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(71) Applicant (for all designated States except US): MOLEC-ULAR DYNAMICS, INC. [/US]; 928 East Arques Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 968 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).

(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, P.O. Box 1327, Piscataway, NJ 08855 (US).

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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S.provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_HEART.txt, created 25 24 January 2001, having 20,186,946 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genomederived single exon nucleic acid probes expressed in human

heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., Proc. Natl. Acad. Sci. USA 70(4):1209-13 (1973); Gilbert et al., Proc. Natl. Acad. Sci. USA 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., Nature 308(5955):153-8 (1984).

More recently, however, the development of high
throughput sequencing methods and devices, in concert with
large public and private undertakings to sequence the human
and other genomes, has altered this investigational
paradigm: today, sequence information often precedes
understanding of the basic biology of the encoded protein
product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast

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amounts of sequence data (see for example Adams et al., Science 252:1651 (1991); Williamson, Drug Discov. Today 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known a priori with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

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With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches - and in particular, with the accumulation of sequence information from multiple genera, from multiple 20 species within genera, and from multiple individuals within a species - there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information. 30

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, Science 280:995 (1998); Pennisi, Science 283: 1822-1823 (1999),

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of 5 a genome's actual expression complexity.

For example, when the C. elegans genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. C. elegans Sequencing Consortium, Science 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of Arabidopsis predicts over 4000 genes, Lin et al., Nature, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the . 15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many 20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence - and most importantly, but not exclusively, regions that function to encode genes - to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting 30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., Proc. Natl. Acad. Sci. USA 88(24):11261-5 (1991); Xu et al., Genet. Eng. 16:241-53 (1994); Uberbacher et al., Methods Enzymol. 266:259-81 (1996); GENEFINDER, Solovyev et al., Nucl. Acids. Res. 22:5156-63 (1994); Solovyev et al.,

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Ismb 5:294-302 (1997); and GENESCAN, Burge et al., J. Mol.
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
however, to give high false positive rates. Burset et al.,
5 Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons. from genomic sequence.
Ansari-Lari et al., Genome Res. 8(1):29-40 (1998)

Identification of functional genes from genomic

10 data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
need to be revised substantially downwards. Nature

15 405:311-199 (2000); Reeves, Nature 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically — and specifically, that permit the expression of regions predicted to encode protein — readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays: A Practical Approach

25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., Genomics 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., Cancer Res. (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast Saccharomyces cerevisiae. Risi et al., Science 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single 10 exon genes, i.e., lack introns, Lopez et al., RNA 5:1135-1137 (1999); Goffeau et al., Science 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex 15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that 20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods 25 and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

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The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the

expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20 least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.

Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

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Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

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In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said 15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single 25 exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The 30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genomederived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes
at high stringency to an expressed human gene. In
particular embodiments, the invention provides single exon
probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,

there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human heart which is a nucleic acid molecule comprising a
nucleotide sequence as set out in any of SEQ ID NOs.: 1
9,980 or a complementary sequence or a fragment thereof

wherein said probe hybridizes at high stringency to a
nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981

35 - 19,771 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

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Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,

10 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in

20 accordance with the second aspect of the invention, with a
first collection of detectably labeled nucleic acids, said
first collection of nucleic acids derived from mRNA of
human heart; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in

sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 9,981 - 19,771, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 9,980.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set

out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

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Detailed Description of the Invention

Definitions

15 As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar 20 or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 25 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural 30 nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, inter alia, in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); 35 in such case, the term "microarray" and phrase "nucleic

acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10⁷, preferably at least 10⁸, more preferably at least 10⁹
liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated

with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

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The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence 15 data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;
FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression

with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3

10 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1 x 10⁻³⁰) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1 x 10⁻³⁰) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

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Methods and Apparatus for Predicting, Confirming,

25 Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present

invention is drawn from one or more databases 100
containing genomic sequence data. Because genomic sequence
is usually obtained from subgenomic fragments, the sequence
data typically will be stored in a series of records

corresponding to these subgenomic sequenced fragments.

Some fragments will have been catenated to form larger
contiguous sequences ("contigs"); others will not. A
finite percentage of sequence data in the database will
typically be erroneous, consisting inter alia of vector

sequence, sequence created from aberrant cloning events,
sequence of artificial polylinkers, and sequence that was
erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence

identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence.

Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the

30 htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than

35 human, such as mouse, rat, Arabidopsis, C. elegans, C.

brigsii, Drosophila, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic

5 sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating

10 message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal

15 stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite

25 function by process 200 are then input into process 300,

where a subset of the input sequences suitable for

experimental confirmation is identified. Experimental

confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is

30 bioinformatic, rather than physical, there are fewer

constraints on the sequences that can be tested, and in

this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

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can be automated.

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FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified inter alia using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be

identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, infra, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added

relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such 20 as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods

thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the
genomic sequence returned by query 20 with public or
private databases containing known repetitive sequence,
vector sequence, artificial sequence, and other artifactual
sequence. Such comparison can readily be done using
programs well known in the art, such as CROSS_MATCH, or by
proprietary sequence comparison programs the engineering of
which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases

25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized

by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also
include formatting of the data as specifically appropriate
for passage to the analytical algorithms of process 25.
Such formatting can and typically will include, inter alia,
addition of a unique sequence identifier, either derived
from the original accession number in genomic sequence
database 100, or newly applied, and can further include
additional annotation. Formatting can include conversion
from one to another sequence listing standard, such as
conversion to or from FASTA or the like, depending upon the
input expected by the subsequent process.

25 Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified 30 within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the

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like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not 10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in 30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when

consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among 10 the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay. 15

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, infra, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% 25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

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Furthermore, consensus can be required among 30 different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset 35 thereof, with another approach, such as comparative

sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

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For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the genespecific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
amplified nucleic acid, considerations such as desired
amplicon length, primer synthesis requirements, putative
exon length, sequence GC content, existence of possible
secondary structure, and the like can be used to identify
and select those ORFs that appear most likely successfully
to amplify. Where subsequent gene expression assay relies

upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

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The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present
invention are particularly useful for identifying potential
coding regions within genomic sequence. In a preferred
embodiment of process 400, therefore, the expression of the
sequences predicted to encode protein is verified. The
combination of the predictive and experimental methods
provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

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Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger

fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

thus input into one or more primer design programs, such as PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can

be added commonly to the ORF-specific 5' primer and a

second, typically different, predetermined sequence

commonly added to each 3' ORF-unique primer. This serves

to immortalize the amplicon, that is, serves to permit

further amplification of any amplicon using a single set of

primers complementary respectively to the common 5' and

common 3' sequence elements. The presence of these

"universal" priming sequences further facilitates later

sequence verification, providing a sequence common to all

amplicons at which to prime sequencing reactions. The

common 5' and 3' sequences further serve to add a cloning

site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can

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conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in

Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning: A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

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After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline

silicon or plastics. Such plastics include
polymethylacrylic, polyethylene, polypropylene,
polyacrylate, polymethylmethacrylate, polyvinylchloride,
polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, or mixtures thereof, can
also be used. Typically, the support will be rectangular,
although other shapes, particularly circular disks and even
spheres, present certain advantages. Particularly
advantageous alternatives to glass slides as support
substrates for array of nucleic acids are optical discs, as
described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying

nucleic acids on support substrates can be constructed
using public domain specifications (The MGuide, version
2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or
can conveniently be purchased from commercial sources
(MicroArray GenII Spotter and MicroArray GenIII Spotter,

Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can
also be effected by printing methods, including those using
ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or

5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and

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upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the

array by a single predicted ORF. Alternatively, genes can
be represented by more than one predicted ORF. For
purposes of measuring differential splicing, more than one
predicted ORF will be provided for a putative gene. And as
is well known in the art, each probe of defined sequence,
representing a single predicted ORF, can be deposited in a
plurality of locations on a single microarray to provide
redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by in situ synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived — either directly or indirectly — from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the de novo construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries — and thus microarrays

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based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as 10 probes on an EST microarray. And as further demonstrated in the examples, infra, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other 15 expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful 20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the 25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, a priori knowledge of the sequence of the 30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays

of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genomederived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

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A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material.

25 Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes

disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

Preferably, at least about 85, 90 or more than 90% of exonincluding probes in the genome-derived single exon microarray of the present invention lack vector sequence.

With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious crosshybridization to a probe vector sequence is reduced.

As a further consequence of excision or

15 amplification of probes from vectors in construction of EST
microarrays, the probes arrayed thereon often contain
artificial sequence, derived from vector polylinker
multiple cloning sites, at both 5' and 3' ends. The probes
disposed upon the genome-derived single exon microarrays

20 need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, 25 independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include 30 artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would 35 contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding 5 region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression 10 measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the 15 probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

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Because of their origin from fully- or partiallyspliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exonspanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., Nature 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the 35 probes in the genome-derived single exon microarrays of the

present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genomederived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in

EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon

microarrays of the present invention.

Conversely, the probes provided on the genomederived single exon microarrays of the present invention
typically, but need not necessarily, include intronic
and/or intergenic sequence that is absent from EST

25 microarrays, which are derived from mature mRNA.
Typically, at least about 50, 60, 70, 80 or 90% of the
exon-including probes on the genome-derived single exon
microarrays of the present invention include sequence drawn
from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly
interfere with measurement of gene expression, and provides
the additional opportunity to assay prespliced RNA, and
thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from in situ

synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on in situ synthesis

5 microarrays are limited to a maximum of about 25 bp. As a
well known consequence, hybridization to such chips must be
performed at low stringency. In order, therefore, to
achieve unambiguous sequence-specific hybridization
results, the in situ synthesis microarray requires

10 substantial redundancy, with concomitant programmed
arraying for each probe of probe analogues with altered
(i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for in situ synthesis microarrays.

A further distinction is that the probes in in

25 situ synthesis microarrays typically are covalently linked
to the substrate surface. In contrast, the probes disposed
on the genome-derived microarray of the present invention
typically are, but need not necessarily be, bound
noncovalently to the substrate.

30 Furthermore, the short probe size on in situ microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over in situ synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the in situ synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in Saccharomyces cerevisiae - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al.,

Nucl. Acids Res. 28:85-86 (2000); Spingola et al., RNA 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as Saccharomyces cerevisiae, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present

invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, infra.

Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of

a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, infra, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a 10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the

genome-derived single exon microarray will identify certain
of the probes thereon as of particular interest. Thus, it
is often desirable that the user be able readily to obtain
sufficient quantities of an individual probe, either for
subsequent arrayed deposition upon an additional support
substrate, often as part of a microarray having a plurality
of probes so identified, or alternatively or additionally
as a solitary solid-phase or solution-phase probe, for
further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of
nucleic acids identical in sequence to, or substantially
identical in sequence to, probes on the genome-derived
single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is 30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates 35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genomederived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered

probe set, or with both.

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If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query including information on identical sequences and information on nonidentical sequences that have diffuse or

focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present

invention rapidly produce functional information from
genomic sequence. Coupled with the escalating pace at
which sequence now accumulates, the rapid pace of sequence
annotation produces a need for methods of displaying the
information in meaningful ways.

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FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual

display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the 5 first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a 10 convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned 25 into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor 30 such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and 35

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last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present
the output from process 200, that is, to present the
bioinformatic prediction of those sequences having the
desired function within the genomic sequence. Functional
sequences are typically indicated by at least one rectangle
83 (83a, 83b, 83c), the left and right borders of which
respectively indicate, by their X-axis coordinates, the
starting and ending nucleotides of the region predicted to
have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired

15 function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

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a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and userselectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG.

3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the 25 probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As 30 noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example,

where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions

15 that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify

20 sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through 25 color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

servers.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for 30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed infra, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using

normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, 10 showing conventions used in the Examples presented infra. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene 15 predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 20 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

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The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of

portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

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As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a

25 significant cause of human morbidity and mortality.

Increasingly, genetic factors are being found that

contribute to predisposition, onset, and/or aggressiveness

of most, if not all, of these diseases. Although mutations

in single genes have on occasion been identified as

30 causative, these disorders are for the most part believed

to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in the United States and other developed countries. In

developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD 5 each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

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CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a 15 severe stenosis or result in arterial occlusion. plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

20 Risk factors for CVD include age and gender. addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the 30 development of CVD. Both insulin-dependent and noninsulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the

The literature is replete with evidence for

development of atherosclerosis.

genetic causes of cardiovascular diseases. For example, studies by Allayee et al., Am. J. Hum. Genet. 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., Am. J. Hum. Genet. 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

major gene plus individual polygenic components.

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The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., Proc. Nat. Acad. Sci. 89: 708-712 (1992) and Rotter et al., Am. J. Hum. Genet. 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., supra, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., Mutat 4: 178-

194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL), that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm

20 Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular 25 risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of hyperlipidemia, intimal thickening occurs. Non-

atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic 35. kidney disease, medullary thyroid cancer, pheochromocytoma,

and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable 5 antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both ' genetic and environmental components. The recent search for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor 15 receptor-2, and "-adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell sodium in 1,800 normotensive members of 16 Utah pedigrees 20 ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major locus increases susceptibility to hypertension.

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From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene, with gender and age dependence. They also suggested that a

single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on 5 other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367 10 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

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As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone, encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or 30 conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular block, familial sinus node disease, progressive cardiac

conduction defect, and familial cardiomyopathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of

Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations in the gene encoding tafazzin (TAZ), or in the FK506binding protein 1A gene (FKBP1A).

linkage of the disorder to DNA markers on band 7q3.

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with agerelated penetrance. The linkage of familial dilated cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

In addition, cardiomyopathy can also be caused by

mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the 20 His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000 25 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott 30 et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United States. Twenty percent of infants with congenital heart

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disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by

several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects

15 have been identified. For example, Greenberg et al., Am.

J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al.,

20 Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several

25 genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who underwent fluorescence in situ hybridization (FISH) testing

with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974)

5 described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, 10 typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, 15 heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, 20 Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, 25 humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

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expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with 20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single 25 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel 30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at

sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

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As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," Proc. Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology, " Arch. Biochem. Biophys. 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (sée, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," Curr. Biol. 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," Proc. Natl.

30 Acad. Sci. USA 96(12):6745-50 (1999); Perou et al.,
"Distinctive Gene Expression Patterns in Human Mammary
Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci.
USA 96(16):9212-7 (1999); Wang et al., "Identification of
Genes Differentially Over-expressed in Lung Squamous Cell

35 Carcinoma Using Combination of cDNA Subtraction and

Microarray Analysis," Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol. 46(3):425-8 (1999)), in drug discovery screens (see, for 5 example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer, " Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression, " Cancer Res. 59(22):5656-61 (1999)). 10

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

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For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead 25 compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile 30 and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements 35 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., Trends Biochem. Sci. 24(5):168-173 (1999) and Zweiger, Trends Biotechnol. 17(11):429-436 (1999); Schena et al.

The invention particularly provides genomederived single-exon probes known to be expressed in heart.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression.

Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, inter alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the

range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form

5 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific

5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present

invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a hybridization reaction in which the probe is not first

bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message — a subset of target sequence that is much reduced in complexity as compared to genomic sequence — even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 - 19,771, respectively, for probe SEQ ID NOS. 1 - 9,980. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 - 19,771 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human cot1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization

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at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally—and functionally—related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly

25 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and

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below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution

10 hybridization, the probes of the present invention can

11 usefully have detectable labels. Nucleic acid labels are

12 well known in the art, and include, inter alia, radioactive

13 labels, such as ³H, ³²P, ³³P, ³⁵S, ¹²⁵I, ¹³¹I; fluorescent

14 labels, such as Cy3, Cy5, Cy5, Cy7, SYBR®

Green and other labels described in Haugland,

Handbook of Fluorescent Probes and Research Chemicals, 7th
ed., Molecular Probes Inc., Eugene, OR (2000), or
fluorescence resonance energy transfer tandem conjugates
thereof; labels suitable for chemiluminescent and/or
enhanced chemiluminescent detection; labels suitable for
ESR and NMR detection; and labels that include one member
of a specific binding pair, such as biotin, digoxigenin, or
the like.

The probes, either in quantity sufficient for 25 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific
5' primers used for genomic amplification had a first
common sequence added thereto, and the ORF-specific 3'
primers used for genomic amplification had a second,
different, common sequence added thereto, a single set of
5' and 3' primers can be used to amplify all of the probes
from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid

amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, inter alia, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, supra.

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The invention particularly provides genomederived single-exon nucleic acid microarrays comprising a 30 plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray

At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo

Alto, CA; Protein Fusion & Purification (pMAL™) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7), Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence

15 translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted 30 in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR ·

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The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the aminomodified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 15 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit 20 subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant 25 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR

15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent 5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 E. coli genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)

25 produced an exact match (BLAST Expect ("E") values less
than 1 e⁻¹⁰⁰) to either an EST (20% of sequences) or a known
mRNA (13% of sequences). A further 22% of the probe
sequences showed some homology to a known EST or mRNA
(BLAST E values from 1 e⁻⁵ to 1 e⁻⁹⁹). The remaining 45% of

30 the probe sequences showed no significant sequence homology
to any expressed, or potentially expressed, sequences
present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

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Function	n of Predic	cted ORFs As	Deduced From Comparative
1	e Analysis		-
		`	
Total	V6 chip	V7 chip	Function Predicted from
			Comparative Sequence
			Analysis
211	96	115 ,	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

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The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)

5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were 15 incorporated during separate reverse transcriptions of $\cdot 1~\mu g$ of polyA $^+$ mRNA performed using 1 μg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1% Superscript II buffer, 0.01 M DTT, 100 μM dATP, 100 μM dGTP, 100 μM dTTP, 50 μM dCTP, 50 μM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μl hybridization solution containing 50% formamide, 5X SSC, 0.2 μg/μl poly(dA), 0.2 μg/μl human cot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
Gen3 scanner, as described. Schena (ed.), Microarray

Biochip: Tools and Technology, Eaton Publishing
Company/BioTechniques Books Division (2000) (ISBN:
1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it

15 attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter,

20 "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the 20 intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more

"novel" genes among those that were up-regulated in only
one tissue, as compared with those that were down-regulated
in only one tissue. In fact, it was found that ORFs whose
expression was measurable in only a single of the tested
tissues were represented in sequencing databases at a rate
of only 11%, whereas 36% of the ORFs whose expression was
measurable in 9 of the tissues were present in public
databases. As for those ORFs expressed in all ten tissues,
fully 45% were present in existing expressed sequence
databases. These results are not unexpected, since genes
expressed in a greater number of tissues have a higher
likelihood of being, and thus of having been, discovered by
EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonlyexpressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large

5 number of even the high expressers were "unknown". Since
the genomic approach used to identify genes and to confirm
their expression does not bias exons toward either the 3'
or 5' end of a gene, many of these high expression genes
will not have been detected in an end-sequenced cDNA

10 library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

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To ascertain the validity of the approach described above to identify genes from raw genomic

20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and

indeed should not, be confirmed by independent assay
methods, or the high throughput, highly parallel advantages
of microarray hybridization assays will be lost. However,
in addition to the two RT-PCR results presented above, the
observation that 1/3 of the arrayed genes exist in

expression databases provides powerful confirmation of the
power of our methodology — which combines bioinformatic
prediction with expression confirmation using genome—
derived single exon microarrays — to identify novel genes
from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed
20 high (normalized) signal in brain, but which showed very
low (normalized) signal (less than 0.5, determined to be
biological noise) in all other tissues, were further
studied. There were 82 sequences that fit these criteria,
approximately 2% of the arrayed elements. The 10 sequences
25 showing the highest signal in brain in microarray
hybridizations are detailed in Table 2, along with assigned
function, if known or reasonably predicted.

Table 2

Function of the Most Highly
Expressed Genes Expressed Only in Brain

• -	1/57274				PCT/US01/00666
	Microarray	Normal	Expressi	Homology	Gene Function
		ized	on Ratio		as described by
	l a =				

	Microarray	Normal	Expressi	Homology	Gene Function
	Sequence	ized	on Ratio	to EST	as described by
	Name	Signal			GenBank
				in	
				GenBank	
	AP000217-1	5.2	+7.7	High	S-100 protein,
					b-chain, Ca ²⁺
					binding protein
	•				expressed in
					central nervous
					system
İ	AP000047-1	2.3		High	Unknown
					Function
1	AC006548-9	1.7	 	High	Similar to
					mouse membrane
1					glyco-protein
					M6, expressed
		}			in central
					nervous system
ľ	AC007245-5	1.5		High	Similar to
				-	amphiphysin, a
					synaptic
					vesicle-
	,				associated
					protein. Ref 21
	L44140-4	1.2	+2.0	High	Endothelial
					actin-binding
					protein found
					in nonmuscle
					filamin
•	ı	ı	1	1	ļ

AC004689-9	1.2	+3.5	174	T Donat a 3
AC004669-9	1.2	+3.5	High	Protein
1				Phosphatase
				PP2A, neuronal/
				downregulates
				activated
				protein kinases
AL031657-1	1.2	+3.0	High	Unknown
				function/
				Contains the
,				anhyrin motif,
	•			a common
				protein
				sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to
				the
				Synaptotagmin I
			:	protein in
		: :	ļ.	rat/present at
]		•		low levels
				throughout rat
				brain
AP000086-1	1.0	+2.7	Low	Unknown, very
				poor homology
				to collagen
AC004689-3	1.0		High	Protein
				Phosphatase
				PP2A, neuronal/
				downregulates
		ĺ		activated
				protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be

5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca²⁺ binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, Neurochem. Res. 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3

10 were both found to be phosphatases present in neurons (Millward et al., Trends Biochem. Sci. 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., J. Neurol. Sci. 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1□ (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., Genomics 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparis	son of Expression R	atio, for each
tissue, of GAPDH		
•		
	AC006064 (n = 4)	Control $(n = 5)$
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again

5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

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For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons 20 selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

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EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

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The protocols set forth in Examples 1 and 2, supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be 5 useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to 10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as 20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

15

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO .: " and additionally by the SEQ ID NO:. of the exon contained within the probe: "EXON SEQ ID NO.: ") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of 30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is. found ("Top Hit Database Source").

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Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS .: . The 5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each 10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for 20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

ORFs must be in the same frame.

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Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as 25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1 \times 10^{-5}) and le-100 (i.e., 1 x 10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, supra, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for 35 analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,980) and probe exon (SEQ ID NOs.: 9,981 - 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- (a) the accession number of the BAC from which
 the sequence was derived ("MAP TO"), thus providing a link
 to the chromosomal map location and other information about
 the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST 25 E value for the "hit";
 - (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Heart

<u>Table 4</u> (413 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human heart.

Page 1 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Exoli Flobes Expressed in Realt	Top Hit Descriptor																																		
JIG EVOII FIOR	Top Hit Database Source																																		
	Top Hit Acession No.																																		
	Most Similar (Top) Hit BLAST E Value		, .																																
	Expression Signal	4.41	17.08	2.14	76.7	1.87	4.97	1.01	0.95	7.45	0.98	3.03	2.62	2.34	3.7	1.52	8.97	. 0.87	0.89	1.71	. 5.94	0.89	0.89	1.03	1.76	0.78	5.08	207	1.92	1.92	9	5.89	4.9	2.9	1.6
	ORF SEQ ID NO:	20209	20647				21381	21467				21713	21907	22020	22875	23121	23192		23309	23781	23838	23858	23859		24402		24617	24629	24834	24835				25490	25678
	Exon SEQ ID NO:	10386	10797	10947							11744			12118	13074	13320	13387		13521	14002		14084					14851	14863	15140	15140	15248	15356	15248	15427	19451
	Probe SEQ ID NO:	442	871	1029	1280	1597	1619	1694	1715	1721	1848	1935	2119	2233	3149	3403	3471	3513	3607	4102	4164	4184	4184	4242	4730	4779	4976	4988	5217	5217	5328	5436	5483	5509	5668

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Table 4
Single Exon Probes Expressed in He

																						1 (Naip1) and general transcription	1 (Naip1) and general transcription	polyprotein mRNA partial cde		puyprotein mikiva, partei cds	OPROTEIN PP89)	chondrial gene for mitochondrial	chondrial gene for mitochondrial	23'
Single Exon Probes Expressed in Heart	Top Hit Descriptor	•																		Homo saplens LSS gene, partial, exons 15, 16, 17 and 18	Haemophilus influenzae Rd section 31 of 163 of the complete genome	Mus musculus Naip3 gene, excn 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gt/2h2) genes, complete cds	Mus musculus Naip3 gene, exon 1: neuronal apoptosis Inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds.	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA nartial cds	Dengue virus troe 3 membrene protein (mtW/M/venvelone alternation (2) and	Mus musculus AT3 gene for antithrombin, complete cds	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP80)	Leuaiscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3
lle Exon Probe	Top Hit Database	Source																		± E	E	N TN	N T	NT ID	<u>a</u>		ISSPROT	Ä G		EST HUMAN 8
Silis	Top Hit Acession No.																			9.9E+00 AJ239028.1	_	9.6E+00 AF242432.1	9.6E+00 AF242432.1				9.3E+00 P11210	9.1	9.1E+00 AF095609.1	
	Most Similar (Top) Hit BLAST E	Value																		9.9E+00	9.8E+00 U32716.	9.6E+00	9.6E+00	9.4E+00 L11433.1	9.4E+00 L11433.1	9.4E+00	9.3E+00 F	9.1E+00 AF09560	9.1E+00 A	8.9E+00 BE97180
	Expression Signal		1.41	1.84	1.61	1.61	1.29	1.3	3.58	1.26	3.7	231	284	2.91	1.73	1.73	2.19	1.62	2.11	13.31	1.54	1.32	1.32	2.72	2.72	5.91	2.97	2.07	2.07	5.51
	ORF SEQ ID NO:		25700				26769	27012	27569	27758	•	28355		28840	28150	28151			25230	25701	26745	28046	28047	22389	22390	22612	27271	24932	24933	25687
	Exon SEQ ID	Š	15599	15769	16244	16244	16577	16820	17364	17534	17961	19472	18266	18555	17906	17906	18606	19094	19280	15500	16549	17805	17805	12499	12499	12820	17083	15163	15163	15587
	Probe SEQ ID	Ö	2690	5863	6382	6382	6697	6942	7494	7684	8070	8219	8330	8666	8757	8757	8792	9464	9760	5691	6999	7955	7955	2631	2631	2893	7206	5239	. 5239	5678

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	Cynops pyrrhogaster CoTbx3 premature mRNA partial crts	Onops pyrhodaster Co Tbx3 premeture mRNA practical ords	Homo saplens insulin receptor substrate 1 (IRS1) mRNA	Zea mays mRNA for legumain-like protease (see2a)	BREFELDIN A RESISTANCE PROTEIN	Thermoplasma acidophilum complete genome: segment 3/5	THROMBOSPONDIN 1 PRECURSOR	THROMBOSPONDIN 1 PRECURSOR	602128876F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE-428556R 5	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	Lycopersicon esculentum Mill, GTPase (SAR2) mRNA, complete cds	Lycopetsicon esculentum Mill, GTPase (SAR2) mRNA, complete calc	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMFODOWAIN PROTEIN 1)	ZING-FINGER PROTEIN 1 (ZING-FINGER HOMEODOMAIN PROTEIN 1)	Arabidopsis thaliana DNA chromosome 4, contro fragment No. 91	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPR INTERGENIC BEGION	ARGININE KINASE (AK)	WD-40 REPEAT PROTEIN MSI3	60S RIBOSOMAL PROTEIN L4 (L2)	DNA MISMATCH REPAIR PROTEIN MUTS	za07c11.r1 Soares melanocyte ZNbHM Homo saplens cDNA clone IMAGE: 291860 5'	za07c11.r1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291880 5	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:	HVPOTHETICAL 1570 KDA BEOTEIN CROSSEN CHEROLOGISCOLES III	IDVI ATE KINASE (19) (HODINIE MONOBLOSEITATE IN CHROMOSOME III	URIDY ATE KINASE (UK) (URIDINE MONOPHOSPHALE KINASE) (UMP KINASE)	PROBABIE CATION, TRANSPORTING ATDASE CONTRACE) (UMP KINASE)	FINV POLYDROTTEIN ICONTAINS COAT BEATERN CHEST COAT BEATERN COAT BEATERN CHEST	Schizophyllum commune unknown mRNA	Mus musculus mixed lineage kinase 3 (MIK3) and two pore domain K+ channel subunit (Konk6) genes.	complete cde
igie Exon Pro	Top Hit Database Source	N .	¥	4 NT	¥	SWISSPROT	Z Z	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	닏	<u>F</u>	SWISSPROT	SWISSPROT	Į.	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	TOGOSSIMS	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	Z	Ŀ	
10 h	Top Hit Acession No.	8.7E+00 AB019788.1	8.7E+00 AB019788.1	5031804 NT	8.1E+00 AJ131719.1		7.5E+00 AL445065.1	P35441	P35441	BF700517.1	7.4E+00 P04929	P04929	7.2E+00 L12051.1	7.2E+00 L12051.1	P28166	P28166	7.1E+00 AL161595.2	P05850	P48610	022469	P35679	P44834	6.8E+00 W03412.1	8.8E+00 W03412.1	P36307	003570	09ZE07	097F07	010309	P03374	6.2E+00 AY010901.1	4	7815514
	Most Similar (Top) Hit BLAST E Value	8.7E+00	8.7E+00	8.4E+00	.8.1E+00	8.0E+00 P41820	7.5E+00	7.5E+00 P35441	7.5E+00 P35441	7.4E+00	7.4E+00	7.4E+00 P04929	7.2E+00	7.2E+00	7.1E+00 P28166	7.1E+00 P28166	7.1E+00	7.1E+00 P05850	7.0E+00 P48610	7.0E+00 022469	6.9E+00 P35679	6.9E+00 P44834	6.8E+00	8.8E+00	8 8F+00 P36307	6.8E+00 CO3570	6.6E+00 09ZE07	6.6E+00.097E07	6.6E+00/010309	8.5E+00 P03374	6.2E+00	00.10	
	Expression Signal	1.71	1.71	1.75	3.68	2.31	2.07	1.53	1.53	2.58	3.83	3.83	4.2	4.2	1.3	1.3	8.48	3.26	2.98	1.85	2.72	1.3	1.45	1.45	1.47	3.82	21	21	217	8.32	1.44	7 18	?
	ORF SEQ ID NO:	25871	25872	20199	26642			26940	26941	25531	27155	27156	22671	22672	26254	26255		28860	27809	28712	26889	28015	26680	26681		27957	27881	27882		27372	27686	25956	2
	Exen SEQ ID NO:	15754	15754	10378	16452	18381	16209	16747	16747	15460	16962	16962	12874	12874	16105	16105	17386	18577	17585	18443	16697	17775	16494	16494	17154	177713	17846	17846	18344	17172	17467	15833	
	Probe SEQ ID NO:	5848	5848	433	7439	8509	6346	8989	6868	5544	7085	7085	2947	2947	6239	6239	7535	8690	7735	8575	83	7925	6614	6614	7277	7863	7796	7796	8471	7296	7616	5928	-

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Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | LYCOPENE BETA CYCLASE | PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)

 | Arabidopsis thallana DNA chromosome 4, contig fragment No. 97

 | VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2; | RHODOPSIN | RHODOPSIN | Bovine immunodeficiency-like virus surface envelone gene 5 and of cds | DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC STIBLINITY | PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR | COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN) | Canis familiaris skeletal muscle chloride channel CIC-1 (Ci CN1) mRNA complete ede
 | Mycobacterium tuberculosis H37Rv complete genome: seament 103/162 | Eunice australis histone H3 (H3) gene, partial cds | PM0-BT0547-310100-002-b04 BT0547 Homo sepiens cDNA | 601875654F1 NIH MGC 55 Homo saplens cDNA clone IMAGE 4099716 だ | 601875654F1 NIH MGC 55 Homo saniens cDNA clone IMAGE 4000748 E | Homo saplens chromosome 21 segment HS21Cngn | Methanococcus lannaschil section 111 of 150 of the complete genome | Archaeoglobus fulgidus section 63 of 172 of the complete genome | 602072585F1 NCI CGAP Bm67 Homo sabiens cDNA clone IMAGE 4215284 F
 | 602072585F1 NCI CGAP Bm67 Home saniens citiva clone IMAGE-4245284 8 | Murine I gene for MHC class II(Ia) associated invariant chain | Plasmodium falciparum R29R+var1 gene, exon 1 | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathlone S-transferase theta 1 (GSTT1) genes. complete cris. | MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) | (NOTE)
 | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) | Wio/gus.X1 Soares, Nrt. I GBC S1 Homo sapiens cDNA clone IMAGE:2360692 3' | GENE 68 PROTEIN | GENE 68 PROTEIN
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| Top Hit
Database
Source | SWISSPROT | SWISSPROT

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 | 5.4E+00 | 5.4E+00 | 5.4E+00 | 5.3E+00 | 5.3E+00 | 5.3E+00 | 5.1E+00 | 5.0E+00
 | 5.0E+00 | 4.8E+00 | 4.8E+00 | 4.7E+00 | 4.7E+00 | 4.7E+00 | 4.6E+00 | 4.5E+00 | 4.4E+00
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 | 157 | A 4R | 7.65 | 3.31 | 3.31
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 | 28749 | | | 20071 | 20071 | 22958 | 26617 | 28986 | 22723
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 | 26187 | 27240 | 26553 | 26618 | 26619
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 | 18477 | 13879 | 16847 | 10251 | 10251 | 13160 | 16434 | 18693 | 12931
 | 12931 | 15671 | 16259 | 18116 | 15306 | 16043
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| Probe
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NO: | 8770 | 8769

 | 8967

 | 6593 | 7769 | 7769 | 4675 | 6710 | 8839 | 7655 | 7959
 | 8610 | 3972 | 6970 | 286 | 287 | 3236 | 6576 | 8881 | 3003
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Table 4
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6617	16497	26684	2.95		4.1E+00 U57503.1	LN.	Par troopolytes mans remarking and TE
7576	17427	27641	231	<u> </u>	4.1E+00 BF6924251	FST HIMAN	FIGURE 1 NIE MCC 52 U.S. CONTROL OF THE CONTROL OF
8259	18139		2.89	4.1E+00	4.1E+00 P09716	SWISSPROT	HYPOTHETICAL PROTEIN DW E4
8339	18216		12.46	4.1E+00	4.1E+00 BE885880.1	EST HUMAN	601507510F1 NIH MGC 71 Home saniens cDNA clane MA CE 20000E2 E1
9672	19231	25241	1.86	4 1 1 1 1 0 0	4 15+00 047978	1000001110	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGF8P-1) (IBP-1) (IGF-
9929	1	26285	1.37	4.0E+00	4.0F+00 O33010	SWISSBOT	BINDING PROTEIN 1)
8768	1 1	28164	217	4.0E+00 P14546	P14546	SWISSPROT	CCT OCHROME COXIDASE BOLVBERTINE !!!
					-		GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GI YCOPROTEIN MY MA IOP ENVELOPE PROTEIN); MATRIX PROTEIN
8835	18648	28934	3.34	4.0E+00 P07564	P07564	SWISSPROT	NS1, NS24, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5);
8835	18648	28935	3.34	4 0F+00 P07564	P07564	TOGGOSIMIS	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS
3459	13375	23181	3.89	3.9E+00	1	LN LN	Nahadim chilingog and 60 for death 11.
4226	14124		0.99	3.9E+00	150	L	Mis miscallis cominal vacials constant to the
6471	15391	25454	2.47	3.9E+00	T	EST HUMAN	MR0-BN0070-300500-028-bns BN0070 June 1991 (MSVSP99) gene, promoter region
5471	15391	25455	247	3.9E+00	3.9E+00 BE814357.1	EST HUMAN	MRO-BN0070-300500-028-h05 BN0070 Home Scripes CUNA
6108	16002	26140	4.46	3.9E+00 P39299		SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL BEGIN ATOB IN AND ENGLINEER SERVICES.
6355	16218	26379	4.68	3.9E+00		Z	Human MHC class Numbhocyte antigen (DPw4 he/e.1) cond.
8840	16719	26913	232	3.9E+00 X65865.1		N.	Xlaevis mRNA for M4 muscarinic recentor
888	17879	28120	3.09	3.9E+00	3.9E+00 Y18000.1	TN.	Homo saplens NF2 gene
8715	18532	28816	5.58	3.9E+00	3.9E+00 AA661489.1	EST HUMAN	nr18a12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2588	12459		2.4	3.8E+00	2.1	Z	Helicobacter owlori strain 199 seedlen 172 at 120 state.
691	16789	26982	1.18	3.8E+00 D44725.1		EST HUMAN	HUMSUPY135 Himan brain cos securir 123 of 132 of the complete genome
3936	13845	23622	10.09	3.7E+00	27		Arabidoosis theliana DNA chromosome 4 contra frames N. 20
8730	18586	28872	2.13	3.7E+00	3.7E+00 BF669279.1	EST HUMAN	602120551F1 NIH MGC 58 Home captain COM 4
8730	18586	28873	2.13	3.7E+00		EST HUMAN	602120551F1 NIH MGC 56 Home series conv. Alone 114 OF 1277748 5
678	10516	20322	2.1	3.6E+00	-	EST HUMAN	AV761055 MDS Homo sertiens CDNA Alma Morell Earles
1022	16899	27090	3.66	3.6E+00	+	LN.	Pseudomonas aeruginosa PA01 section 8 of 529 of the complete access
7022	16899	27091	3.66	3.6E+00		NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

Page 6 of 413 Table 4 Single Exon Probes Expressed in Heart

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חושים בעמון ומופס בעלופספת וון נופשון	Top Hit Descriptor	Escherichia coli glycerophosphate dehydrogenase (gipD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds.	Confessoridium felis heaf shock profein 70 (NSD20) and the first of th	Bressica nature RP86d mRNA complete cite	Homo sapiens chromosome 21 segment HS21C078	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT	Saccharomyces oerevisiae MSS1 gene, complete cyle	Homo saplens DiGeorge syndrome critical region, centraments and	Homo sapiens KIAA0480 gene product (KIAA048n) mRNA	Homo saplens KIAA0480 gene product (KIAA0480) mRNA	D.reito zp50 POU gene	D.rerio zp-50 POU gene	PHOSPHOGLYCERATE KINASE CYTOSOI IC	PHOSPHOGLYCERATE KINASE, CYTOSOLIC	NADH-UBIQUINONE OXIDOREDICTASE CHAIN A	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	Chlamydomonas reinhardii chloronlast DNA for moo verta, verta, verta, moda	Chlamydomonas reinhardtii chloroplast DNA for rnsg wefa wefa weda and	PERIPLASMIC INIFEL HYDROGENASE SMALL SUBLINIT MICE LYDBOCEN VASE STALL STALL	Scerevisiae friconine deaminase (II V1) nene complete cas	Oryglas latibes OIGC6 gene for guandyl cyclase C. complete cds	Sus scrofa choline acetyliransierase dene promoter region	HYPOTHETICAL 1425 KD PROTEIN C23E2 02 IN CHROMOSOME I	TYPE I IODOTHYRONINE DEIODINASE (TYPE-1 STREIODINA SECTION (TYPE-1 FINE PROPERTY OF THE PROPER	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I SIDEIODINASE) (DIOI) (TYPE 1 DI) (SDI)	GLUTAMATE (NWDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 20) (NR20) (NR30) (NR30)	DEOXYHYPUSINE SYNTHASE (DHS)	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN B, MAJOR ENVELOPE PROTEIN E, NONSTRUCTURAL PROTEINS NS1, NS28, NS48, AND NS48, HEI ICASE (NS3); BNA, DIBECTED BNA, DISC.	retinoic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
ביים ביים	Top Hit Database Source	<u>5</u>	Į.	Z	F	SWISSPROT	F	E	<u>F</u>	Z.	LN L	LN LN	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	IN.	Ę	SWISSPROT	뉟	ΙN	Z.	SWISSPROT.	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	Þ
5	Top Hit Acession No.	M96795.1	3.5E+00 AF221538.1	3.4E+00 AF254577.1		P04052	3.4E+00 AF013167.1	3.4E+00 L77570.1	7662155 NT	7662155 NT	3.2E+00 X96422.1	X96422.1	P12783	P12783	P18931	P18931	Y13655.1	Y13655.1		3.2E+00 M36383.1	3.2E+00 AB016081.2	L33836.1	Q10135	P49894	P49894	214957	P49365	233515	
	Most Similar (Top) Hit BLAST E Value	3.6E+00 M96795.	3.5E+00	3.4E+00	3.4E+00	3.4E+00 P04052	3.4E+00	3.4E+00	3.3E+00	3.3E+00	3.2E+00	· 3.2E+00 X96422.1	3.2E+00 P12783	3.2E+00 P12783	3.2E+00 P18931	3.2E+00 P18931	3.2E+00 Y13655.1	3.2E+00 Y13655.1	3.2E+00 P13061	3.2E+00	3.2E+00	3.2E+00 L33836.1	3.1E+00 Q10135	3.1E+00 P49894	3.1E+00 P49894	3.1E+00 Q14957	3.1E+00 P49365	3.1E+00 P33515	3.1E+00 S56660.1
	Expression Signal	3.76	1.0	3.57	1.02	2.41	3.17	1.92	1.41	1.41	1.39	0.79	2.68	2.66	2.08	2.06	2.35	2.35	6.33	1.17	1.69	4.32	2.42	4.35	4.35	3.8	4.78	3.78	3.35
	ORF SEQ ID NO:	-	22934	21260	22298				24679				25415			25826	26609	26610		27567	27932		25574	27067	27068		28009		
	Exen SEQ ID NO:	18110	13133	11400			17739	_				┙			15713	15713	16427	16427	17098	17361	17687	18863	15497	16877	16877	17238	17770	17908	18591
	Probe SEQ ID NO:	8228	3209	1496	2532	6354	7889	8818	5036	5036	492	3938	5439	5439	5808	5808	6269	6269	7221	7491	.7837	8080	5582	7000	8	7334	7920	8759	8774

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					ilio	gle Exon Pro	Single Exon Probes Expressed in Heart
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2807	12737	22635	1.06	3.0E+00	8923984 NT	F	Homo saplens hypothetical protein PRO0889 (PRO0889), mRNA
5273		24970	1.63	3.0E+00	3.0E+00 X53096.1	Ę	Saureus genes encoding Sau96i DNA methyltransferase and Sau66i restriction endomiclasse
6245	16111		9.5	3.0E+00 P18406		SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7164	17041		1.45			N _T	Briapus DNA for myrosinase
8374	18251	28501	6.51	3.0E+00 P51842		SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8374	18251	28502	e.	3 05 100		TOGGOIMO	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE
1964	11858	21747	2.56	2 9F+00	25.2	TN ISSUED	Chlamidanhia maimaina AB30 and En Son Eu
6129	15976	26112	1.63	2.9E+00		Ę	Financial despite production and a security of the complete genome
6282	16146	26300	4.47	2.9E+00 014514		SWISSPROT	BRAIN SPECIFIC ANGIOGENESIS INHIBITOR 4 DREGIDEDS
6282	16146	26301	4.47	2.9E+00 014514		SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECLIRSOR
6410	16271	26433	5.19	2.9E+00 P46589		SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SI IREADE ANTIGENIA
1441	11346	21212	5.79	2.8E+00		NT	Buxus harlandii maturase K (malk) gene, partial cds; chloroplast gene for chloroplast product
1615	11519		3.12	2.8E+00	AL1615	N-	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6325	16188	. 26350	4.78	2.8E+00		ᅜ	Mus musculus endomucin (LOC53423), mRNA
230	10199	20012	4.63	2.7E+00		N	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
88	10199	20013	4.63	2.7E+00	9026799	닏	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
2408	15327	25377	1.75	2.7E+00		NT	Homo sepiens apoA polymorphism Kringle IV gene, exons 1 and 2
7185	17062		2.21	2.7E+00	1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7996	17846		2.16	2.7E+00	.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo saplens cDNA
4576	14467	24253	4.35	2.6E+00	2.6E+00 AF068749.1	¥	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5405	15324	25373	1.97	2.6E+00	6755601		Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6405	15324	26374	1.97	2.6E+00	6755601 NT		Mus musculus SRV-box containing gene 13 (Sox13), mRNA
6533	16391		5.45	2.6E+00	-	¥	Mus musculus SH2-containing inositol 5-phosphatase (Shin) gens, evene 16 through 27, and event.
9699	16576	26767	1.2	2.6E+00	2.6E+00 AJ132180.1	¥	faba bean necrotic yellows virus C2-Eq gene, Isolate Ervotian EV1-93
9699	16576	26768	1.2	2.6E+00	1	Ę	faba bean necrotic vellows virus C2-Eq gene isolaria Frantian EV1.03
7567	17418	27634	2.95	2.6E+00	2.6E+00 AL161540.2		Arabidopsis thallana DNA chromosome 4, continuit no. 40
7927	11111		1.52	2.6E+00	9055193 NT		Mus musculus cleavage and polyadenylation specificity factor 3 (Cnst3) mRNA
9711	19649		2.31	2.6E+00	2.6E+00 11419220 NT		Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ARCRA), menta
1448	11353	21216	2.08	2.5E+00		M	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Table 4
Single Exon Probes Expressed in Heart

		1	Т	T	T	Т	T	Т	7	T	T	T	Т	T	Т	T	Т	T	T	T	7	Т	Т	Т	Т	Т	٦	T	Ŧ	7	7	7	\neg
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Aspergillus nidulans recO gene for DNA helicese avvnc 1 4	TEICHOIC ACID BIOSYNTHESIS PROTEIN F	QV4-FT0005-110500-205-007 FT0005 Home saniens CDNA	Rice DNA for aldolase C-1, complete cds	Mus musculus EIF4H gene paritial cds. I IMK4 gene complete cds: and ETN	Chicken alpha-3 collagen type VI mRNA, 3' end	Homo saplens double C2-like domains, alpha (DOC2A) mRNA	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 4)	CD27L RECEPTOR PRECINSOR / LOST ACTIVATION ANTICEN CRASS / F2.23	CD27L RECEPTOR PRECURSOR (T.CEL) ACTIVATION ANTICEN CD27 (174)	Helicobacter pviori, strain J99 section 47 of 132 of the commission of the commissio	IRC2-PT0004-031299-011-d05 PT0004 Homo seniens cONA	ENDOCHITINASE B PRECURSOR (CHN.B)	SKIN GRANULE PROTEIN PRECURSOR	SKIN GRANULE PROTEIN PRECURSOR	Hisapiens CTGF gene and promoter region	XYLULOSE KINASE (XYLULOKINASE)	hre3f08.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMA GE-3133187 9	hrestoext NCI CGAP Kid11 Homo sepiens oDNA done IMAGE:3133487 %	Bacillus subtilis chromosomal DNA, region 75 degrees; glpPFKD operon and downstream	Frantaria y ananassa sidoshito constant	Generations artificial single chain antibody complete cds	Ros fairms nortial with canafar after the contract to	Rettus norvedicus ATPasa Ca++ transmettine ublimitimus (At-2-2) DAVA	MAJOR CENTROMERE AUTOANTIGEN R (CENTROMERE BEOTTEIN BY CENTROMERE)	M.mazei dhaK and dhaJ genes homologues coding for DnaK and Dna I	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)	602069121F1 NIH MGC 58 Home contains cONA class (MA CE 1000475 2)	602069121F1 NIH_MGC_58 Homo saplens cDNA clone IMAGE:4068173 5			
gle Exon Pro	Top Hit Database Source	Į	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST HUMAN	NT	TN	NT LN	N I	SWISSPROT	SWISSPROT	SWISSPROT	N	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	TN	SWISSPROT	EST HUMAN	EST HUMAN	TN	5	LN	FZ	L	SWISSPROT	TN	SWISSPROT	EST HUMAN	EST_HUMAN
ZIIS	Top Hit Acession No.	2.5E+00 AJ271844.1	1	P13485	P13485	P13485	2.5E+00 AW949158.1	D50307.1	1.5		4503352 NT					6.1				-		-	-					978554					-
	Most Similar (Top) Hit BLAST E Value	2.5E+00	2.5E+00 P13485	2.5E+00 P13485	2.5E+00 P13485	2.5E+00 P13485	2.5E+00	2.5E+00 D50307.1	2.5E+00	2.4E+00 M24282.1	2.4E+00	2.4E+00 P02843	2.4E+00 P26842	2.4E+00 P26842	2.4E+00 AE001486	2.4E+00	2.4E+00 P24091	2.4E+00 P13673	2.4E+00 P13673	2.4E+00 X92511	2.4E+00 P09099	2.4E+00 BE326702	2.4E+00 BE326702	2.4E+00 Y14079.1	2.4E+00 AF158652	2.3E+00 Z46724.1	2.3E+00 AJ401081	2.3E+00	2.3E+00 P07199	2.3E+00 X60265.1	2.3E+00 Q11127	2.3E+00 BF541987	2.3E+00 BF541987
	Expression Signal	2.08	2.33	233	1.71	1.71	1.34	1.75	2.28	0.86	7.62	4.19	2.14	214	263	1.71	9.45	2.5	2.5	2.18	6.49	1.67	1.67	1.77	2.52	9.36	1.28	222	2.3	1.53	1.81	2.6	2.6
	ORF SEQ ID NO:	21217	25537	25538	25537	25538	26598	27334		22707	24485	25664	26802	26803			27194	27853	27854	27911		28002	28003	28558	28839	20802		26431		26613	27364	29083	29084
	Exon SEQ ID NO:	11353	15468	15468	15468	15468	16419	17141	18861	12907	14699	15569	16613	16613	16659	16903	17002	17621	17621	17670	17731	17764	17764	18302	18554	11140	13934	16269	19766	16431	17165	18793	18793
	Probe SEQ ID NO:	1448	5552	5552	5886	5886	6561	7264	9086	2880	4816	2857	6733	6733	6780	7026	7125	777.1	1111	7820	7881	7914	7914	8428	8665	1233	4031	6408	6479	6573	7289	8888	8988

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Top Hit Descriptor	2_72 Homo sapiens cDNA clone IMAGE:3918843 5	otein alpha subunit GNA-3 (gna-3) gene, complete cyla	Exant (nan-coding exan)	exon1 (nan-codina exan)	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (LOW-DENSITY LIPOPROTEIN RECEPTIVE WITH 11 LICAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LICAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LICAND-BINDING REPEATS)	R(1)(>	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR REPEATS) (1811) (2	7 7 Homo saniens CDNA close MAAGE: 30E0777 2	TURAL PROTEIN MU-2	H FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)	Co10 Homo sapiens cDNA clone IMAGE:1058379 3'	205910.r1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5	9 Homo sapiens cDNA clone IMAGE:3948581 5'	OTEINA	qm69b03.x1 Soares, placenta_8b9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965.3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN):	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965.3'	57 Homo saniens cDNA clone IMACE: AZESOA ET	Homo sapiens ovarian granulosa cell 13 0 kDa protein FGR74 homotos mDNA	UROMODULIN PRECURSOR (TAMM-HORSFALL LIRINARY CLYCODROTEIN) /TUBY	TEIN	receptor alpha gene, enhancer region and unstream region	UI-H-BI3-aki-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo saniens cDNA chope IMACE-2724560 2	OTEIN PRECURSOR (FETUIN-A)	yy08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654	
Top Hit Descriptor	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cas	Rat gene for regucalcin, exon1 (non-coding exon)	Rat gene for regucatch, exon1 (non-coding exon)	ELATED RECEPTOR PRECURSOR (SORTING PROTEIN-REI ** LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DEI ** RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR REL	BINDING REPEATS) (LR11) (>	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-REI CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DEI RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR REL BINDING REPEATS) (1,811) (>	600943401T1 NIH MGC 17 Homo seriens cDNA close MACE: 3050777 3	MINOR VIRION STRUCTURAL PROTEIN MU-2	INSULIN-LIKE GROW TH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)	nl95b02.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'	ares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAG	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 51	TRANSPOSON TY1 PROTEIN A	qm69b03.x1 Soares, placenta_8tx9weeks_2NbHP8tx98W_Homo sapiens cDNA similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN):	qm69b03.x1 Scares_placenta_8tp9weeks_2NbHP6tp9W Homo sapiens cDNA similar to ch-Y01433.61 ITATHIONE DEDOVIDAGE (U. 1994)	601855591F1 NIH MGC 57 Homo saniens cDNA close 1846 E-4075204 E-	ovarian granulosa cell 13 0 kDa protein hGR74 hrmdox mBNA	N PRECURSOR (TAMM-HORSFALL LIBINARY CLYCOBROTT	S KD PROTEIN	Mus musculus pre-T cell receptor alpha gene, enhancer region and unstream region	-08-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAG	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)	yy08a10.s1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:270 TRANSCRIPTION INITIATION FACTOR TEILIN (HI IMANN).	AU123630 NT2RM2 Homo sapiens CDNA dans NT2DN/200524 21
Top Hit Database Source	T HUMAN				TOGGS	Т	SORTILIN-REL CONTAINING I RECEPTOR RI SWISSPROT BINDING REP		Т		П		EST_HUMAN 601594733F1 N	Г	qm69b03.x1 So EST_HUMAN similar to gb:Y00	gm69b03.x1 So EST HUMAN similar to ch-Yor	Т		SWISSPROT UROMODULIN	SWISSPROT EARLY E1A 28 KD PROTEIN	Г	EST_HUMAN UI-H-BI3-aki-e-0	ГΤ	yy08a10.s1 Soal EST HUMAN TRANSCRIPTIC	Г
Top Hit Acession No.			D67071.1 NT	2.2E+00 D67071.1 NT				83.1			7	2.1	78.1		2.2E+00 Al290373.1 ES	2.2E+00 A 290373.1 ES	Σ.					3.1		2.1E+00 N29575.1 ES	2
Most Similar (Top) Hit BLAST E Value				H	Í		2.2E+00 O88307							2.2E+00 Q04706			L	2.2E+00	2.2E+00 P07911	2.2E+00 P10407	2.1E+00	2.1E+00	2.1E+00 O70159	2.1E+00	2.1E+00
Expression Signal	4		3.82		10.08	2.51	10.08	90.6	3.3	2.89	3.14	51.56	11.83	2.1	1.56	1.56	2.28	2.88	4.5	4.67	6.81	1.19	3.72	4.7	1.99
ORF SEQ ID NO:	25333		23891		24973				25853	26005		26514			27865	27866	27902	28066	28132	28895	20304		26206	26087	
Exan SEQ ID NO:	Li	ı	ı	14114	15198					15882	15113	16344	17250	19468	17633	17633	17662	17825	17888	18700	12670	13455	16057	15955	16826
Probe SEQ ID NO:	9304	8936	4216	4216	5276		5276	9699	5835	5978	6155	88	33		7783	7783	7812	7975	8739	888	224	3539	8074	6195	6948

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Table 4
Single Exon Probes Expressed in Heart

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 | - 1 | 1 | 1 | - 1 | - 1 | 1

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| Top Hit Descriptor | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds | Oryctolagus cuniculus Na+,K+-ATPase beta 1 subunit mRNA, complete cds | PUTATIVE RRNA METHYLTRANSFERASE SPB1 | R.norvegicus mRNA for collagen alpha1 type i | R.norvegicus mRNA for collagen alpha1 type I | ht13c05.x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE: LIVER (HLIMAN): | hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 1 NEB /HIMAAN | Escherichia coli 0157 DNA, map position at 46 min. complete cds.
 | Escherichia coli 0157 DNA, map position at 46 min. complete cds | Escherichia coli 0157 DNA, map position at 48 min., complete cds | HSPD22703 HM3 Homo sepiens cDNA clone s4000117808 | Gallus gallus mitochondrion, complete genome | Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA | Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltpr1), mRNA

 | CTD-BINDING SR-LIKE PROTEIN RA4 | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
 | CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA | ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD) | PROTEIN B8 PRECURSOR
 | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit
 | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase engine cultural | (athE) genes, complete cds | HEDGEHOG RECEPTOR (PATCHED PROTEIN) | 601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5
 | 601893489F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4139038 5 | EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS) | yh72c08.r1 Soares placenta Nb2HP Homo sepiens cDNA clone IMAGE:135278 5' | Homo saplens PRO0530 mRNA, complete cds | HYPOTHETICAL 75.5 KD PROTEIN IN SDH1-CIMS/YTA3 INTERGENIC REGION |
| Top Hit
Database
Source | TN | LN LN | SWISSPROT | Į. | N
T | EST_HUMAN | EST HUMAN | N N
 | N N | TN | EST_HUMAN | Z | N | Ę

 | SWISSPROT | SWISSPROT | SWISSPROT
 | EST_HUMAN | SWISSPROT | SWISSPROT
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 | | 뒫 | SWISSPROT | EST HUMAN
 | EST_HUMAN | SWISSPROT | EST HUMAN | NT | SWISSPROT |
| Top Hit Acession
No. | AF180527.1 | AF204927.1 | P25582 | Z78279.1 | | AW664496,1 | AW664496.1 | AB008676.1
 | AB008676.1 | AB008676.1 | F31500.1 | 5834843 | 6754389 | 1 1

 | Q63627 | P02467 | P02467
 | 6.1 | |
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 | | .1 | | 9.1
 | 2.1 | | | 9.1 | |
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Value | 2.0E+00 | 2.0E+00 | 2.0E+00 | 2.0E+00 | 2.0E+00 | 2.0E+00 | 2.0E+00 | 2.0E+00
 | 2.0E+00 | 2.0E+00 | 2.0E+00 | 2.0E+00 | 1.9E+00 | 1.9E+00

 | 1.9E+00 | 1.9E+00 | 1.9E+00
 | 1.9E+00 | 1.9E+00 | 1.8E+00
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 | | 1.8E+00 | 1.8E+00 | 1.8E+00
 | 1.8E+00 | 1.8E+00 | 1.8E+00 | 1.8E+00 | 1.8E+00 P36062 |
| Expression
Signal | 1.23 | 1.43 | 3.13 | 4.6 | 4.6 | 2.09 | 2.09 | 3.8
 | 3.8 | 3.8 | 3.3 | 5.81 | 4.67 | 4.67

 | 2.27 | 2.58 | 2.58
 | 3.36 | 1.86 | 1.71
 | 4.48
 | | 4.48 | 222 | 1.9
 | 1.3 | 2.09 | 1.21 | 3.29 | 3.76 |
| ORF SEQ
ID NO: | 20935 | 21076 | | 21890 | 21891 | 23692 | 23693 | 26751
 | 26752 | 26753 | 27237 | 24998 | 25412 | 25413

 | | 26999 | 27000
 | | | 22773
 | 22799
 | | 22800 | | 25723
 | 26078 | 27210 | 27369 | | |
| Exon
SEQ ID
NO: | 11089 | 11219 | 11462 | 11991 | 11991 | 13917 | 13917 | 16558
 | 16558 | 16558 | 17047 | 19613 | 15357 | 15357

 | 15950 | 16805 | 16805
 | 16909 | 17033 | 12981
 | 13009
 | | 13009 | 15492 | 15820
 | 15946 | 17017 | 17169 | 17749 | 18801 |
| Probe
SEQ ID
NO: | 1178 | 1313 | 1557 | 2102 | 2102 | 4011 | 4011 | 6678
 | . 6678 | 6678 | 7170 | 9629 | 5437 | 5437

 | 6047 | 6927 | 6927
 | 7032 | 7158 | 3054
 | 3082
 | | 3082 | 2227 | 5712
 | 6043 | 7140 | 7293 | 7899 | 8998 |
| | Exon Signal No: Signal Value Signal Accession No: Signal Value | Exon SEQ ID NO: Signal Value Value 11089 20935 1.23 2.0E+00 AF180527.1 NT Put Hit Accession Sequence Source | Exon
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Page 11 of 413 Table 4 Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Chlamydomonas reinhardii alternative oxidase 1 (AOX1) cene. nuclear cene encoding mitro-hondrial profeso	c1b) mRNA	e IMAGE:4135586 5'	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)		clone IMAGE:1678137 3'	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)	DNA	DNA	OUP-TF I)	9 IMAGE:4140084 5'			lomo sapiens cDNA not directional	tu82d07.xf NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2257549 3' similar to contains MSR1.tf MSR1 repetitive element:	4750b01.xt Soares_testis_NHT Homo sapiens cDNA done IMAGE:1753417.3' similar to contains L1.tt L1	of the second se	exons 1.2 and 3 and complete cols			ns cDNA clone IMAGE:341689 5' similar to	SIMAGE:43105913'	(SMARCA6) mRNA complete cde	(SMARCA6) mRNA complete cds			Pu	DNA
Single Exon Probes Expressed in Heart	, ,	Chlamydomonas reinhardtii alternative oxidase	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA	601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135586 5	LEVANSUCRASE (BETA-D-FRUCTOFURAN TRANSFERASE)	Homo sapiens chromosome 21 segment HS21C080	oz43h05.x1 Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:1678137 3'	LEVANSUCRASE (BETA-D-FRUCTOFURAN TRANSFERASE)	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)	601894255F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:4140084 51	HOMEOBOX PROTEIN DLX-3	HOMEOBOX PROTEIN DLX-3	67B7 Human retina cDNA Tsp5091-cleaved sublibrary Homo saniens cDNA not directional	tu82d07.x1 NCI_CGAP_Gas4 Homo saplens of MSR1 repetitive element;	qf50b01.x1 Soares_testis_NHT Homo sapiens	Home saniers lens entitledirm-derived arouth feather sone alternativals and	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1.2 and 3 and commister case	Mus musculus ST6GalNAcill gene, exon 2	B.napus gene encoding endo-polygalacturonase	2d25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA done IMAGE:341689 5' similar to db:D29805 N-ACETYL ACTOSAMINE SYNTHASE (HI MANN)	602186095T1 NIH MGC 45 Homo sapiens cDNA clone IMAGE-4310591 3'	Homo saplens proliferation-associated SNF2-like protein (SMARCAB) mRNA complete cds	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA complete cds	Mus musculus ST6GalNAcili gene, exon 2	Mus musculus ST6GalNAcili gene, exon 2	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
gle Exon Pro	Top Hit Database Source	Ę	ΕV	EST_HUMAN	SWISSPROT	Z	EST HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	ECT LIMAN	TN TN	N.	N	Z	EST HUMAN	EST HUMAN	LN LN	Ŗ	N.	NT	IN	EST_HUMAN
Sin	Top Hit Acession No.	1.8E+00 AF314254.1	9506404 NT	BF316805.1	Q60114	AL163280.2	AI141067.1	Q60114	1.7E+00 BE063546.1	BE063546.1	Q9TTR8	BF308000.1	060479	060479	W22424.1	AI678443.1	A1408573 4	5	4.1			-	7:	2.	1.7				7.1
	Most Similar (Top) Hit BLAST E Value.	1.8E+00	1.8E+00	1.8E+00 BF31680	1.7E+00 Q60114	1.7E+00 AL16328(1.7E+00 AI141067	1.7E+00 Q60114	1.7E+00	1.7E+00 BE06354	1.7E+00 Q9TTR8	1.7E+00 BF30800	1.7E+00 O60479	1.7E+00 O60479	1.7E+00 W22424.	1.7E+00 AI678443	4 7E+00 Altos573	1.6E+00 AF19933	1.6E+00 AF077374	1.6E+00 Y11344.1	1.6E+00 X98373.1	1.6E+00 W58426.	1.6E+00 BF570077	1.6E+00 AF155827	1.6E+00 AF155827	1.6E+00 Y11344.1	1.6E+00 Y11344.1	1.6E+00 L04808.1	1.6E+00 BE69726
	Expression Signal	4.01	2.4	1.34	1.92	3.25	1.02	0.84	1.48	1.48	3.58	1.29	2.15	215	1.78	1.37	9.00	16.73	3.61	. 1.96	1.48	2.62	5.14	1.44	1.44	3.14	3.14	2.19	2.64
	ORF SEQ ID NO:				20849	22013	22101	24037	25424	25425	25673		27355	27356	28977	25306	25185	21775	21783	21788		22658		23928	23929	24657	24658	25546	26317
	Exon SÉQ ID NO:	19584	19119	19429	11008	12110	12202	14252	15369	15369	15575	16891	19467	19467	18686	19044	19351	11882	11891	11896	12122	12858	13854	14154	14154	14830	14890	15474	16160
	Probe SEQ ID NO:	9428	9204	8968	1092	2225	2321	4356	5448	5448	5664		7282	7282	8874	9384	0986	1989	1997	2003	2238	2934	3946	4255	4265	5016	5016	6558	9629

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						VTN								A PONT	Cylully Vo						SOR	SOR												
Single Exon Probes Expressed in Heart	Top Hit Descriptor	VIRULENCE FACTOR MVIN HOMOLOG	Mus musculus SIL, MAP 17, CYP a, SCL & CYP b denes	M.musculus COL3A1 gene for collagen alpha-l	M.musculus COL3A1 gene for collagen alpha-l	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6 19/1TV	QV4-LT0016-090200-100-d07 LT0016 Homo saplens cDNA	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA	Homo sapiens transglutaminase type I (Trasel) gene, promoter region	Homo sapiens unknown mRNA	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5	Rettus norvegicus Jun dimerization protein 2 (Idp-2) mRNA, complete cds	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome	Mus musculus a disintectin and metalloproteinase domain (ADAM) 15 (materialin) (Adams - DAM)	Potato virus A RNA complete genome, isolate (1	Mus musculus T-cell lymphoma invasion and metastasis-1 (Tiam1) mRNA	Potato virus A RNA complete genome isolate II	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE-31603 5	601478745F1 NIH MGC 68 Homo sapiens cDNA clone IMAGE:3881555 5'	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRFCLIRSOR	HYPOTHETICAL 118.4 KD PROTEIN IN BATZ-DALS INTERGENIC REGION PRECURSOR	RC0-TN0078-150900-034-g05 TN0078 Homo sepiens cDNA	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'	ze38g06.r1 Soares retina NZb4HR Homo sapiens cDNA clone IMAGE:361306 5	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 31	Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA	Thermoplasma acidophilum complete genome; segment 3/5	Rattus norvegicus 5 - Lipoxygenase (Alox5), mRNA	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
Jie Exon Pro	Top Hit Database Source	SWISSPROT	Ę	N.	₽ F	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	Z.	EST HUMAN	Z	LN	 	¥	Z	Z	N N	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	7	Z	5	7	47	NT
Sing	Top Hit Acession No.	246378	1.6E+00 AJ297131.1		(52046.1	F41290.1	1.6E+00 AW835644.1	1.6E+00 AW835644.1	1.6E+00 AF005631.1				1.5E+00 AE002201.2	6752961 NT	AJ131402.1	6678350 NT	2.1	5.1		1.5E+00 BE785356.1							.1	(07380.1	6753287 NT	1.5E+00 AL445065.1	6978492 NT	7661685 NT	7661685	F053357.1
	Most Similar (Top) Hit BLAST E Value	1.6E+00 Q46378	1.6E+00/	1.6E+00 X52046.	1.6E+00 X52046.	1.6E+00 T41290.1	1.6E+00/	1.6E+00	1.6E+00/	1.6E+00 AF10431	1.6E+00	1.5E+00 U53449.	1.5E+00 /	1.5E+00	1.5E+00	1.5E+00	1.5E+00 AJ13140	1.5E+00	1.5E+00 R17879.	1.5E+00 E	1.5E+00 P47179	1.5E+00 P47179	1.5E+00 E	1.5E+00 E	1.5E+00 A	1.5E+00 A	1.5E+00 AL134197	1.5E+00 X07380.1	1.5E+00	1.5E+00 A	1.5E+00	1.4E+00	1.4E+00	1.4E+00 AF05335
	Expression Signal	1.21	3.56	1.3	1.3	1.29	1.25	1.25	5.86	3.25	1.65	4.29	1.76	1.79	2.46	2.02	222	0.82	2.71	1.42	29.13	29.13	7.56	1.71	1.96	1.96	3.91	10.73	7.	2.89	1.42	1.28	1.28	0.95
	ORF SEQ ID NO:		26958	26646	26647	27679	27946	27947	25601	29047	_	19812	20014		22135	22237	22135	23054	25880		26268	26269	27747		27951	27952	28802					19808	19809	
	Exon SEQ ID NO:	16561	16760	19465	19465	17462	17702	17702	15520	18752	19379	10017	10200	10541	12239	12344	12239	13249	15762	16096	16116	16116	17521	17632	17706	17706	18520	18641	18946	19178	19243	10014	10014	12116
	Probe SEQ ID NO:	6681	6881	7444	7444	7611	7852	7852	8217	8944	8902	30	231	605	2359	2468	3099	3329	5856	6230	6250	6250	7671	7782	7856	7856	8702	8828	9223	9596	0696	27	27	2231

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Table 4
Single Exon Probes Expressed in Heart

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Probe E SEQ ID SE NO:	Exen ORF SEQ ID ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
658	10498		1.67	1.3E+00	1.3E+00 Z73640.1	LN	M.mucedo gene encodina 4. Dihydromethyl-trisnyrate dehydrogenese
_	10810	20659	2.74	1.3E+00	2.1	Į.	Cantharellus sp. partial 25S rRNA gene. isolate Tibet
1113	11028		16.5	1.3E+00	Γ	NT.	Homo sapiens putative psihHbA pseudodene for hair kerafin exons 2 to 7
1275		21033	10.9	1.3E+00	4507998 NT	F	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
		21034	10.9	1.3E+00	4507998 NT	F	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
	11241		1.62	1.3E+00	1.3E+00 U61730.2	NT	Cotx lacryma-jobl dihydrodipicolinate synthase (dapA) gene. complete cds
1593	11497		2.09	1.3E+00	1.3E+00 AE002338.2	Ę	Chlamydia muridarum, section 66 of 85 of the complete genome
	12083		2.1	1.3E+00	1.3E+00 AB030447.1	Į.	Opprinus carplo MRPb and MASPb genes for mannose-binding lectin-associated serine protease (WASP) and MASP-related profein, complete rols
2503	12378		219	1.3E+00	5.2	EST HUMAN	601661233R1 NIH MGC 72 Homo saniens cONIA clans IMAGE:2015045 21
	12835	22632	1.12	1.3E+00	6755621	1 1	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
				•		,	Fugu rubribes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane brotein 1955) sunantic usercle asserviated informal manufactors and a subunit sunantic usercle asserviated informal manufactors and a subunit sunantic sunantic usercle asserviated informal manufactors and a subunit sunantic sunanti
		23258	1.03	1.3E+00	1.3E+00 AF016494.1	Ā	enhancer protein (PCOLCE) genes, complete c>
		22632	0.82	1.3E+00	. 6755621 NT	5	Mus musculus alpha-specifin 1, erythroid (Spna1), mRNA
		24607	0.98	1.3E+00	1.3E+00 AJ252087.1	FA	Plasmodium reichenow partial 83/AWA-1 gene for apical membrane antigen 1
		24608	0.98	1.3E+00	1.3E+00 AJ252087.1	Į.	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
		25674	7.76	1.3E+00	4.1	EST_HUMAN	PMp-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
		25675	7.76	1.3E+00	4.1	EST_HUMAN	PMo-CT0289-291199-004-f08 CT0289 Homo saplens cDNA
		25889	1.33	1.3E+00		F	D.melanogaster no-on-transient A gene product, complete cds
		26901	1.25	1.3E+00	1.3E+00 AJ009912.1	Z	Sus scrafa pip gene
丄		26988	3.06	1.3E+00	1.3E+00 BE963379.2	9.2 EST HUMAN	601657145R1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:38661953'
	16931	1	1.55	1.3E+00	9910247	5	Homo sapiens GL004 protein (GL004), mRNA
┙		1	5.44	1.3E+00	4.1	N	Homo sapiens heparan glucosaminyi N-deacetylase/N-sulfotransferase-2 gene, complete cds
		27560	2.31	1.3E+00		IN	S.alba phr-1 mRNA for photolyase
7487	17357	27561	2.31	1.3E+00	1.3E+00 X72019.1	F	Salba phr-1 mRNA for photolyase
7574 1	17425	27639	1.45	1.3E+00 000754		SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
L		27690	127	1.3E+00	1.3E+00 Al927629.1	EST HUMAN	wo85a07.x1 NCI CGAP Kid11 Homo saniens cDNA clone MAGE:2483400 3
		27751	4.9	1.3E+00	_,	ST HUMAN	601657145R1 NIH MGC 67 Home septens cONA clone MAAGE-3886105 3
l		27961	1.6	1.3E+00	1.	F	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
		27968	1.39	1.3E+00	1.3E+00 M29953.1	N	Campylobacter Jeluni kanamycin phosphotransferase (anhA-7) gene complete calc
┙			4.3	1.3E+00 Q14117		SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
8277 1	18157 2	28398	2.34	1.3E+00 P25299		SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
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art	Top Hit Descriptor	eue	HN9 Homo sapiens cDNA clone IMAGE-2739888 31	085 gene, partial cds	DNA 23.9kB fragment	Cavia porcellus Inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene. complete crts.	P Brn67 Homo sapiens cDNA clone IMAGE:4158452 5'	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE CI VCOPROTEIN)	zi22d08.s1 Soares fetal liver spleen 1NFLS S1 Homo sepiens cDNA clone IMAGE-434535 3*	EIN PRECURSOR (CLONE PFHRP-(II)	EIN PRECURSOR (CLONE PFHRP-III)	EIN PRECURSOR (CLONE PFHRP-III)	al protein PRO3077 (PRO3077), mRNA	ane synthase mRNA, complete cds	rus complete genome	rus complete genome	coupled receptor 14 (GPR14) gene, complete cds	KIAA0874 protein, partial cds	chromosome 4, contia fragment No. 63	chromosome 4, contia fraament No. 63	PROTEIN TRBE PRECURSOR	e, intron 2	A, complete cds	ike serine protease LPC (PC7) gene, exons 1 to 9, partial cds	3-906_1 FT0175 Homo sapiens cDNA	e, intron 2	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glra?) mRNA	gene, exons 1-23	chromosome 4, contig fragment No. 21	vitc density 95 (DLG4) gene, complete cds	cL gene, partial	A, complete cds	3-c05 ST0191 Homo sapiens cDNA	· DNA, fragment D	0-e03 BN0090 Homo sapiens cDNA
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Mus musculus desmin gene	xp09e03.xt NCI CGAP HN9 Homo saniens cDNA clone IMAGE-2739868 3'	Human mRNA for KIAA0085 gene, partial cds	Bacillus subtilis genomic DNA 23.9kB fragment	Porcellus Inwardly-rectifying potassium channel Kir2.2 (KCNJ12)	602023185F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5	LYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (M	108.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDN/	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA	Elasis oleifera sesquiterpene synthase mRNA, complete cds	pea seed-borne mosaic virus complete genome	pea seed-borne mosaic virus complete genome	Homo saplens G-protein coupled receptor 14 (GPR14) gene, camplete cds	Homo saplens mRNA for KIAA0874 protein, partial cds	Arabidopsis thallana DNA chromosome 4, contin fragment No. 63	Arabidopsis thallana DNA chromosome 4, contin fragment No. 63	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR	Homo sapiens LHX3 gene, intron 2	G.gallus T-cadherin mRNA, complete cds	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9. partial cds	MR0-FT0175-050900-203-906_1 FT0175 Homo sapiens cDNA	Homo sapiens LHX3 gene, intron 2	s norvegicus Glycine receptor alpha 2 subunit (glycine receptor, n	Rattus rattus cardiac AE3 gene, exons 1-23	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21	Homo saplens post-synaptic density 95 (DLG4) gene, complete cds	T. pinnatum chloroplast rbcL gene, partial	G.gallus T-cadherin mRNA, complete cds	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA	D.fhydel ayf repeat cluster DNA, fragment D	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
=xon Probes t	Top Hit Database Source	Mus	HUMAN		Baci	Cavi	EST_HUMAN 6020	Т	П	T	Т	SWISSPROT HIST	Г	Elae	bea	bead	HoH	Hom	Arab	Arab	SWISSPROT CON	면원	G.ga		EST_HUMAN MR0	Hom	Rath	Rath	Arab	Hom	T.pin	G.ga	EST_HUMAN MR3		EST_HUMAN QV4
ingle L		토	EST	Ę	토	¥	EST	SWI	EST	SWE	SWIS	SWK	8924234 NT	<u>5</u>	뉟	Ę	¥	호	Ę	본	SWE	Ę	ΙN	Ϋ́	EST	Ŋ	34 NT	토	뉟	Ę	뉟	Ę	EST	ΤN	EST
ν 	Top Hit Acession No.	1.3E+00 Z18892.2	1.3E+00 AW274791.1	1.3E+00 D42042.1	1.3E+00 Z98682.1	1.3E+00 AF187873.1	1.3E+00 BF348043.1	P33464	1.2E+00 AA676246.1	P05228	P05228	P05228	89242	1.2E+00 AF080245.2	1.2E+00 AJ252242.1	1.2E+00 AJ252242.1	1.2E+00 AF140631.1	1.2E+00 AB020681.1	1.2E+00 AL161563.2	1.2E+00 AL161563.2	1	1.2E+00 AF188740.1	1.2E+00 M81779.1	1.2E+00 U75902.1	1.2E+00 BF373570.1	1.2E+00 AF188740.1	6980951 NT	1.2E+00 M87060.1	1.2E+00 AL161509.2		Y09200.1	M81779.1	1.2E+00 AW813276.1	X74885.1	1.2E+00 BE003113.1
	Most Similar (Top) Hit BLAST E Value	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00 P33464	1.2년+00	1.2E+00 P05228	1.2E+00 P05228	1.2E+00 P05228	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00 P54910	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00 Y09200.1	1.2E+00 M81779.1	1.2E+00	1.2E+00 X74885.1	1.2E+00
	Expression Signal	2.23	1.81	2.82	2.71	2.35	3.24	2.68	8.14	1.33	1.33	1.33	2.19	5.53	1.77	1.77	1.05	0.95	5.41	5.41	2.9	0.78	0.99	7.28	1.49	1.09	1.39	1.64	1.28	1.82	5.44	0.94	1.96	2.47	3.28
	ORF SEQ ID NO:	28424		28923	28999		25263		20384	20578	20579	20580		20901	20943	20944	21746	22789	22851	22852		23038		23350	23598	23038	23981		24102	24145			25379	25753	25783
	Exon SEQ ID NO:	18178	18510	18639	18705	19033	19139	19499	10571	10735	10735	10735	10786	11058	11097	11097	11857	12999	13053	13053	13172	13232	13233	13564	13814	13232	14196	14267	14316	14354	14379	13233	15329	15647	15676
	Probe SEO ID 8 NO:	8299	8646	8826	8895	9362	9533	9544	634	908	806	808	860	1145	1187	1187	1963	3072	3128	3128	3249	3311	3312	3650	3904	4201	4298	4371	4422			4584	5409	5739	5769

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Table 4
Single Exon Probes Expressed in Heart

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Single Extri Fronces Expressed in reading	Top Hit Descriptor	Ciglutamicum pta gene and ackA gene	C.glutamicum pta gene and ackA gene	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA	Mus musculus DSPP gene	AV734585 cdA Homo sapiens cDNA clone cdAAFH03 5'	L.lactis pyrD and pyrF genes	Homo sapiens mRNA for KIAA1204 protein, partial cds	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01	H.saplens ENO3 gene for muscle specific enolase	PMO-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds	Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds	Homo sapiens chromosome 21 segment HS21C003	Bacillus halodurans genomic DNA, section 9/14	Human mRNA for KIAA0227 gene, partial cds	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA	U-HF-BR0p-alk-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens chromosome 21 segment HS21C013	Homo saplens hypothetical protein FLJ10749 (FLJ10749), mRNA	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA	wf54h11x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to	XWella fastidina sociin 32 of 230 of the complete general	Xylella fastidiosa section 32 of 228 of the complete geneme	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA	Homo sapiens hypothetical protein FL 10749 (FI 110749) mRNA	R.unicornis complete mitochondrial genome	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds	African swine fever virus, complete genome
וום בעחוו גווחי	Top Hit Database Source	NT	Ŋ	EST_HUMAN	EST HUMAN	Į.	EST_HUMAN	F	N	EST_HUMAN	<u>F</u> V	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	Z	ᅜ	Z	FZ.	F	EST_HUMAN	EST_HUMAN	NT	NT	M	NT	for Links	PINOU I PIN	LN	E	Z	与	N	Į.
Sillo	Top Hit Acession No.			1.2E+00 AA759254.1	W813276.1	1.1	5.1		0.1	0.1				17.1	1.1				5.1		93.1	1.1E+00 AW575889.1	1.2	3.2	. 8922641 NT	8922973 NT	4 4Exon Alebesses 4	T	9,1	5729757	8922641 NT	5835331 NT		
	Most Similar (Top) Hit BLAST E Value	1.2E+00 X89084.1	1.2E+00 X89084.1	1.2E+00 /	1.2E+00 AW81327	1.2E+00 AJ002141	1.2E+00 AV73458	1.2E+00 X74207.1	1.2E+00 AB03303	1.2E+00 AW37721	1.2E+00 Z32850.1	1.2E+00 D11745.1	1.2E+00 X56832.1	1.2E+00 AW8178	1.2E+00 BE16076	1.2E+00 U50147.1	1.2E+00 /	1.2E+00	1.2E+00 /	1.1E+00 D86980.1	1.1E+00 A	1.1E+00 A	1.1E+00 AL163213	1.1E+00 AL16321	1.1E+00	1.1E+00	1 100	1 1F+00 AFORSBR	1 1F+00 AF00388	1.15+00	1.1E+00	1.1E+00	1.1E+00 L	1.1E+00 U18466.1
	Expression Signal	1.87	1.87	32.83	1.82	2.55	1.9	2.4	3.45	1.74	3.08	1.8	3.28	. 2.03	23.47	4.87	2.5	15.4	1.49	1.13	1.39	0.92	6.61	6.61	0.93	1.26	6	1.16	116	17.81	0.99	5.89	1.18	2.92
	ORF SEQ ID NO:	25815	25816	25841	. 25949	26121	26392	26544	27055	27285	27480	27601	27786	28826		28145	28787	25067		20217	21496	21628	23009	23010	23165		73274	23357	23358	23378	23565		24520	24573
	Exon SEQ ID NO:	15704	15704	15729	15823	15986	19463	16367	16861	17095	17274	17391	17561	18542	18576	17901	18877	19572	19025	10400	11627	11753	13209	13209	13358	13426	12447	13571	13571	13592	13773	14022	14740	14800
	Probe SEQ ID NO:	5798	96/9	5823	5918	6139	6369	6208	6984	7218	7407	7540	7711	8653	8689	8752	9114	9330	9349	456	1726	1857	3288	3288	3441	3510	2534	3657	3657	3678	3862	4122	4860	4921

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Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | E.faecalis pbp5 gene | Rettus norvegicus Aguaporin 4 (Ago4), mRNA | 601652776R1 NIH MGC 58 Homo saniens chivia clone IMAGE: 3875885 2 | qd85c03.x1 Soares testis NHT Home seniens cDNA clane IMAGE:1728280 3 | Herpes simplex virus type 1 (strain KOS) III 41 gene | Herpes simplex virus type 1 (strain KOS) 111 41 nene | Arabidopsis thaliana DNA chromosome 4. contid fragment No. 84 | 602082582F1 NIH MGC 81 Homo sertiens cDNA clone IMAGE-4246828 E | Homo saplens mRNA for KIAA0934 protein, parifal cds

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 | Girardia tigrina mRNA for homeodomain transcription factor (so gene)
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Source 14874 24638 1.16 1.16+00 X78425.1 NT 15370 25426 1.204 1.16+00 6978530 NT NT 16380 25446 1.29 1.16+00 A118582.1 EST HUMAN 16286 25446 1.93 1.16+00 A118582.1 NT 16296 25456 7.63 1.16+00 A1418582.1 NT 16508 25456 7.63 1.16+00 A1418582.1 NT 16508 25456 7.63 1.16+00 A1416188.2 NT 17608 27733 1.65 1.16+00 A1416168.2 NT 17608 27731 1.65 1.16+00 A14161616.2 NT 17634 27815 2.65 1.16+00 A14161616.2 NT 17834 28182 2.65 1.16+00 A1461</td> <td>Exon No: ORF SEQ ID ID NO: Expression Signal Signal Signal Signal ID NO: Top Hit Acession Value No. Top Hit Acession No: Top Hit Acession Source Noise Top Hit Acession No: Top Hit Acession No:<!--</td--><td>Exon ORF SEQ Expression Most Similar Top Hit Acession Top Hit Acession Top Hit Acession NO: Signal 1.16
1.15+00 X78425.1 NT 14874 24638 1.16 1.15+00 X78425.1 NT 15370 25426 1.20 1.15+00 6978530 NT NT 15380 25440 1.29 1.15+00 Al138582.1 EST HUMAN 16283 26446 1.93 1.16+00 Al138582.1 NT 16296 26458 7.63 1.16+00 Al138582.1 NT 16508 26459 3.22 1.16+00 Al161588.2 NT 17608 27733 1.65 1.16+00 Al161588.2 NT 17608 27731 1.65 1.16+00 Al161516.2 NT 17834 27815 20.08 1.16+00 Al161516.2 NT 17834 28182 2.65 1.16+00 Al161516.2 NT 13426 3.41</td><td>Exon No: ORF SEQ ID ID NO: Expression Signal Signal Signal Signal ID NO: Top Hit Acession No: Top Hit Acession No: Top Hit Acession Source Nature Top Hit Acession No: Top Hit Acession Source Source Top Hit Acession No: Top Hit Acession</td><td>Exon
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 A14161588.2 NT 1650 27733 1.65 1.1E+00 A161588.2 NT 17608 26789 3.22 1.1E+00 A161588.2 NT 17608 27733 1.65 1.1E+00 A161588.2 NT 17609 27733 1.65 1.1E+00 A161588.2 NT 17640 27733 1.65 1.1E+00 A161516.2 NT 17834 28182 2.65 1.1E+00 A161516.2 NT 18253</td> <td>Exon
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Table 4
Single Exon Probes Expressed in

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6861	16740	26932	2.7		1.0E+00 Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
6861	16740	26933	2.7		1.0E+00 Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
6967	19466		2.01	1.0E+00	1.0E+00 BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
7064	16941	27133	1.9		1.0E+00 M38427.1	닏	Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,
7339	17207	27405	1.78		1.0E+00 BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Hamo saplens cDNA clane IMAGE:3899421 5'
7460	17320	27526			6753429	۲	Mus musculus chloride channel calcium activated 1 (Cica1), mRNA
7460	17320	27527	1.28		6753429 NT	۲	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
7544	17395	27607	. 2.03		1.0E+00 AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
7546	17397	27609	1.2		1.0E+00 U44952.1	NT	Xenopus laevis zona pellucida C giycoprotein precursor (XIZPC) mRNA, complete cds
7546	17397	27610	1.2		1.0E+00 U44952.1	ΙN	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
7916	17766	28005	2.83		1.0E+00 AV758825.1	EST_HUMAN	AV75825 BM Homo sapiens cDNA clone BMFAW C04 5
7985	17835	28075	17.08		1.0E+00 AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
7985	17835	28076	17.08		1.0E+00 AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
9193	18928		2.05		1.0E+00 P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
9513	19126		1.51	1.0E+00	1.0E+00 AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo saplens cDNA
9869	19350		1.67		1.0E+00 AB040950.1	ΙN	Homo sapiens mRNA for KIAA1517 protein, partial cds
1553	11458				9.9E-01 AF245455.1	TN	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1553	11458	21316	0.84		9.9E-01 AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2298	12467	22360			9.9E-01 AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3553	13468		1.18		9.9E-01 AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5461	15381	25441	9.22		9.9E-01 P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
7336	17204		1.38		9.9E-01 U65667.1	N	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene
7510	17298		2.43		9.9E-01 Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
8097	17988	28237			9.9E-01 AJ005029.1	TN	Danio rento mRNA for Eph-like receptor tyrosine kinase rtk8
512	10454	20265	232		9.8E-01 P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
3732	13644	23429	0.82		9.8E-01 BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3732	13644	23430	0.82		9.8E-01 BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6272	16137	26292	4.61		9.8E-01 AJ302158.1	LN	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- like protein, isolate JM983

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Table 4

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Top Hit Descriptor	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- like protein, isolate JM983	601110258F1 NIH MGC 16 Homo septens cDNA clone IMAGE: 3350750 F	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360750 5	Homo saplens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrendent colorabethanks and a companies (CRTR), adrendent colorabethanks and a companies (CRTR).	we62e04.x1 Soares thymus NHFTh Homo saniens CNA class IMAGE 22 / Ego. 21	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds	Triticum aestivum stribe rust resistance protein V410 (V410) gene generalists ad-	Salmonella tyohimurium adenina-methyliransferase (m.m.) and south-firm	UI-H-BI4-aci-e-07-0-UI st NCI CGAP Suba Homo sanians CNN slow (MA CE SARE)	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen dentiunition	Bromus inemis putative cytosolic physihroniusom mass of months about the cytosolic physikatonius putative cytosolic physikatonius produce and the cytosolic physikatonius physikatonius produce and the cytosolic physikatonius physikat	Bromus Inermis putative cytosolic phosphoducom riase (pg.11) mRNA complete cos	PM2-UM0053-240300-005-F12 IM0053 Home seniors (FBILI)	Homo sepiens KIAA0914 cene product (KIAA0014)BNA	Parvovirus B19 DNA, patient C, genome position 2448, 2004	Parvovirus B19 DNA, patient C, genome position 2448,2004	P.falciparum complete gene map of plastid-like DNA (IR-A)	AV752805 NPD Homo sapiens cDNA close NPDRACAGE 87	AV762805 NPD Homo sepiens cDNA clone NPDBAG06 5'	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial	601675639F1 NIH MGC 21 Home sarians aDNA alexa MA OF SOCIAL TO	601875639F1 NIH MGC 21 Home carions abna 21 1 1 1 2 1 1 2 1 1 1 2 1 1 2 1 1 2 1 2 1 1 2 1	RC1-CT0295-241199-011-b02 CT0295-Home septems chiva	Bartonella clarridosiae RNA polymerase bate subunit (mg8) and a matici ad-	Pimpinella brachycarpa zinc finger protein (ZEP4) mRNA complete cuts	601466703F1 NIH_MGC 67 Homb sapiens cDNA clone IMAGE:3850020 57	Homo saplens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) ancogene homolog) (EGFR), mRNA	Homo saplens phytanoyi-CoA hydroxylase (PHYH) gene, exon 5
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Top Hit Acession No.	AJ302158.1	BE258705.1	BE258705.1	U52111.2	AI660384.1	,	7.		-				4.1	662375							\-	l					11419857	9.3E-01 AF242382.1
Most Similar (Top) Hit BLAST E Vafue	9.8E-01	9.8E-01	9.8E-01	9.8E-01	9.7E-01	9.7E-01	9.7E-01	9.7E-01	9.7E-01	9.7E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01 /	9.6E-01	9.6E-01	9.5E-01	9.5E-01	9.5E-01	9.4E-01 /	9.4E-01	9.4E-01	9.4E-01	9.3E-01
Expression Signal	4.61	4.43	4.43	1.62	1.01	2.37	1.86	1.74	4.52	1.39	6.8	6.8	1.3	0.92	3.46	3.46	1.37	4.15	4.15	1.52	1.6	1.6	1.17	3.37	1.67	1.64	£.	1.11
ORF SEQ ID NO:	26293	28487	28488			26266	27023	27025			24016	24017	24036	24729	25498	25499		28912	28913	24989	23410	23411	27336					
Exon SEQ ID NO:	16137	18239	18239	19061	14974	16114	16830	16832	18382	19419	14234	14234	14251	14953	15435	15435	16769	18622	18622	19646	13627	13627	17143	13090	13106	19029	19564	11601
Probe SEQ ID NO:	6272	8362	8362	9408	5108	6248	6952	6954	8510	9926	4337	4337	4355	5083	5517	5517	06890	808	8808	9709	3715	3715	7266	3165	3181	9354	9708	1700
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Table 4
Single Exon Probes Expressed in

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Table 4
Single Exon Probes Expressed in Heart

Exon Most Similar Most Similar Most Similar Top Hit Acession Top Hit Acession NO: Signal (Top) Hit Acession (Top) Hit Acession Top Hit Acession Top Hit Acession 15413 25476 2.08 8.9E-01 AF02518.1 NT 15692 28065 3.47 8.9E-01 AF00394.1 NT 16784 28065 3.28 8.8E-01 AF00394.1 NT 18724 28065 3.28 8.8E-01 AF00394.1 NT 18724 28065 3.28 8.8E-01 AF00394.1 NT 18725 22130 1.58 8.8E-01 AF00394.1 NT 12233 22130 1.09 8.7E-01 AF121970.1 NT 12773 22560 4.64 8.7E-01 AF121970.1 NT 14816 2.78 8.7E-01 AF121970.1 NT 14876 29067 4.16 8.7E-01 AF10939.1 EST HUMAN 1653 4.16 8.7E-01 AF10789.1 RT HUMAN 1674 2906 4.16 8.7E-01 AF10789.1												_				_	_		_			_										
Exon NO: ID NO: ID NO	בילויסססס ווו ופמון	Top Hit Descriptor	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel close of several contractions.	Rabbit MHC framment R1 A DE DNA	Xylella fastidiosa, sertion 90 of 209 of the complete grown	Chlamydobhlla pneumonlae AR39 section 21 of 64 of the commission	PUTATIVE F420-DEPENDENT NADD REDICTAGE	Maerudinosa (HUB 5-24) DNA from plasmid PMA4	Synechocystis sp. PCC6803 cmmheir genome 13/27 15/2502 1740542	Homo sepiens SOS1 (SOS1) dene nertiel ode	Homo sepiens AT-hinding transcription factor 1 (ATDEA) DNIA	INDESTITE INC. CRAP P.4.1 Home content COMA class MACE AND CONTENTS	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-	indicated i.z-uloxygeriase beta-to-P protein OnbA (onbA), OnbC (onbC), ortho-halobenzoate 1,2- Idioxygenase alpha-ISP protein OhhB (onbB) בייל הייל הייל.	Pseudomonas aerucinosa DA01 senton 524 of 520 of 41.	OVO-NN1021-100800-337-03 NN1021 Long configure genome	60182368481 NIH MGC 70 Homo seniors CONA class (MACE) Access of	601823684R1 NIH MGC 70 Home capiene color invasional s	AV661898 GLC Homo sanians of NA character of CAVANTS.	Rat IGFII gene for insulindike growth forter il	zd44e03.r1 Soares fetal heart NbHH19W Homo santens cDNA clone IMACE:245516 FT	Homo sepiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, carebrotendinous	Arabidoosis thaliana DNA chromosome 4 confin fromment No. 25	Drosobhla melanoraster marlin (Dmarlin) mBNA mampleta of	Chicken lipoprotein linease gene	Chicken Innovated Inservence	Grus canadensis recombination activeting protein 1 (DAC 4)	GIIS canadensis recombination activistics activistics and a 1000-100 gene, patient cos	Bacillus halodurans cenomic DNA section 1974	601067107F1 NIH MGC 10 Home senions cDNA clane MA CE: 2 Acococ cr	Ovanidium caldarium cene for SinC, complete cite	Oyanidium caldarium gene for SigC, complete cds
Exon NO: ID NO: ID NO	21 1122 218	Top Hit Database Source	L Z	Į.	L Z	Z	SWISSPROT	¥	۲	Ę	F	EST HUMAN		K	NT.	h-	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST_HUMAN		Ę	Į.	- L	Ę	E	2	¥	EST HUMAN	L	LV.
Exon ORF SEQ Expression (TT Signal No: Signal No: Signal No: No: Signal No:		Top Hit Acesslon No.	AF026198.1	X60986.1	AE003944.1	AE002186.2	026350	228337.1	D90911.1	AF106953.2	5901893	AA595863.1		AF121970.1	AE004963.1	3F363970.1	7	=	 -			4503210	2									
Exon ORF SEQ Express NO: NO: Sign: N		Most Similar (Top) Hit BLAST E Value	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.8E-01	8.8E-01	8.8E-01	8.7E-01	8.7E-01	8.7E-01		8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.6E-01.)	8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.GE-01	8.6E-01.	8.6E-01	8.6E-01/	8.6E-01	8.5E-01	8.5E-01/	8.5E-01
Exon SEQ ID NO: 16413 15692 16776 18304 18776 18776 18776 18672 10409 10767 1738 12509 15509 15509 15509 15509 15774 15509 17774 15509 17774 15509 17774 17774 17774 17774 17774 17774 17774 177774 177774 1777774 1777		Expression Signal	. 208	1.32	3.47	4.74	3.28	2.98	1.75	1.54	1.09	4.64		2.51	1.45	5.47	4.16	4.16	278	1.66	3.62	1.01	0.81	1.29	11.82	11.82	2.14	2.14	1.52	2.75	1.36	1.36
		ORF SEQ ID NO:								20218	22130	22560	,		27681	28343	29067	29068			20618	22012	23273	23427	25586	25587	26065	26066		26469	28013	28014
Probe 1 2494 1 24442 1 24442 1 24442 1 3430 1 34				1	\Box	18987	14336	18304	19722	10401	12233	12773		14816	17464	18090	18776	18776	19534	10409	10767	12109	13482	13642	15509	15509	15934	15934	16506	16304	17774	17774
		Probe SEQ ID NO:	5494	5786	8990	9285	4442	8430	9108	457	2353	2845		4938	7613	8206	8970	8970	9488	466	840	2224	3568	3730	5595	5595	6030	6030	9299	6443	7924	7924

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		Т	T	Т	T	T	Т	Ţ	Т	Т	Т	Т	Т	Т	T	T	Т	02	7	Т		Ţ	T	\neg	7	7	_	\top	\top	7	-
Single Excit Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens human immunodeficiency virus hare I enhancer-hinding grahein 4 /Lin/ED41 Dhia	Rettus norvegicus protein tyrosine phosphalase, non-recentor type 5 (Phys.) mBNA	Mus musculus mper1 gene for period1 complete cds	Mus musculus NK cell receptor 284 dene promoter region and martial add	Human fibroblast growth factor receptor 3 (FGFR3) gene infrom 7	Human fibroblast growth factor receptor 3 (FGFR3) gene, infrom 7	Pyrococcus abyssi complete genome: segment 5/6	Thermus thermophilus cytochrome c-552 (cyt.A) and Che.B (cyt.B) genes complete ad-	Arabidopsis thaliana DNA chromosome 4, contin fragment No. 18	Nicottana tabacum mRNA for chloroplast ribosomal protein I 10, complete cde	Streptomyces antibioticus polyketide biosynthetic gene cluster	Cenis familiaris MHC DLA Class II DRB pseudomene DRR2	Canls familiaris MHC DLA Class II DRB pseudonene DRB?	Canis familiaris MHC DLA Class II DRB pseudonene DRR2	Canis familiaris MHC DLA Class II DRB pseudocene DRR2	Arabidopsis thaliana DNA chromosome 4. contin frament No. An	nn01f12.y5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR	Drosobila melanoraster I ist homelon mRNA complete at	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the	Phytophthora infestans mitochondrion complete census	Homo caniano EDA3B common femilia anti-	Reffus norweding mRNA for RDLO 4 complete and	Mus musculus trophinin (Tinn) gene complete ade	1.3-CT0219-161199-031-CD8 CT0219 Home serions of NA	Rattus norvegicus mRNA for RPHO-1, complete cds	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isoproplymalate (alpha-IPM) synthetise (nertial) and DNA polymerses enhalocation	Homo sepiens thioredoxin-related profein mRNA commists and	MCKUSICK-KAUFMANIBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
IIE EXUII PIO	Top Hit Database Source	۲	NT	TN	Į.	NT	N N	F	N	L	F	N	N.	F	NT	N	N F	EST HUMAN		N.	MŦ	5	Į į	LN	Z	ST HUMAN	N	T	NT	7	ISSPROT:
Sillo -	Top Hit Acessian No.	11418543 NT	9507008 NT	8.1	2			Υ.		2	1						2	8.3E-01 AI791952 1	T	8.3E-01 AF108133.1		2472	8.3E-01 AF020503 1	_	_		_			_	
	Most Similar (Top) Hit BLAST E Value	8.5E-01	8.5E-01	8.5E-01 AB03081	8.4E-01	8.4E-01 L78726.1	8.4E-01 L78726.1	8.4E-01 AJ248287	8.3E-01 M93437.1	8.3E-01 AL161506	8.3E-01 AB010875	8.3E-01 Y19177.1	8.3E-01 U46916.1	8.3E-01 U46916.1	8.3E-01 U46916.1	8.3E-01 U46916.1	8.3E-01 AL161540	8.3E-01	8.3E-01	8.3E-01	8.3F_04.1A	8.3E-01	8.3E-01 A	8.2E-01 AB000489	8.2E-01 A	8.2E-01 AW376990	8.2E-01	8.2E-01 AW37943	8.2E-01 Z12126.1	8.2E-01 AF052659	8:2E-01 Q9JI70
	Expression Signal	2.52	2.63	1.29	0.84	2.7	2.7	3.13	231	2.64	1	3.11	1.12	1.12	0.95	0.95	2.13	4.2	1.23	3.1	2.46	246	2.03	2.99	1.51	1.14	1	3.26	3.58	1.53	6.66
	ORF SEQ ID NO:			25243	23785	25145	25146		20486	22774	23434	23619	24570	24571	24570	24571	24839		27914	27962	28204		28760	21789			24691	26154	26330	27871	28028
	Exon SEQ ID NO:	19643	19075	19238	14008	19443	19443	17571	10858	12983	13651	13839	14796	14796	14796	14796	15145	17424	17672	17717	17953	17967	18488	11898	11934	12513	14917	15016	19462	17638	17787
	Probe SEQ ID NO:	9430	9436	9683	4108	5378	5378	7721	724	3056	3739	3930	4917	4917	5177	5177	5222	7573	7822	7867	8062	9076	8623	2006	2043	2646	5045	6122	6308	7788	7937

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	. Top Hit Descriptor	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA	OVARIAN TUMOR LOCUS PROTEIN	w14d02.r1 Soares_placenta_Bto9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HLIMAN):	Mus musculus mRNA for NIPSNAP2 protein	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds	Homo sapiens MHC class 1 region	Homo saplens MHC class 1 region	NEURONAL MEMBRANE GLYCOPROTEIN M6-B	NEURONAL MEMBRANE GLYCOPROTEIN M6-B	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA	RC0-TN0080-220800-025-d10 TN0080 Homo sepiens cDNA	Thermotoga manitima section 23 of 136 of the complete genome	Staphylococcus aureus partial pta gene for phosphate achitransferase allele 15	Bos taurus futb and rtif genes	602072473F1 NCI CGAP Brn87 Homo sagiens cDNA clone IMAGE-4215004 51	Salmiri boliviensis olfactory receptor (SBO27) gene, partial ods	Mus musculus gene for oviductal diveopratein, complete cds	Neisseria meningitidis serograup A strain 22491 complete genome: semment 7/7	G.gallus mRNA for nicolinic acetylcholine recentor (nAChR) heta 3 submit	RCO-NN1012-270300-021-h06 NN1012 Homo sabiens cDNA	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	Ureaplasma urealyticum section 31 of 59 of the complete genome	Homo sapiens mRNA for KIAA1452 protein, pertial cds	Haemophilus influenzae Rd section 54 of 163 of the complete genome	Oryctolagus cuniculus mRNA for mitsugumin 29, complete cds	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	601192033F1 NIH MGC 7 Homo saplens cDNA clone IMAGE:3535785 5	Mus musculus embigin (Emb), mRNA	Mus musculus embigin (Emb), mRNA	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
	Top Hit Database Source	SWISSPROT	TN.	SWISSPROT	EST HUMAN	Т		N	,	SWISSPROT	SWISSPROT	EST HUMAN	T	Γ	Ę		T HUMAN	Г	LN LN	NT.		EST HUMAN			LΝ	Į,	TN	F	Į.	EST_HUMAN				NT
	Top Hit Acession No.	Q9JI70	8.2年-01 L10127.1	P10383	8.2E-01 H87398.1	8.2E-01 AJ001261.1	8.1E-01 AF191839.1	8.1E-01 AF055066.1	8.1E-01 AF055066.1	013491	Q13491	8.1E-01 BE938558.1	8.1E-01 BE938558.1	8.1E-01 AE001711.1	7.0	2.1	BF530962.1					8.0E-01 AW901489.1		0.1	5.1			7.9E-01 AF130459.1		2.1	6753745 NT	6753745 NT		
	Most Similar (Top) Hit BLAST E Value	8.2E-01 Q9JI70	8.25-01	8.2E-01 P10383	8.2E-01	8.25-01	8.1E-01	8.1E-01	8.1E-01	8.1E-01 Q13491	8.1E-01	8.1E-01	8.1E-01	8.1E-01	8.0E-01 AJZ7151	8.0E-01 AJ13277	8.0E-01 BF53096	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	7.9E-01 D11476.1	7.9E-01 AE00213	7.9E-01 AB04088	7.9E-01 U32739.1	7.9E-01	7.9€-01	7.9E-01 AF22868	7.9E-01 BE26361;	7.9E-01	7.9E-01	7.9E-01 Z47210.1	7.9E-01 Z47210.1
	Expression Signal	6.66	2.81	9.	6.65	1.73	1.29	281	2.81	2.49	249	1.94	1.94	1.84	3.02	3.76	1.83	2.73	1.14	1.8	5.65	284	3.78	1.16	65.97	1.37	5.24	2.29	2.75	0.92	1.02	1.02	0.84	0.84
-	ORF SEQ ID NO:	28029		. 29064	29069	25284		23130	23131	26020	26021	28879	28880	25343		20070		22761	22993		24115		20211				22006	22007	23193		24188	24189	24720	24721
	Exan SEQ ID NO:			18772	18777	19083	12593	13329	13329	15897	15897			18909	10142	10250	11884	12967	13194	13557	14327	16541	10390	10631	11491	11538	12102	12103	13388	14103	14401	14401	14945	14945
	Probe SEQ ID NO:	7937	8809	9968	8971	9451	2731	3412	3412	2992	5992	8775	8775	9166	170	285	1990	3039	3273	3643	4432	6661	446	869	1587	1634	2216	2217	3472	4204	4508	4508	5075	5075

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Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17 | P.sativum GR gene | Giardia lambila variant-specific surface profein G3M-B (vsnG3M-R) mRNA nertial Ac | SWALL HYDROPHOBIC PROTEIN | Homo sapiens KIAA1072 protein (KIAA1072), mRNA | NEURAL-CADHERIN PRECURSOR (N.CADHERIN) | HSC1KH041 normalized infant brain cDNA Homo sanians cDNA clare c-1/kh04 | EST371637 MAGE resequences. MAGF Homo sabiens cONA

 | Rattus norvegicus transmembrane receptor Uncott mRNA complete cots
 | Sphenodon punctatus alpha enolase mRNA, partial cds | D.discoideum racGAP gene | Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACSS) gene | Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA complete and | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II abba | chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butwoohilin-like (NG9) hurtwoohilin-like (NG9) hurtwoohilin-like
 | CITRATE SYNTHASE | Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7
(GalNAc-T7) (GALNAC-T7) mRNA

 | Homo saplens PRO1975 mRNA complete cde | Coturnix coturnix latonica sub-species janonica hata artin mBNA mortici ade | Cotumix cotumix labonica sub-species labonica hela-actin mRNA partial cac | RAFFINOSE INVERTASE (INVERTASE) | RAFFINOSE INVERTASE (INVERTASE) | yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE-127755 2
 | Vennereirom hiteratum ADD all tosses | Archaeonlohus fululdus complete casamo | Arabidopsis thallana 3-methylorotonyl-CoA carboxylase non-biotinylated subunit (MCCR) mRNA commission | operation (Constitution) | Arabidopsis thallana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |
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| Top Hit
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| Top Hit Acession
No. | M29930.1 | X90996.1 | U01912.1 | P19719 | 7662471 | , | Z43785.1 | AW959567.1

 | U87305.1
 | AF115856.1 | Y10159.1 | L 29260.1 | AF184345.1 | | AF050157.1
 | 033915 | 8393408

 | AF118085.1 | | 3.1 | P16553 | P16553 | 308600.1
 | | 17621 | | 2. | Ξ |
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| Most Similar
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Value | 7.9E-01 | 7.9E-01 | 7.9E-01 | 7.9E-01 | 7.9E-01 | 7.9E-01 | 7.8E-01 | 7.8E-01

 | 7.8E-01
 | 7.8E-01 | 7.8E-01 | 7.8E-01 | 7.7E-01 | | 7.7E-01
 | 7.7E-01 | 7.7E-01

 | 7.7E-01 | 7.7E-01 | 7.7E-01 | 7.7E-01 | 7.7E-01 | 7.7E-01
 | | | | 7.6E-01 | 7.6E-01 |
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| Expression
Signal | 1.01 | 2.43 | 4.78 | 3.95 | 2.36 | 2.48 | 1.76 | 3.2

 | 67.0
 | 2.32 | 1.27 | 1.42 | 6.33 | | 1.85
 | 2.8 | 0.8

 | 4,45 | 2.88 | 2.88 | 1.44 | 1.44 | 1.95
 | 2.8 | 6.14 | | 4.04 | 4.04 |
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ID NO: | | 26790 | | | | 28682 | | 22016

 | 24278
 | 25709 | 27399 | | 19932 | |
 | 22436 |

 | 23259 | 23979 | 23980 | 25386 | 25387 | 25630
 | 19932 | | | 25720 | 25721 |
 |
| Exon
SEQ ID
NO: | 14954 | 16601 | 17373 | | | | 10784 | 12114

 | 14491
 | 15607 | 17199 | 19623 | 10112 | | 10641
 | 12545 | 13234

 | 13464 | 14195 | 14195 | 15335 | 15335 | 15541
 | 10112 | 19004 | 9,61, | 12618 | 15618 |
 |
| , Probe
SEQ ID
NO: | 5084 | 6721 | 7504 | 7781 | 8372 | 8543 | 828 | 2229

 | 4603
 | 2698 | 7323 | 9424 | 138 | | 709
 | 2680 | 3313

 | 3549 | 4297 | 4297 | 5415 | 5415 | 5626
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Source 4 14954 1.001 7.9E-01 M29930.1 NT 4 14954 25790 2.43 7.9E-01 X90996.1 NT 4 17373 27582 4.78 7.9E-01 U01912.1 NT | SEQ ID NO: Signal Cap Hit Acession Cap Hit Acession Cap Hit Top Hit Acession Cap Hit Acession | Exon NO: ORF SEQ ID NO: Expression Signal NO: (Top) Hit Top Hit Acession Signal NO: Most Simal No: Top Hit Acession No: Top Hit Acessio | Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Top Hit Acession No. Top Hit Acession No. | Exon NO: ORF SEQ ID NO: Expression Signal Most Similar (Top) Hit Top Hit Acession Source No: Top Hit Acession No: Source Source No: Source Source No: No: Source No: <td>Exon NO: ORF SEQ ID NO: Expression Signal NO: Most Similar (Top) Hit Top Hit Acession Source No: Top Hit Acession No: Acession No: Source Source No: Source Source No: Source No:</td> <td>Exon NO: ORF SEQ ID ID NO: Expression Signal (Top) Hit Top Hit Acession No. Source Source No. Source No. Source <</td> <td>Exon NO: ORF SEQ ID ID NO: Expression Signal (Top) Hit Top Hit Acession No. Source Source No. Source No. Source No. Source No. Source No. No. No. Source No. No. No. No. No. No. No.<</td> <td>Exon NO: ORF SEQ ID ID NO: Expression Signal (Top) Hit Top Hit Acession No. Top Hit Acession</td> <td>Exon NO: ORF SEQ ID ID NO: Expression Signal Most Similar Top Hit Acession No. Source Source No. No. Source No. Source No. No.</td> <td>Exon NO: ORF SEQ ID NO: Expression Signal NO: Most Similar Top Hit Acession NO: Top Hit Acess</td> <td>Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Top Hit Acession No: Top Hit Acession No:</td> <td>Exon No: ORF SEQ ID NO: Expression Signal No: Most Similar Top Hit Acession No: Top Hit Acession Source Nature Top Hit Acession No: Top Hit Acession Source Nature Top Hit Acession No: Top Hit Acession Source Nature Top Hit Acession No: Top Hit Acession No: Top Hit Acession Source Source Top Hit Acession No: Top Hit Acession No: Top Hit Acession Source Top Hit Acession No: Top Hit Acession No: Top Hit Acession Source Top Hit Acession No: Top H</td> <td>Exon No: ORF SEQ ID NO: Expression Signal No: Most Similar Top Hit Acession No: Top Hit Acession No: Top Hit Acession Signal No: Most Similar Top Hit Acession No: Top Hit Acession Source No: Top Hit Acession No:<td>Exon No: ORF SEQ Bignal Expression (Top) Hit Top Hit Acession Signal Most Similar (Top) Hit Top Hit Acession Plabase No: Top Hit Acession Plabase Source Nature Source Source Source Plabase Source Plabase Source Source Nature Top Hit Acession Plabase Source Source Plabase Source Source Plabase Source Plabase Plabase Source Plabase Plaba</td><td>Exon
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Page 26 of 413 Table 4 Single Exon Probes Expressed in Heart

		7	Т	Т	T	Т	Т	Т	T	Т	Т	Т	7	Т	Т	\neg	\neg	$\overline{}$			_	_	Т	Т	Т	7	_	_	_	—
Single Extra Flobes Expressed in Heart	Top Hit Descriptor	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK	Mus musculus advilla (Advil-panding) mDNA	Mus musculus edvillin (Advilbendina), mana	Mus musculus cytochrome P450, 259, phencharbital Inducible three of Charles and Charles	MUSCARINIC ACETY CHOLINE RECEPTOR M2	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	H. aspersa mRNA for neurofilament NF70	H.aspersa mRNA for neurofilament NF70	Arabidopsis thaliana DNA chromosome 4, contid fragment No. 88	Homo sapiens mRNA for KIAA0895 protein nartial cals	Homo sapiens chromosome 21 segment HS2/C101	Homo saniens FRA38 common fracile paston disclaration to the series of t	C14203 Clontech human gorta noly4 + mRNA (#8572) Home control of the Cartest C	Homo sapiens fivorihetical profein FI. 140703 (FI. 140703) - DMA	Homo sapiens dentin sialophrenhometein measurem (Dobb)	Synechocystis sp. PCC8803 complete genome 9/27 1058487-1488888	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome	tn14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu	Homo sapiens mRNA for KIAA0534 profein nartial cde	Malva pusilla actin (Act1) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C046	601573026F1 NIH MGC 9 Homo seniens cDNA clone IMAGE: 3824474 F	Mus musculus complement component 1 inhibitor (CABA) MRNA	ta13h01.x1 NCI CGAP Lym5 Homo saniens cDNA clone IMAGE: 2042085.2	Borrelia burgdorferi (section 52 of 70) of the complete genome	Homo sepiens HT017 mRNA, complete cds	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b. mRNA	Mus musculus antigen (CD72) gene	Mus musculus anticen (CD72) gene
gie Exori Pior	Top Hit Database Source	IN	¥	Į.	NT	/ISSPROT	T	Į.	NT	Z	N FN	ΙN	Į.	T HUMAN				Þ	T HUMAN	Т	Ę	N	EST HUMAN		T HUMAN	Z	NT			Į.
	Top Hit Acessian No.	AF146793.2	6857752 NT	6857752 NT	6753577 NT	•	P30372						7.5E-01 AF020503.1		22672	4F163151.2	Γ	_		-	-	2	7.4E-01 BE747503.1	753217		7.3E-01 AE001166.1	1	5360211 NT	ľ l	
	Most Similar (Top) Hit BLAST E Value	7.6E-01		7.6E-01	7.6E-01	7.6E-01 P30372	7.6E-01 P30372	7.6E-01 X86347.1	7.6E-01 X86347.1	7.6E-01	7.6E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.4E-01 AI598146.	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.4E-01 AI472641.	7.3E-01	7.3E-01 AF225421		7.3E-01	7.3E-01 L35772.1
	Expression Signal	1.41	2.04	2.04	1.28	7.62	7.52	2.31	231	4.81	2.74	1.52	223	0.88	13.92	3.57	1.87	1.42	1.23	26.0	1.22	4.43	7.23	3.28	1.59	0.95	4.76	1.1	5.61	5.61
	ORF SEQ ID NO:	26770	26796	26797	27252	27414		28837	28838				20315	23040	19900		25209	25190	20869	22076	23366	23889	27328			24194	24277		26010	26011
	Exon SEQ ID NO:	16579	16606	16606		17215		_				10444	10508		10083	19042	19329	19368	11029	12177	13579	14111	17135	18828	18901	14408	14490	14994	15889	15889
	Probe SEQ ID NO:	6699	6726	6726	7184	7347	7347	8664	8664	8948	9073	502	569	3315	4573	9381	9828	9884	1114	2295	3665	4213	7258	9041	9150	4515	4602	5127	5984	5984

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Table 4
Single Exon Probes Expressed in Heart

1		Т	Т	T	Т	Т	7	Т	7	Τ-	Т	7		-	_	1		Т	$\overline{}$		7	-	т	-	-	_	_	~	-, -
	Top Hit Descriptor	V. alginolyticus sucrase (scrB) gene, complete cds	V. alginolyticus sucrase (scrB) gene. complete cds	225b08.s1 Sogres fetal liver spleen 1NFI S S1 Homo saniens CONA John INA CE 424770 21	225508.s1 Soares fetal liver spleen 1NFI S.S1 Homo saniens CDNA Advantil NA CE 424700 or	Rattus norvegicus initiation factor-2 kinase (elf-2a) mRNA complete edita	N. tabacum NelF-4A13 mRNA	Gallus gallus gene for melanocortin 2-receptor complete ods	Fowlpox virus, complete genome	Giardia Infestinalis variant-emerifin e urfone prodoin (com 447 c)	602035589F1 NCI CGAP Bring Hum sanians child class (MACE: 1492555	Linesenteroides gene for surrose abosabandase (FC > 4.4.7)	Homo sepiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete ods; and L-type calcium channel a>	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes.	complete cds; and L-type calcium channel a>	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds	Voz. i toso in i vin _wiseso namo sapiens oDNA clone IMAGE:4275381 5	Aeropyrum bernix genomic DNA section 6/7	Rana catesbelana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha	Homo saplens partial TCF-4 dene for T-cell transcription factor 4 months 45 46	Mus musculus otodelin (Otod), mRNA	Mus musculus otogelin (Otog) mRNA	602155438F1 NIH MGC 83 Home saniens cDNA clone IMAGE:4708344 F1	602155438F1 NIH MGC 83 Home saniens china china livia CE-4206344 E	Drosophile melanogaster 6-ovruvovltetrahydronterin synthese (hr) gang complete ed.	601496330F1 NIH MGC 70 Home seniens CDNA clone INA CE 3808405 ET	ZUOGh11.s1 Soares testis NHT Home saniens con a close IMA CE 724400 2	Homo sapiens mRNA for KIAA0614 protein, partial cyls	Homo saplens mRNA for KIAA0614 protein, partial cds
TO LINE OIG	Top Hit Database Source	Ē	된	EST HUMAN	EST HUMAN	Σ	N.	N-	뒫	5	EST HUMAN	Į.	NT		IN I	NI CCT LIMAN	NT NT	Ę	Ę	Z	¥		T HUMAN	EST HUMAN		7	EST HUMAN	Т	
	Top Hit Acesslan No.	7.3E-01 M26511.1	7.3E-01 M26511.1	7.3E-01 AA678019.1	7.3E-01 AA678019.1	7.2年-01 [29281.1	7.2E-01 X79140.1	7.2E-01 AB009605.1	7.2E-01 AF198100.1	7.2E-01 AF065606.1	7.2E-01 BF338350.1		7.2E-01 AF196779.1		7.2E-01 AF 1907 / 9.1	7.2E-01 AF230061.1	7.2E-01 U82623.1	7.2E-01 AP000063.1	7.1E-01 D21070 1	AJ270777.1	7305360 NT	7305360 NT	7.1E-01 BF681034.1					7.0E-01 AB014514.1	7.0E-01 AB014514.1
	Most Similar (Top) Hit BLAST E Value	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.25-01	7.2E-01	7.2至-01	7.2E-01	7.2E-01	7.25-01	7.2E-01	7.2E-01	i i	7.25.04	7.25-01	7.2E-01	7.2E-01	7.15-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.0E-01	7.0E-01
	Expression Signal	7.42	7.42	3.29	3.29	2.54	3.68	1.46	1.16	2.14	1.31	2.41	1.16	4	2 5	2000	4.78	4.08	10.38	10.8	2.93	2.93	1.56	1.56	6.97	2.25	1.61	1.04	1.04
	ORF SEQ ID NO:				28871		21687	22186	22748	23124	23494	24335	24706	70776	26004	28011	28256		20431	22745	23793	23794	25625	25626	26162	27746		20966	20967
	Exon SEQ ID NO:			_		Ì	11809		12956		13707	14546	14934	14034	16801	17772	18009	19160	10610	12952	14014	14014	15538	15538	16022	17519	19550	11118	11118
	Probe SEQ ID NO:	6454	6454	8729	8729	814	1914	2412	3028	3406	3795	4660	5064	5064	6023	7922	8121	9570	677	3024	4114	4114	5623	5623	6149	7669	9363	1209	1209

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Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element; | yz73e07.s1 Soares_muliple_sclerosis_ZNbHMSP Homo saplens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element: | Homo sapiens chromosome 21 segment HS24C404 | Escherichia coli K-12 MG1655 section 143 of 400 of the complete assessment | AV763842 MDS Homo sapiens cDNA clane MDSCHE04 5 | AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5 | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial ods | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
 | In 28a09 ST NCI CIGAP Gaed Homo caniens and Alexa 1146 OF Joses 220 St | Chlamydia muridanim, section 3 of 85 of the complete concess | Mus musculus mRNA for immunoalchulin damma hasay chair waichlo | Arabidopsis theliana DNA chromosome 4 contra frament N. ep. | Arabidopsis thaliana DNA chromosome 4 contin fragment No. 60 | Homo saplens DAN gene, complete cds | Homo saplens DAN gene, complete cds
 | FORKHEAD BOX PROTEIN CZ (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK
HEAD PROTEIN 1) (MEH-1 PROTEIN) (TPANSCEIDTION EACTOR FIG. 1.3) | Glardia intestinalis carbamate kinase dene, complete ods | Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470 | aj 5a05.s1 Scares_parathyroid_tumor_NbHPA Homo saplens cDNA clone IMAGE:1402256.3' similar to ab.X56411 mat ALCOHO! DEHYDROGENASE CLASS II DI CLAMA (LILIAAN). | Rat(hooded) prolactin gene : exon iii and flanks

 | Homo saplens hevin (HEVIN) mRNA | Homo sapiens mRNA for KIAA1345 protein, partial cds | Stagonospora avenae bol1 gene for beta-glurosidase, exms 1.4 | Stagonospora avenae bgl1 gene for beta-cilicosidase, exms 1.4 | Mus musculus zinc finger protein (Pea3) mRNA complete cals | Mus musculus zinc finger protein (Peg3) mRNA, complete cis
 | Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds |
| Top Hit
Database
Source | EST_HUMAN | EST HUMAN | Ί. | L | EST_HUMAN | EST_HUMAN | Į | FN
 | | | NT | Į. | NT. | LN | N
N
 | SWISSPROT | ¥ | Ę | EST HUMAN | N

 | Z | N- | LN L | N- | ٦ | NT.
 | ĻΝ |
| Top Hit Acession
No. | N62412.1 | N62412.1 | AL163301.2 | AE000253.1 | AV763842.1 | AV763842.1 | U69674.1 | U69674.1
 | AA593530.1 | AE002271.2 | Y17373.1 | AL161573.2 | AL161573.2 | |
 | | | | 5.1 |

 | 4758521 | 5.1 | 5.1 | 2 | |
 | |
| Most Similar
(Top) Hit
BLAST E
Value | 7.0E-01 | 7.0E-01 | 7.0E-01 | 7.0E-01 | 7.0E-01 | 7.0E-01 | 6.9E-01 | 6.9E-01
 | 6.9E-01 | 6.9E-01 | 6.9E-01 | 6.9E-01 | 6.9E-01 | 6.9E-01 | 6.9E-01
 | 6.9E-01 | 6.8E-01 | 6.8E-01 | 6.8E-01 | 6.8E-01

 | 6.8E-01 | 6.8E-01 | 6.8E-01 | 6.8E-01 | 6.8E-01 | 6.8E-01
 | 6.8E-01 AF164151 |
| Expression
Signal | 1.4 | 1.4 | 1.95 | 8.1 | . 2 | 2 | 15.73 | 15.73
 | 2.21 | 1.63 | 0.85 | 2.73 | 2.73 | 3.56 | 3.56
 | 2.37 | 1.03 | 1.16 | 1.58 | 1.26

 | 0.83 | 1.52 | 2.34 | 2.34 | 2.59 | 2.59
 | 1.79 |
| ORF SEQ
ID NO: | 22/73 | 22174 | | | | | 20725 | 20726
 | 21049 | 22911 | 23117 | 26726 | 26727 | 28719 | 28720
 | | 20713 | | 21362 | 24153

 | 24420 | 27622 | 28566 | 28567 | 28593 | 28594
 | 28757 |
| Exon
SEQ ID
NO: | 12277 | 12277 | 14864 | 16759 | 18336 | 18336 | 10878 | 10878
 | 11196 | 13107 | 13316 | 16532 | 16532 | 18450 | 18450
 | 19543 | 10866 | 12506 | 11502 | 14363

 | 14634 | 17407 | 18311 | 18311 | 18331 | 18331
 | 18485 |
| Probe
SEQ ID
NO: | 2399 | 2399 | 4989 | 6880 | 8463 | 8483 | 954 | 954
 | 1288 | 3182 | 3399 | 6652 | 6652 | 8682 | 8582
 | 9016 | 941 | 2639 | 2799 | 4469

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Page 29 of 413 Table 4 Single Exon Probes Expressed in Heart

		(NFKB1) gene, complete	(NFKB1) gene, complete	786310 3' similar to	gene, complete cds,	rely spliced					. !						II EIN GPI1	and the second	iplete cas i), transmembrane domain		ry haemochromatosis	Hele cas					
Single Exult Plobes Expressed in Heart	Top Hit Descriptor	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Homo sepiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;	Drosophila melanogaster Mst85C gene, complete cds; NMDMC Isoform (Nmdmo) gene, complete cds, alternatively sniliced; and transcription feeter (Dalah)	Mus musculus Wiskott-Aldrich syndrome protein (West) gene, complete das, alternativ	Stuberosum mRNA for alucose-6-phosphate dehinfronenses	xe95g12x1 NCI CGAP Co17 Homo septens CDNA clone IMAGE: 7874508 21	Dendrobium fimbriatum mRNA for phosphoenolovnivate carhovase partial	Helicobacter pylori, strain J99 section 47 of 132 of the complete general	Gallid herpesvirus 2. complete genome	Gallid herpesvirus 2, complete genome	Pseudomonas aerudinosa PA01 section 167 of 520 of the complete and	Helicobacter pviori, strain 199 section 47 of 132 of the complete genome	CM3-HT0769-010600-197-03 HT0769 Home confine only	N-ACETY GLUCOSAMINY -PHOSPHATION INOSITOL BIOSSAUTHER DESCRIPTION	Homo saciens St. 171 profein (St. 11.2) mDNA martial add.	Homo sapiens lens epithelium-derived growth factor gene alternativals existed	Homo sepiens sema domain, seven thrombospondin repeats (type I and type I -like), transmembrane domain (TM) and short extensing domain (sexumbosis) to (CEANARA).	Cabicans random DNA marker 282bn	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene. RoRet gene, and sodium phospheta brancher hubran.	Mus musculus kinesin light chain 2 (Kh2) mRNA	AV660506 GLC Home sepiens cDNA clane Cl CGID04 3	Homo sapiens chromosome 21 segment HS21C078	Vibrio cholerae chromosome II. section 39 of 93 of the complete chromosome	H. vulgaris Na.K-ATPase alpha subunit mRNA complete Ale	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
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16985 27176 1.75 .6.1E-01 11431065 NT 17286 27492 19.47 8.1E-01 AF236117.1 NT 17286 27493 19.47 6.1E-01 AF236117.1 NT	7108	16985	27175	1.75	6.1E-01	11431065		Homo sapiens mitogen-activated protein kinase kinase kinase kinase (MAPAKA) mRNA
17286 27493 19.47 6.1E-01 AF236117.1 NT 17286 27493 19.47 6.1E-01 AF236117.1 NT	7108	16985	27176	1.75	. 6.1E-01	11431065		Homo saplens mitogen-activated protein kinase kinase kinase kinase 4 (MAPAKA) mRNA
17286 27493 19.47 6.1E-01 AF236117.1 NT	7419	17286	27492	19.47	6.1E-01	1		Homo saplens G-protein coupled receptor EDG-7 mRNA, complete cds
	/419	17286	27493	19.47	6.1E-01	-		Homo saplens G-protein coupled receptor EDG-7 mRNA, complete cds

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Table 4
Single Exon Probes Expressed ir

	Top Hit Descriptor	A3) dane, complete cds	ratein, complete cds	lex 3. mu 2 subunit (CI A20) mRNA	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene complete cds	G, Nv, L genes, French strain 07-71		UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 31	Musca domestica insecticide-susceptible strain vnitane-sensitiva entirma parameter and Anna Anna Anna Anna Anna Anna Anna	main onty 1 protein even 4			Homo sepiens genes for leukotriene B4 recentor RI T2 leukortriene R4 recentor BI T4 seminate au		19 kD isoform	19 kD isoform	cDNA clone IMAGE-2095621 3'	ed 2)-like 3 (NFF21 3) mRNA	sterase (Pde3e) mRNA	no sapiens cDNA	3 of the complete genome	21C067	(2/C067	spo	Homo seniens fow density linanoratein recentur, colothad assets II /I DOM	or reserved protect in (Later 2) gene, exon 1 and partial cds	no sapiens cDNA	(Cd48) mene partial cds	Ilbha 1 AT) gana promoter region	-phosphate decarbowless complete and	MICROTUBULE-ASSOCIATED PROTEIN 14 ICONTAINS: MAPA 1 (GHT CHAIN I CO	יין ביין וביין וביין ביין ביין ביין ביין
Single Exon Probes Expressed in Heart		Homo saciens dopamine transporter (SLC6A3) gane, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens adaptor-related protein complex 3. mu 2 subunit (Cl A20) mRNA	Human respiratory syncytial virus strain Cl	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71	D(2) DOPAMINE RECEPTOR	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_S	Musca domestica insecticide-susceptible s	Homo sapiens partial LMO1 gene for LIM domain onty 1 protein exms 1	SEGMENTATION PROTEIN FUSHI TARAZU	SEGMENTATION PROTEIN FUSHI TARAZU	Homo sapiens genes for leukotriene B4 rek	PEROXISOMAL MEMBRANE PROTEIN PERS (PEROXIN-3)	Gallus gallus mRNA for Hyperion protein. 419 kD Isoform	Gallus gallus mRNA for Hyperion protein, 419 kD isoform	#08f07.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE 20185621 3	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NEE213) mRNA	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a) mRNA	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA	Haemophilus influenzae Rd section 16 of 163 of the complete genome	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C067	Rattus norvegicus cenexin 2 mRNA, partial cds	Homo sepiens low density linearstein re-	THYMIDYLATE KINASE (DTMP KINASE)	PM1-DT0041-190100-002-h03 DT0041 Homo saniens chNA	Mus spretus strain SPRET/FI CD48 antigen (Cd48) gene partial cds	Oryctolagus cuniculus alpha 1 anti-trvasin (alpha 1 AT) gene promoter region	Aspergillus oryzae pyrG gene for orolidine-5'-ohosphate decarboylase complete cds	MICROTUBULE-ASSOCIATED PROTEIN	SIM1 PROTEIN
gie Exon Pro	Top Hit Database Source	뒫	Σ	·	Ę	F	SWISSPROT	EST_HUMAN	Z	ĽŽ	SWISSPROT	SWISSPROT	F	SWISSPROT	TN	N FN	EST HUMAN	N.	Į.	EST HUMAN	Z	N N	NT	NT	ĪN	SWISSPROT	EST HUMAN	₽ FN	IN	N	SWISSPROT	SWISSPROT
	Top Hit Acession No.	AF119117.1	D87675.1	5802999 NT	6.0E-01 AF065253.1	AJ233396.1	20288	4W139713.1	J38813.1	4,777661.1		202835	6.0E-01 AB008193.1	201497	1,1131892.1	4J131892.1	6.0E-01 AI420623.1	11421663 NT	FN 8055303	3E157617.1	J32701.1	AL163267.2	NL163267.2	5.9E-01 AF162756.1	\F065440.2		4W937175.1	NF064626.1		5.9E-01 AB017705.1		40472
	Most Similar (Top) Hit BLAST E Value	6.1E-01 AF11911	6.0È-01 D87675.	6.0E-01	6.0E-01	6.0E-01 AJ23339	6.0E-01 P20288	6.0E-01 AW1397	6.0E-01 U38813.	6.0E-01 AJZ7766	6.0E-01	6.0E-01 P02835	6.0E-01	6.0E-01 Q01497	6.0E-01 AJ131892	6.0E-01 AJ13189;	6.0E-01	6.0E-01	6.0E-01	6.0E-01 BE15761	5.9E-01 U32701.1	5.9E-01 AL16326	5.9E-01 AL163267	5.9E-01	5.9E-01 AF065440	5.9E-01 Q9X013	5.9E-01 AW93717	5.9E-01 AF064626	5.9E-01 L42320.1	5.9E-01	5.9E-01	5.8E-01 P40472
	Expression Signal	1.59	0.92	264	1.76	1.02	1.56	2.58	261	6.2	4.19	4.19	1.69	1.43	1.78	1.78	2.74	1.64	2.1	2.18	1.25	4.85	4.85	4.12	21	2.67	3.1	236	1.91	2.18	4.15	1.44
	ORF SEQ ID NO:		20243				24918	25086		26375	26794	26795	27727		28541	28542			25065		20752	22954	22955		25917	28203	28454	28669	25342			21637
	Exon SEQ ID NO:	17628	10429	10490	11245	13656	15151	15260	15845	16213	16605	16605	17503	17744	18286	18286	18651	19115	19554	19484	10907	13156	13156	14029	15795	17952	18205	18401	18908	19057	19193	11763
	Probe SEQ ID NO:	7778	486	549	1339	3744	5227	5339	5940	6350	6725	6725	7653	7894	8411	8411	8838	9500	9787	6086	984	3232	3232	4129	5889	8061	8328	8529	9165	9404	9614	1867

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Single Exon Probes Expressed in Heart

							The second of th
Probe SEQ (D NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3902					5.8E-01 BF695738.1	EST HUMAN	601852474F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE-A076134 F
4413	- 1	24090	2.81	5.8E-01	5.8E-01 AB009077.1	N	Vigna radiata mRNA for proton bytophosphatase complete cole
4690			1.04		5.8E-01 AF110846.1	Z	Medasella scalaris sev-letha homeline (Meney) gang partiel and element
6753		25768	1.29		5.8E-01 D78659.1	EST HUMAN	HUM500E068 Human placenta poly4+ (Telliwers) Home sonions o'DNA state CEN grants and
6077	16060		2.3		5.8E-01 Se5091.1	Z	cyclic AMP-regulated phosphoprotein frats, mRNA, 1030 nfl
6604			2.62	5.8E-01	5.8E-01 H41571.1	EST HUMAN	yn91b03.s1 Soares adult brain N2b5HB557 Homo sapiens cDNA clone IMAGE:175757 3' similar to ob:578187 M-PHASE INDI ICER PHASEDIATAGE 3' similar to
6764	16643	26830	2.23	5.8E-01	5.8E-01 P14328	SWISSPROT	SPORE COAT PROTEIN Spor
6764			2.23	5.8E-01	5.8E-01 P14328	SWISSPROT	SPORE COAT PROTEIN SPOR
7153			8.64	5.8E-01	5.8E-01 AJ270774.1	F	Homo sapiens partial TCF-4 dene for T-cell transcription forther 4
8358	ı	28483	8.47	5.8E-01	5.8E-01 AJ243213.1	뉟	Homo saplens partial 5-HT4 recentor nene exerce 2 to 8
8396			3.23	5.8E-01	5.8E-01 BF700092.1	EST HUMAN	602127577F1 NIH MGC 56 Homo samians cDNA clans IMA OE 4264425 F1
8482			1.78	5.8E-01	5.8E-01 BF700092.1	EST HUMAN	602127577F1 NIH MGC 56 Homo saniens CDNA clone IMAGE 4284403 5
3186	13111	22915	1.48	5.7E-01	5.7E-01 Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO14)
3460	13376		2.43	5.7E-01	5.7E-01 AB033503.1	IN	Pobulus eurameticana reace. 2 mRNA for 4 aminomalonesses
3829	13741	23533	1.65	6.7E-01	6.7E-01 AF011581.1	IN.	Homo sapiens T cell receptor beta chain (BV6S7*2-B 14S4) mBNA metal care
5201	15064	24827	2.24	5.7E-01	5.7E-01 U78517.1	L L	Rettus norveolous cAMP-remigrated missing anniholation and consequences.
5836		25854	3.72	5.7E-01	2	EST HUMAN	60/45/962F1 NIH MGC 66 Home seniors child April 1870 F-25 F-25 F-35 F-35 F-35 F-35 F-35 F-35 F-35 F-3
6100	15110	24874	1.41	5.7E-01		Į.	Botyds cheres strain T4 cDNA library under conditions of although the conditions of all the conditions o
6564		26603	212	5.7E-01 P00373		SWISSPROT	PYROLINE-5-CARBOXYLATE REDI (CTASE (PSCR) (PSC BEDI (CTASE)
9124			1.68	5.7E-01	5.7E-01 BE715051.1	EST HUMAN	MR3-HT0736-180700-003-a02 HT0736 Homo saniens citala
3318	_	23043	1.21	5.6E-01	33.2	N.	Homo sapiens mRNA for KIAA0740 protein, partial cds
3318	-1	23044	1.21	5.6E-01	3.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3808		23509	0.83	5.6E-01	12	NT	Arabidopsis thaliana DNA chromosome 4, contin fragment No. 13
4146	\perp	23818	0.83	5.6E-01		N.	Chicken TBP gene, exon8, complete cds
711		27180	4.18	5.6E-01		EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 F
7411		27181	4.16	5.6E-01	Γ	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSEns 5'
9023	18817		2.46	5.6E-01		Π	601514007F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE:3015457 F
9137	18893	28794	1 73	נטעני	5 6E 01 0 0 0 0 5 5 5 4		ng75g10.s1 NCI_CGAP_Pr6 Homo saplens cDNA clone IMAGE:940674 similar to contains element PTR7
9524	L		1 35	E GE OF DECENE	3	J.	representation
9919		-	00 6	A 6E 04	5	T	AND THE REPORT OF THE POLY SECTION IN THE PROPERTY OF THE POLY SECTION IN THE POLY SEC
			1	1 1 2 3 1 1	1	LO LICONIAIN	ovz132029F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4271334 5'

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Table 4
Single Exon Probes Expressed in Heart

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onigio Exore i lobos Expressed III lleall	Top Hit Descriptor	Rattus norvegicus Propionyl Coenzyme A carboxylase heta notymentide (Broth) Bhila	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P36; NUCLEOPROTEIN P10]	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30: NI ICI EODBOTEIN P40:	Homo sanians streetiller viralicidir articity 2 (6 constitution)	volt8a10.s1 Spares adult hrain NOAFHRESV Home continue CRIV.	Rabbit oral papillomavirus, complete negoties appreis active clone (MAGE:1782663)	FOS-RELATED ANTIGEN-1	Homo sapiens KIAA0929 protein Msz2 interacting nuclear farnet (MilNT) homology (KIAA0929)	Homo sapiens KIAA0929 protein Msx2 interacting nuclear terract (Minut) pages 1 (2000)	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds: and unknown genes	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes,	OV4-NN0040-070400-160-04 NN0040 Uses	Chlemydophila nnei monise AB30 south 74.504.54	Drosobila melammaster mRNA for 15 15, bets complete genome	602076545F1 NIH MGC 62 Homo sanians china MAA CE 2222500 E1	NITRATE REDUCTASE INADPHT/NR\	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) WEBDOSIN LIFAXOS CHAIN	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)	wB7g04x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);	Homo sepiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B	(bi), and complement component C2 (C2) genes;>	Pressiva detacea var. capitata prosprioripase DZ (PLDZ) gene, complete ods Ressira olement var continta al en el	Diagona diciance val deputate prosprintipase U2 (PLU2) gene, complete cds.	Homo saniens protein tyrosine phoesphotoms (coepior-type, zeta polypeptide 1 (PTPRZ1) mRNA	Homo sepiens secreted C-type lectin precursor (LSLCL) gene, complete cds	
מומעיים מופ	Top Hit Database Source	N F	SWISSPROT	SWISSPROT	5902085 NT	EST HUMAN	NT	SWISSPROT	Į.	IN	NT IN	F	EST HUMAN	LN	Z	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	Ė	LV	Į.	Į.			
,	Top Hit Acession No.	8393912 NT	i	į .		H46219	6.5E-01 AF227240.1	5.5E-01 P48755	7657266 NT	7657268 NT	6.4E-01 AF232006.1			Γ	Γ		Γ	Q60675	Q60675	5.4E-01 AI858398.1		5.3F-01 AF113010 1		6328	4506328 NT	5.3E-01 AF087658.1	
	Most Similar (Top) Hit BLAST E Value	5.5E-01	5.5E-01 P03341	5.5E-01 P03341	5.5E-01	5.5E-01	6.5E-01	5.5E-01	6.4E-01	5.4E-01	6.4E-01	5.4E-01	5.4E-01	5.4E-01	5.4E-01	5.4E-01	5.4E-01 P36858	5.4E-01	5.4E-01	5.4E-01	요 3도 01	53501	5.3E-01	5.35-01	5.3E-01	5.3E-01	
	Expression Signal	1.09	2.88	2.88	1.34	1.39	3.1	1.29	3.74	3.74	2.61	261	2.24	2.78	2.23	2.01	2.87	4.51	4.51	2.12	200	0.91	0.91	8.24	8.24	292	
	ORF SEQ ID NO:	20949	22423	22424			22926	23335	19933	19834	20316	20317	21006		21998		28557	28996	28997		20260	21877	21878	22508	22509	22931	
	Exon SEQ ID NO:	11103	12533	12533	12815	12955		13548	10113	10113	10509	10509	11157	11949	12095	17588	18301	18702	18702	18862	10447	11982	11982	12617	12617	13129	
	Probe SEQ ID NO:	1193	2668	2668	2888	3027	3196	3634	139	139	570	270	1250	2059	2208	7738	8427	8892	8892	9087	505	2083	2093	2755	2755	3205	

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Table 4
Single Exon Probes Expressed in Heart

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and the control of th	Тар Hit Descriptar	Mycoplasma denitalium section 9 of 51 of the complete account.	242h12.v5 Soares ovary fumor NhHOT Home spalene - DNA NA SE-2	242h12 v5 Series over timor NHOT Home conjune DNA 11.	7e73c12.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE (SOMERASE PREC) IRSOR (HI IMAN)	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA done MAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECI IRSONA done MAGE:3288118 3' similar to gb:J02783	Roridula gorganias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast modified	601339867F1 NIH MGC 53 Homo seniens cDNA clare IMACE seconds 5:	og30e05.s1 NCI_CGAP_Br7 Home sapiens cDNA clone IMAGE:1441376 3' similar to gb;J02811 APOI POPROTFIN D PRECI PSOD ALI IMAAN.	Drosophila melanogaster helix-loop-helix mRNA complete cds	NUCLEAR FACTOR OF ACTIVATED T CELLES, STIPPED COMMING TRANSCRIPTION FACTOR NFATS) (NF-ATS)	Homo saplens phospholinid commission of a comm	Homo sabjens chromosome 21 section USACOS	Homo saplens mBNA for KTA A0740 Profess	Chlamydobhlia abadins strain S7813 BOMBOA - La BOLLBOA	Azotobacter vinelandii ind gene for incaitate della Polyired A precursor, genes, complete eds	Botrylis cineras strain T4 cONA library mode.	am77g05.s1 Stratagene schizo brain S11 Homo serviers CONA Acres MAACE Agents	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3)	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	with minescales variation receptor-like protein 1 (Vrl1), mRNA	nomo sapiens PELO IA (PELO TA) gene, complete cds	OFFEDINGLE ACTOR RECEPTION CANAMA (PAR CANAMA) (PETRICICA ACTOR CANAMA) (PETRICICA ACTOR CANAMA) (PAR CANAMA) (PETRICICA ACTOR CANAMA)	DELTA)	Human adrenodoxin reductase gene, exons 3 to 12	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
101 1 10V 0:6	Top Hit Database Source	Z	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	ļ L	EST HUMAN	EST HUMAN	M	SWISSPROT	LN	Ę	Ę	Į.	Z		T HUMAN					T LI IRAANI	1	SWISSPROT	F	E E
	Top Hit Acessian No.	5.3E-01 U39687.1	5.3E-01 AI820921.1	5.3E-01 AI820921.1	5.3E-01 BE645620.1	5.3E-01 BE645620.1	5.3E-01 L01950.2	5.3E-01 BE566291.1	5.3E-01 AA916053.1		оелмес	6.2E-01 AF224492.1	AL 163285.2	5.2E-01 AB018283.2	T		-	-	5.2E-01 AF020269.1		1108444	2	4 2	T			-
	Most Similar (Top) Hit BLAST E Value	5.3E-01	5.3E-01	6.3E-01	5.3E-01	5.3E-01	5.3E-01	5.3E-01	5.3E-01	5.2E-01 L20770.1	5.2E-01 Q9WV30	6年01/	5.2E-01	5.2E-01	5.2E-01 U65942.1	5.2E-01 D73443.1	5.2E-01/	5.2E-01/	5.2E-01	1	5.25-01 0826/1.2	5 2F-04 AE443052	5 2F-01 A		5.2E-01 P18516	5.1E-01 M58509.1	5.1E-01 AJ233944
	Expression Signal	1.29	1.75	1.75	1.91	1.91	2.15	5.62	2.46	11.31	7.69	2.83	5.04	2.75	1.9	1.22	1.76	1.9	1.13		2 2	1 28	246		3.43	1.89	3.28
	ORF SEQ ID NO:		25098		25447	25448		28946		20568	20904	20930		21886	22798			23114		23287	10707	27837	25221			20347	20381
	တ	_]		15270	15387	15387	17038	18658	19551	10728	11061	11086	11739	11988	13008	13124	13278	13314	13494	1340R	14826	17611	19260		19370	10537	10569
	Probe SEQ ID NO:	4117	5350	5350	5467	5467	7161	8846	9015	799	1148	1174	1843	2099	3081	3199	3359	3397	3580	3582	4949	7761	9719		9887	g .	632

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Table 4
Single Exon Probes Expressed in Heart

		T	T			T	T	Ī	T	T	ment.		T	2	es,		gu	 Š				T	Ж		<u>—</u>					T
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Polyangium vitellinum (strain Pl vt1) 16S rRNA gane	R.novedicus mRNA for mammalian fusca protein	602139319F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE-4208417 F	w83b12.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE-2427283 3	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	yi94a09.s1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:146872.3	Human regenerating protein (reg) gene, complete cds	65B1 Human retina cDNA Tsp5091-deaved sublibrary Homo saniens cDNA mot Aircutional	601556863F1 NIH MGC 58 Homo saplens cDNA clone IMAGE:3826767 5	nac51f10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element. TAR1 repetitive element:	Homo saplens postmeiofic sentenation increased 2, like 9 (PMS2) of mBNA	Homo saplens postmeiotic segregation increased 2-like 9 (PMS-19), mRNA	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL DNA biosvorthesis initiation	protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gldA) genes,	complete cos; and termination factor Rho (rho) gene>	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA). ATP operan (athCDGAHEE) and priteins chromosome containing.	complete ods; and termination factor Rho (rho) genes	Mus musculus anti-DNA immunoglobulin light chain low mRNA antibody 3835, 138 partial add	Homo sapiens mRNA for KIAA1184 protein, partial cds	Xenopus laavis smooth muscle beta-tropomyosin mRNA, complete cds	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 57	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN & ALDHA D. CHILOGEDASES)	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4ALPHA-	GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,8-GLUCOSIDASE (DEXTRIN 6-41 PHA-D-GLUCOSIDASE)	601445024F1 NIH MGC 65 Homo satiens cDNA clone IMAGE 3840438 F	Oryzias latibes gene for membrane quanylyl cyclase OIGC1 complete cds	Mus musculus MRC OX-2 antigen homolog gene expres 2-5 and complete ede	Homo saplens chromosome 21 segment HS21C102	NUCLEAR ENVELOPE PROTEIN CUT11
Jie Exon Prob	Top Hit Database Source	N-	NT.	EST HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	F	EST HUMAN	EST_HUMAN		¥				Z		둗			닏	EST_HUMAN	TORGESIME		SWISSPROT	T	Į.	1	Ę	SWISSPROT
ŽIIS	Top Hit Acessian No.	5.1E-01 AJ233944.1		7.					5.1E-01 W22302.1	5.1E-01 BF030207.1	5.1E-01 BF439882.1	4885552 NT	488552 NT		F OF ON A COROSTO 4			1.1		-		5.0E-01 BF317212.1				İ			02.2	
	Most Similar (Top) Hit BLAST E Value	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.1E-01 P96380	5.1E-01	5.1E-01 J05412.1	5.1E-01	5.1E-01	5.1E-01	5.0E-01	5.0E-01		מים מים	9.05-01,		5.0E-01	5.0E-01 U55574.1	5.0E-01	5.0E-01 M92304.1	5.0E-01	6.0E-01 P35573		5.0E-01 P35573	5.0E-01	5.0E-01 A	5.0E-01	5.0E-01	5.0E-01 013961
	Expression Signal	3.28	1.06	1.44	3.84	2.86	1.57	4.54	3.57	3.62	2.03	1.37	1.37		4 22	26.1		1.32	0.84	3.44	5.62	3.61	2.26		2.25	1.27	. 9.32	2.26	2.02	2.94
	ORF SEQ ID NO:	20382			23667			27650	27653			21871	21872		21882	70017		21883	23388	23495		26644	27614		27615		29099			
	Exon SEQ ID NO:	10569	11536	11870	13891	13994	15980	17435	17437	19478	19100	11977	11977		11986	3		11986	13601	13709	16839	16455	17401		17401	17791	18806	18913	19349	19358
	Probe SEQ ID NO:	632	1632	1977	3984	4094	6133	7584	7586	9230	9473	2087	2087		2097			2097	3688	3797	6961	7442	7550		7550	7941	9003	9170	9828	9869

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	EQ Expression (Top) Hit Acession Signal BLAST E No. Source Source	1.98 4.9E-01 BF571462.1 EST HUMAN 602076649F1 NIH MGC 62 Homo seriens cDNA clone IMA CE 2.1 A343860 F1	1.39 4.9E-01 U40869.1 NT	2.46 4.9E-01 AF020931.1 NT	2.46 4.9E-01 AF020931.1 NT	1.76 4.9E-01 AB040051.1 NT	.1 EST HUMAN	16863 NT		EST HUMAN		Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for melotic recombination, complete	AA659878.1 FST HIMAN	4.8E-01 5031650 NT	3.82 4.8E-01 AL161492.2 NT	3.82 4.8E-01 AL161492.2 NT	1.16 4.8E-01 A1820744 1 EST HIMAN	2.04 4.8E-01 X83502.1 NT	1.1 N.1	2.26 4.8E-01 BE790632.1 EST HUMAN	8.36 4.7E-01 BF217173.1 EST_HUMAN	5.77 4.7E-01 AF102673.1 NT	2.06 4.7E-01 U41069.1 NT	2.43 4.7E-01 AW889448.1 EST HUMAN	1.36 4.7E-01 AW341561.1 EST HUMAN	1.2/ 4.6E-01 AW818638.1 EST HUMAN	4 28 4.0E-01 Breeds300.1 EST HUMAN	0.97 4.6F-04 M44287 4 NT	3.38 4.6E-01 090643	3.38 4.6E-01 Q90643 SWISSPROT	1.78 4.6E-01 BE734781.1 EST_HUMAN
							L																								
	ORF SEQ ID NO:	702 20541	760 21634	388 25688	388 25689	67 26429	174	89.	46	.33	36	00 25153	22	93	21 26601		93 26679		11		30 25953			28832			07 23384		80 25111		23 25372
	Probe Exon SEQ ID SEQ ID NO: NO:	772 10702		5679 15588		1		7359 19768		9851 19733	4577 14136	5381 15300	6018 15922	6330 16193		6563 16421	6613 16493	8111 18001					9692 49570		3674 42509		L	1_		\coprod	5404 15323

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Table 4
Single Exon Probes Expressed in

Probe No. 10. Exam Sec ID No. 10. CMPS SEQ ID Septembrane No. 10. Top Hit No. 10. Top Hit No. 10. Top Hit Securo AcE-OI ALASTER. Top Hit No. 10. Top Hit Securo AcE-OI ALASTER. Top Hit AcE-OI ALASTER. Top Hit Securo AcE-OI ALASTER. Top Hit AcE-OI ALASTER.						5	מום ביעסון ג וסי	Single Exon Probes Expressed in Heart
15334 25384 3.29 4.6E-01 AIZ47679.1 EST_HUMAN 15334 25385 3.29 4.6E-01 AIZ47679.1 EST_HUMAN 16339 25393 1.58 4.6E-01 P20050 SWISSPROT 16040 26181 1.47 4.6E-01 D62332.1 NT 16040 26182 1.47 4.6E-01 D62332.1 NT 17230 27430 28.48 4.6E-01 D62332.1 NT 17580 27431 26.48 4.6E-01 D62332.1 NT 17580 27431 26.48 4.6E-01 AF6202 SWISSPROT 17580 27803 1.33 4.6E-01 AF16534.1 EST_HUMAN 18245 28495 4.78 4.6E-01 AF16534.1 EST_HUMAN 17916 28160 5.45 4.6E-01 AF16369.1 NT 17916 28161 5.45 4.6E-01 AF16369.1 NT 11765 21640 1.73 4.6E-01 AF16369.1 NT 11765 21640 1.73 4.6E-01 AF16669.1 NT <t< td=""><td>Probe SEQ ID NO:</td><td>Exan SEQ ID NO:</td><td>ORF SEQ ID NO:</td><td>Expression Signal</td><td>Most Similar (Top) Hit BLAST E Vatue</td><td>Top Hit Acesslan No.</td><td></td><td>Top Hit Descriptor</td></t<>	Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acesslan No.		Top Hit Descriptor
15334 25385 3.29 4.6E-01 Al247679.1 EST_HUMAN 15339 25393 1.58 4.6E-01 P200500 SWISSPROT 16040 25181 1.47 4.6E-01 U62332.1 NT 16040 25182 1.47 4.6E-01 BF6232.1 NT 16722 25916 13.48 4.6E-01 BF6232.1 NT 17230 27431 26.48 4.6E-01 P55202 SWISSPROT 17580 27802 1.33 4.6E-01 P55202 SWISSPROT 17580 27803 1.33 4.6E-01 P55202 SWISSPROT 18245 28496 4.6E-01 P6816334.1 EST_HUMAN 18245 28496 4.6E-01 P6816334.1 EST_HUMAN 18245 28496 4.6E-01 P6816334.1 EST_HUMAN 18245 28496 4.6E-01 AF019369.1 NT 19005 1.43 4.6E-01 AF019369.1 NT 19006	5414	15334	25384	3.29	4.6E-01	AI247679.	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN.;
15339 25393 1.58 4.6E-01 P20050 SWISSPROT 16040 26181 1.47 4.6E-01 U62332.1 NT 16722 26916 1.47 4.6E-01 U62332.1 NT 16722 26916 13.48 4.6E-01 BF627389.1 EST_HUMAN 17230 27430 26.48 4.6E-01 P55202 SWISSPROT 17580 27802 1.33 4.6E-01 P55202 SWISSPROT 17580 27803 1.33 4.6E-01 P55202 SWISSPROT 17581 27803 1.33 4.6E-01 P55202 SWISSPROT 17580 27803 4.78 4.6E-01 P55202 SWISSPROT 18245 28495 4.78 4.6E-01 P65202 SWISSPROT 18245 28495 4.78 4.6E-01 P6716369.1 NT 17915 28161 5.45 4.6E-01 P6716369.1 NT 17916 28161 1.43 4.6E-01 </td <td>5414</td> <td>15334</td> <td>25385</td> <td>3.29</td> <td>4.6E-01</td> <td>AI247679.1</td> <td>EST HUMAN</td> <td>qh59h02.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 ВUTYROPHILIN :</td>	5414	15334	25385	3.29	4.6E-01	AI247679.1	EST HUMAN	qh59h02.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 ВUTYROPHILIN :
16040 Z6181 1.47 4.6E-01 U62332.1 NT 16040 26182 1.47 4.6E-01 U62332.1 NT 16722 26916 13.48 4.6E-01 BF687399.1 EST_HUMAN 17230 27430 26.48 4.6E-01 P55202 SWISSPROT 17230 27802 1.33 4.6E-01 AB15634.1 EST_HUMAN 17580 27803 1.33 4.6E-01 AB15634.1 EST_HUMAN 18245 28495 4.78 4.6E-01 BE185449.1 EST_HUMAN 18245 28495 4.78 4.6E-01 BE185449.1 EST_HUMAN 18245 28496 4.78 4.6E-01 BE185449.1 EST_HUMAN 17915 28496 4.78 4.6E-01 AF018369.1 NT 17916 28496 4.78 4.6E-01 AF018369.1 NT 17916 28496 4.78 4.6E-01 AF018369.1 NT 17716 28496 4.6E-01	5418	15339	25393	1.58	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
16040 26182 1.47 4.6E-01 U62332.1 NT 16722 26916 13.48 4.6E-01 BF697399.1 EST_HUMAN 17230 27430 26.48 4.6E-01 P55202 SWISSPROT 17580 27802 1.33 4.6E-01 APF5202 SWISSPROT 17580 27803 1.33 4.6E-01 APF5202 SWISSPROT 17580 27803 1.33 4.6E-01 APF5202 SWISSPROT 18245 28496 4.78 4.6E-01 APF6491 EST_HUMAN 18245 28496 4.78 4.6E-01 APF018369.1 NT 17015 28160 5.45 4.6E-01 APF018369.1 NT 17015 28161 5.45 4.6E-01 APF018369.1 NT 17015 28161 5.45 4.6E-01 APF018369.1 NT 17765 27640 1.73 4.6E-01 APF01831.1 NT 17765 27640 1.73 4.6E-	6057	16040	26181	1.47	4.6E-01	U62332.1	Ā	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
16722 26916 13.48 4.6E-01 BF697399.1 EST_HUMAN 17230 27431 26.48 4.6E-01 P55202 SWISSPROT 17230 27431 26.48 4.6E-01 P55202 SWISSPROT 17580 27803 1.33 4.6E-01 AIP15634.1 EST_HUMAN 18245 28495 4.78 4.6E-01 BE185449.1 EST_HUMAN 18245 28496 4.78 4.6E-01 BE185449.1 EST_HUMAN 18245 28496 4.78 4.6E-01 AF019369.1 NT 17015 28161 5.45 4.6E-01 AF019369.1 NT 17015 28161 5.45 4.6E-01 AF019369.1 NT 17016 28161 4.6E-01 AF019369.1 NT 1775 2745 4.6E-01 AF019369.1 NT 1775 2746 4.6E-01 AF019369.1 NT 1776 27640 1.73 4.6E-01 AF019369.1 NT <td>6057</td> <td>16040</td> <td>26182</td> <td>1.47</td> <td>4.6E-01</td> <td>U62332.1</td> <td>Į.</td> <td>Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds</td>	6057	16040	26182	1.47	4.6E-01	U62332.1	Į.	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
17230 27430 26.48 4.6E-01 P55202 SWISSPROT 17230 27431 26.48 4.6E-01 P55202 SWISSPROT 17580 27803 1.33 4.6E-01 AI915634.1 EST_HUMAN 18236 28495 4.78 4.6E-01 AI915634.1 EST_HUMAN 18245 28496 4.78 4.6E-01 BE185449.1 EST_HUMAN 18245 28496 4.78 4.6E-01 BE185449.1 EST_HUMAN 17815 28161 5.45 4.6E-01 AF019369.1 NT 17815 28161 5.45 4.6E-01 AF019369.1 NT 19491 2.21 4.6E-01 AF019369.1 NT 1775 2.650 A.6E-01 AF019369.1 NT 1776 2.7630 A.6E-01 AF019369.1 NT 1776 2.7640 A.6E-01 AF019369.1 NT 1778 4.6E-01 AF019369.1 NT 1778 4.6E-01	6843	16722	26916	13.48	4.6E-01	BF697399.1	EST HUMAN	602130953F1 NIH MGC 56 Homo sanlens cDNA close MACE:4787858 5
17230 27431 26.48 4.6E-01 P55202 SWISSPROT 17580 27803 1.33 4.6E-01 AI915634.1 EST_HUMAN 18236 2.86 4.6E-01 AI915634.1 EST_HUMAN 18245 28495 4.78 4.6E-01 BE185449.1 EST_HUMAN 18245 28496 4.78 4.6E-01 BE185449.1 EST_HUMAN 17015 28161 5.45 4.6E-01 AF019369.1 NT 17015 28161 5.45 4.6E-01 AF019369.1 NT 17016 28161 5.45 4.6E-01 AF019369.1 NT 17005 1.73 4.6E-01 AF019369.1 NT 1776 27630 1.73 4.6E-01 AF019369.1 NT 1776 27630 1.73 4.6E-01 AF019369.1 NT 1776 27630 1.73 4.6E-01 AF019369.1 NT 1776 27558 4.6E-01 AF019369.1 NT	7363	17230	27430	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
17580 27802 1.33 4.6E-01 Al915634.1 EST HUMAN 17580 27803 1.33 4.6E-01 Al915634.1 EST HUMAN 18245 28495 4.78 4.6E-01 BE165449.1 EST HUMAN 18245 28496 4.78 4.6E-01 BE165449.1 EST HUMAN 17915 28160 6.45 4.6E-01 AF018369.1 NT 17915 28161 5.45 4.6E-01 AF018369.1 NT 17915 28161 5.45 4.6E-01 AF018369.1 NT 17915 28161 5.45 4.6E-01 AF018369.1 NT 11765 27639 1.73 4.6E-01 AF018369.1 NT 11765 27640 1.73 4.6E-01 AF01831.1 NT 12769 2258 4.87 4.6E-01 AF01831.1 NT 13796 2258 4.87 4.6E-01 AF01831.1 NT 13850 1.73 4.6E-01 AF01831.1 NT 1386 2258 4.87 4.6E-01 AF01831.1 SWISSPROT 1386	7363	17230	27431	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NÁTRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
17580 27803 1.33 4.6E-01 Al915634.1 EST HUMAN 18236 2.86 4.6E-01 P98163 SWISSPROT 18245 28495 4.78 4.6E-01 BE18549:1 EST HUMAN 18245 28496 4.78 4.6E-01 BE18549:1 EST HUMAN 17915 28160 5.45 4.6E-01 AF019369.1 NT 17905 28161 5.45 4.6E-01 AF019369.1 NT 17905 1.43 4.6E-01 AF019369.1 NT 11765 27630 1.73 4.6E-01 AF120134.1 NT 11765 27630 1.73 4.6E-01 AE001931.1 NT 11765 27630 1.73 4.6E-01 AE001931.1 NT 12769 22558 4.5E-01 AE001931.1 NT 13760 22558 3.97 4.5E-01 AE01931.1 NT 13850 1.6 4.5E-01 AE01931.1 NT 13850 1.41 4.5E-01 AE01931.1 SWISSPROT 13889 23666 1.6 4.5E-01 AE01 AE01931.1 SYI	7730	17580	27802	1.33	4.6E-01	AI915634.1	EST HUMAN	Wg73812.x1 Soares NSF F8 9W OT PA P S1 Horne servious cDNA closs (NAS) Services
18236 2.86 4.6E-01 P98163 SWISSPROT 18245 28495 4.78 4.6E-01 BE185499:1 EST HUMAN 18245 28496 4.78 4.6E-01 BE185499:1 EST HUMAN 17915 28160 5.45 4.6E-01 AF019369:1 NT 17905 1.43 4.6E-01 AF019369:1 NT 19491 2.21 4.6E-01 AF120134:1 NT 11765 21640 1.73 4.6E-01 AE001931:1 NT 11765 21630 1.73 4.6E-01 AE001931:1 NT 11765 21640 1.73 4.6E-01 AE001931:1 NT 12769 22558 4.8F-01 AE01931:1 NT 13261 22956 1.05 4.5E-01 AE077080:1 EST HUMAN 13850 1.41 4.5E-01 AE077080:1 EST HUMAN 13850 1.41 4.5E-01 AE077080:1 EST HUMAN 18889 23665 <	7730	17580	27803	1.33	4.6E-01	AI915634.1	EST HUMAN	wg73e12.x1 Soares NSF F8 9W OT PA P 31 Home saniers cDNA clone IMA CE:2270766 3
18245 28495 4.78 4.6E-01 BE18549:1 EST HUMAN 18245 28496 4.78 4.6E-01 BE18549:1 EST HUMAN 17915 28161 5.45 4.6E-01 AF019369.1 NT 19005 1.43 4.6E-01 AF019369.1 NT 19491 2.21 4.6E-01 AF120134.1 NT 11765 21640 1.73 4.6E-01 AF120134.1 NT 12769 22568 4.87 4.6E-01 AF01931.1 NT 13765 22568 4.87 4.6E-01 AF01931.1 NT 13760 22558 4.87 4.6E-01 AF01931.1 NT 13760 22568 4.87 4.6E-01 AF01931.1 NT 13860 22568 4.87 4.6E-01 AF01931.1 NT 13860 22568 4.87 4.6E-01 AF01931.1 NT 13860 22568 4.87 4.6E-01 AF01931.1 AF01931.1	8359	18236		2.86	4.6E-01		SWISSPROT	PUTATIVE VITELL OGENIN RECEPTOR PRECI IRSOR AND COLOR
18245 28496 4.78 4.6E-01 BE185449.1 EST_HUMAN 17915 28161 5.45 4.6E-01 AF019369.1 NT 19005 1.43 4.6E-01 AF019369.1 NT 19491 2.21 4.6E-01 AF120134.1 NT 11765 21640 1.73 4.6E-01 AF120134.1 NT 12769 22568 4.87 4.6E-01 AF01931.1 NT 13196 22558 4.87 4.6E-01 AF01931.1 NT 13251 23056 1.05 4.6E-01 AF01931.1 NT 13850 22558 4.87 4.6E-01 AF01931.1 NT 13850 22558 4.87 4.6E-01 AF01931.1 NT 13850 22558 4.87 4.6E-01 AF01931.1 NT 13860 22558 4.87 4.6E-01 AF01932.1 NT 13860 23056 1.66 4.6E-01 AF02837.1 SWISSPROT	8368	18245	28495	4.78	4.6E-01		EST HUMAN	IL5-HT0730-100500-075-405 HT0730 Homo seniens CPNA
17915 28160 5.45 4.6E-01 AF019369.1 NT 17915 28161 5.45 4.6E-01 AF019369.1 NT 19005 1.43 4.6E-01 D53316.1 EST_HUMAN 19491 2.21 4.6E-01 AF120134.1 NT 11765 21640 1.73 4.6E-01 AE001931.1 NT 11765 21640 1.73 4.6E-01 AE001931.1 NT 12769 22558 4.87 4.6E-01 AE001931.1 NT 13196 22558 4.87 4.6E-01 AE01931.1 NT 13251 23056 1.05 4.6E-01 AF126378.1 NT 13850 1.61 4.6E-01 AF126378.1 NT 13889 23665 1.41 4.6E-01 AF126378.1 SWISSPROT 13889 23666 1.46 4.6E-01 AF126378.1 EST_HUMAN 15079 23666 1.46 4.6E-01 AF126378.1 EST_HUMAN	8368	18245	28496	4.78	4.6E-01		EST HUMAN	IL5-HT0730-100500-075-005 HT0730 Homo saniens cDNA
17915 28161 5.45 4.6E-01 AF019369.1 NT 15005 1.43 4.6E-01 D53316.1 EST HUMAN 19491 2.21 4.6E-01 AF120134.1 NT 11765 21640 1.73 4.5E-01 AE001931.1 NT 11769 22558 4.5E-01 AE01931.1 NT 12769 22558 4.5E-01 AE01931.1 NT 13196 22596 3.97 4.5E-01 AE077089.1 EST HUMAN 13251 23956 1.05 4.5E-01 AE738378.1 NT 13850 1.41 4.5E-01 AE728378.1 NT 13889 23665 1.1 4.5E-01 AVB73495.1 EST HUMAN 15079 4.5E-01 AWB73495.1 EST HUMAN	8766	17915	28160	5.45	4.6E-01	_	IN	Human thiopunine methyltransferase (TPMT) gene exon 10 and complete c4c
19005 1.43 4.6E-01 D53316.1 EST_HUMAN 19491 2.21 4.6E-01 AF120134.1 NT 11765 21640 1.73 4.6E-01 AE001931.1 NT 12769 22558 4.87 4.5E-01 AE01931.1 NT 13196 22996 3.97 4.5E-01 AE077086.1 EST_HUMAN 13251 23956 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 AE20378.1 SWISSPROT 13889 23665 1.1 4.5E-01 AE2047 SWISSPROT 1579 4.5E-01 AF126378.1 EST_HUMAN	8766	17915	28161	5.45	4.6E-01	<u>-</u>	N	Human thiopunine methyltransferase (TPMT) gans exon 10 and complete cds
19491 2.21 4.6E-01 AF120134.1 NT 11765 21630 1.73 4.5E-01 AE001931.1 NT 12769 22568 4.87 4.5E-01 AE001931.1 NT 13196 22596 3.97 4.5E-01 AA677086.1 EST_HUMAN 13251 23056 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 AF126378.1 SWISSPROT 13889 23865 1.1 4.5E-01 AF126378.1 EST_HUMAN 15079 4.5E-01 AW873495.1 EST_HUMAN	9313	19005		1.43	4.6E-01		EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-105F03
11765 21639 1.73 4.5E-01 AE001931.1 NT 12769 22558 4.87 4.5E-01 AE001931.1 NT 13196 22996 3.97 4.5E-01 AF126378.1 SWISSPROT 13251 23056 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 AF126378.1 SWISSPROT 13889 23665 1.1 4.5E-01 AF126378.1 SWISSPROT 15079 4.5E-01 AW873495.1 EST_HUMAN	9978	19491		221	4.6E-01	-	L	Linanflus iamainensis maturase (mat/) nene eklemelee sees
11765 21640 1.73 4.6E-01 AE01931.1 NT 12769 22558 4.87 4.5E-01 AA077086.1 EST_HUMAN 13196 22996 3.97 4.5E-01 Q05783 SWISSPROT 13251 23056 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 AF126378.1 SWISSPROT 13889 23665 1.1 4.5E-01 AF126378.1 SWISSPROT 15079 4.5E-01 AW873495.1 EST_HUMAN	1869	11765	21639	1.73	4.5E-01	-	Į.	Demococcus radiodurans R1 section 88 of 220 of the complete characters.
12769 22558 4.87 4.5E-01 AA677086.1 EST_HUMAN 13196 22986 3.97 4.5E-01 Q05783 SWISSPROT 13251 23056 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 Q28247 SWISSPROT 13889 23665 1.1 4.5E-01 AI708908.1 EST_HUMAN 15079 4.02 4.5E-01 AW873495.1 EST_HUMAN	1869	11765	21640	1.73	4.6E-01	L	ķ	Deinococcus radiodurans R1 section 68 of 220 of the complete chromater.
13196 22996 3.97 4.5E-01 Q05783 SWISSPROT 13251 23056 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 AZ8247 SWISSPROT 13889 23665 1.1 4.5E-01 AI708908.1 EST_HUMAN 15079 4.02 4.5E-01 AW873495.1 EST_HUMAN	2841	12769	22558	4.87	4.5E-01	_	T HUMAN	255402.s1 Sogres fetal liver spleen 1NFLS S1 Homo saniens CDNA clane 1MACE 254476 or
13251 23056 1.05 4.5E-01 AF126378.1 NT 13850 1.41 4.5E-01 AF126378.1 NT 13889 23665 1.1 4.5E-01 AI708908.1 EST_HUMAN 15079 4.02 4.5E-01 AW873495.1 EST_HUMAN	3276	13196	22996	3.97	4 55-04			BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
13850 1.41 4.5E-01 Q26247 SWISSPROT 13889 23665 1.1 4.6E-01 Al708908.1 EST_HUMAN 15079 4.02 4.5E-01 AW873495.1 EST_HUMAN	3331	13251	23056	1.05	4.5E-01		T	Mus musculus DNA polymerase encilon colonici (Pala) con
13889 23665 1.1 4.5E-01 Al708908.1 EST HUMAN 15079 4.02 4.5E-01 AW873495.1 EST HUMAN	3942	13850		1.41	4.5E-01		SWISSPROT	COLLAGEN ALPHA 5/1V/ CHAIN
15079 4.02 4.5E-01 AW873495.1 EST_HUMAN	3982	13889	23665	1.1	4.5E-01		Т	as96e09.x1 Barstead aorta HPLRB6 Homo saniens cDNA clone IMA CE: 2353490.21
l	4085	15079		4.02	4.5E-01	-	П	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'

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Table 4
Single Exon Probes Expressed in Heart

							onigo Exoni copo Expressed III legit
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4862		24522	0.94	4.5E-01	4.5E-01 BE983445.2	EST HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5406			1.45	4.5E-01	4.5E-01 AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
5983	15888		1.47	4.5E-01 Q00956	Q00956	SWISSPROT	COAT PROTEIN
6488	16346		2.49	4.5E-01	4.5E-01 AI858849.1	EST HUMAN	W32e02x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SW I/SNF COMPLEX 170 KDA SUBUNIT.
6897		26970	3.14	4.5E-01 AI64850	AI648596.1	EST HUMAN	#256g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644.3
7100			1.54	4.5E-01	11444786 NT	LN	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183) mRNA
7991		28082	25.09	4.5E-01		EST HUMAN	EST02531 Fetal brain, Stratagene (cat#938206) Homo saniens cDNA clone HFRCY47
7991	17841	28083	25.09	4.5E-01		EST_HUMAN	EST02531 Fetal brain, Stratagene (catt936206) Homo sapiens cDNA clone HFBCY17
8237		28369	2.42	4.5E-01	_	EST_HUMAN	xo14h01.x1 NCI_CGAP_UB Homo sepiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE Q84252 VIRAL INTEGRATION SITE PROTEIN INT-8, [1]
9036	19724		2.25	4.6E-01	BE871461.1	EST HUMAN	601449201F1 NIH MGC 65 Homo sanjens cDNA circue IMAGE-382061 5
9694	19245		1.44	4.5É-01	BF337531.1	EST HUMAN	602035275F1 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGE-4183290 F
9763			2.15	4.5E-01	11422099 NT	7	Homo saplens testis-specific kinase 2 (TESK2), mRNA
9974		24987	1.83	4.5E-01	4.5E-01 AF238234.2	Į.	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
1991	11885		2.47	4.4E-01	6680503 NT	Ę	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2340		22118	3.59	4.4E-01 P49765		SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274		22994	66.0	4.4E-01 AF0587		LN LN	Rattus norvegicus SynGAP-b mRNA, complete cds
3274		22995	66.0	4.4E-01	4.4E-01 AF058790.1	LN	Rattus norvegicus SynGAP-b mRNA, complete cds
3277	13198	22398	1.87	4.4E-01 BF0567;	28.1	EST_HUMAN	7J91402.y1 NCL CGAP Br16 Homo sapiens cDNA clone IMAGE:3393795.5'
4141	14041		1.33	4.4E-01 BE3787	07.1	EST HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5
4924	_ [0.93	4.4E-01	96.1	EST_HUMAN	MR0-HT0078-131299-007-905 HT0078 Hamo sapiens cDNA
5326		25050	1.99	4.4E-01 P04929		SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326	_}	25051	1.99	4.4E-01 P04929		SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
848	15409	25474	1.3	4.4E-01 S65019.		TN	mucin [rats, Spregue-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial 390 ntl
2499	15418	25481	1.98	4.4E-01	4.4E-01 AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5
5624	15539	25827	1.6	4.4E-01 AI19841	3.1	EST_HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN;
5624	16539	25628	1.6	4.4E-01 A119841	3.1	EST_HUMAN	qi82h11.X1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN
5782	i	25798	1.79	4.4E-01	4.4E-01 AW080795.1	EST HUMAN	xc27e08.x1 NCI_CGAP_Co18 Home sapiens cDNA clone IMAGE:2585510 3' similar to TR:095154 095154 AFLATOXIN B1-ALDEHYDE REDUCTASE
6582	16462		10.84	4.4E-01 Z11679.		NT	S.tuberosum mRNA for induced stolon tip protein (partial)
						İ	

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		T	7	1	П	T	T	T	Ţ	\neg	T	Т	7	T	Т	Т	7	Т	٦	T	T	Т	Ţ.	$\overline{}$	Т	T	Т	Т	Т	7	7	7	Т	$\overline{}$
Single Exon Probes Expressed in Heart	Top Hit Descriptor	ZINC FINGER X CHROMOSOMAI PROTEIN	4039f09.x1 NCI CGAP Lu5 Homo sapiens CDNA clame IMA CE : 1040624 21	GLYCOPROTEIN B PRECLISCOR (GLYCOPROTEIN 44)	TYROSINE-PROTEIN KINASF RECEPTOR TIE.1 PRECIDEND	beta -HKA=H K-ATPase hela-suhuni frats. Genomic. 8083 at. 50000000	beta -HKA=H,K-ATPase beta-subunit frats. Genomic Ross of segment 2 of 2]	Mus musculus sodium channel, tone X, alpha polymentide (Scrafon), month	Homo sabiens chromosome 21 segment HS210782	Autographa californica nucleonolyhedrovinis, complete gannas	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HUB22A)	Callithrix jacchus MW/LW opsin gene, upstream flanking region	Callithrix jacchus MW/LW oosin gene unstream flanking meios	QV4-SN0024-200400-183-b01 SN0024 Homo saniems CINA	CM2-DT0003-010200-077-c01 DT0003 Home sepiens cDNA	MR0-BN0070-270300-008-004 BN0070 Homo serviens CDNA	Aquifex aeolicus section 30 of 109 of the complete genome	Human somatostatin I gene and flanks	Callithrix lacchus MW/LW onsin gene unstream flanking region	Cellithrix jacchus MW/LW obsin dene, unstream flanking region	Arabidopsis thallana DNA chromosome 4 contin fragment No. 14	Xestia с-підгит granulovirus, complete genome	Saimin sciureus olfactory receptor (SSC186) gene, partial cds	Coturnix coturnix japonica ifing gene	DNA GYRASE SUBUNIT B	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'	Methanococcus voltae flagella-related protein C-l (flaC-flal) genes, complete cds	h74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE-2968554 5	hh74e10.y1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2988554 5'	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' sImilar to	Equus caballus microsafellite FX027	RC3-BN0034-290200-013-512 BN0034 Home saviens - CINA	RC3-BN0034-290200-013-012 BN0034 Homo seniens cDNA	Streptomyces coelicolor whilt gene
Jie Exon Proc	Top Hit Database Source	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	N I	N	F	NT	¥	SWISSPROT	NT	¥	EST HUMAN	EST HUMAN	П	1	Ę					N I	NT		T_HUMAN			EST_HUMAN	EST HUMAN	Т	EST HUMAN	Т	Ϋ́
JI JIC	Top Hit Acession No.	062836	A1268650.1					6677874 NT	2.2	9627742		8.1	8.1	50.1	99.1	7.1	8.1		3.1		22	9635250 NT		78.1					4.3E-01 AW630048.1	4.3E-01 AW170559.1	Γ			
	Most Similar (Top) Hit BLAST E Vatue	4.4E-01 062836	4.4E-01 A1268650	4.4E-01 P28922	4.4E-01 P35590	4.4E-01 S76404.1		4.4E-01	4.4E-01 AL18328	4.4E-01	4.4E-01 P54725	4.3E-01 AF15521	4.3E-01 AF15521	4.3E-01 AW8665	4.3E-01 AW93526	4.3E-01 AW99947	4.3E-01 AE00069	4.3E-01 J00306.1	4.3E-01	4.3E-01 AF155218	4.3E-01 AL161502	4.3E-01	4.3E-01 AF17982	4.3E-01 A	4.3E-01 033367	4.3E-01 BF34800	4.3E-01 U97040.1	4.3E-01 A	4.3E-01 A	4.3E-01	4.3E-01	4.3E-01	4.3E-01 A	4.3E-01 AJ003022
	Expression Signal	1.29	1.99	2.45	4.67	1.33	1.33	2.29	3.29	5.34	1.76	1.98	1.98	1.1	0.96	0.93	1.53	1.15	1.02	1.02	1.11	1.06	3.04	3.86	4.01	2.54	2.83	1.65	1.65	1.27	2.64	1.98	1.98	2.02
	ORF SEQ ID NO:	27422	27798		27903	28025		25329		25224		20178	20179	21350		22742		23737	20178	20179			25592	26064	-			27674	27675	27967	26195	28673	28674	
	Exon SEQ ID NO:	17222	17573	17574	17663	17785		18996	19663	19267	19326	10351	_]		12771	12950	13145	13961	10351	10351	14755	14929	15514	15933	15996	16235	16/8/	17459	1/408	17722	16049	18409	18409	19390
	Probe SEQ ID NO:	7354	7723	7724	7813	7935	7935	9236	9306	9731	9824	405	405	1585	2843	3022	3221	4059	4306	4306	4875	2029	2000	6029	2010	250	6069	200	800	7872	8302	8537	8537	9916

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		_	÷		_	_	_			_					_					_			_			_					_	_	
Single Excit Plobes Expressed in Heart	Top Hit Descriptor	CELL DIVISION PROTEIN FISH HOMOLOG PRECLIRSOR	In224a09.s1 NCI CGAP GCB1 Homo seniens cDNA clane MAA GE-1288ags 21	Xivella fastidiosa, section 93 of 229 of the complete genome	dl94b01.x1 Soares NhHMPu S1 Homo seniens cDNA clone IMAGE-18700AF 21	QVo-LT0015-180200-127-h01 LT0015 Home sepiens cDNA	SOX-8 PROTEIN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA	nj69h01.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DR-1 RETA CHAIN /HIMANN	VIT7e01.r1 Soares infant brain 1NIB Homo saniens cDNA clone MAGE-28278 5'	601879721F1 NIH MGC 55 Homo sapiens cDNA clone IMAGE-4108403 51	RC3-CT0254-060400-029-004 CT0254 Homo saniens china	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'	Brca1=breast cancer gene frats, WF, spleen. Genomic, 419 nt segment 2 of 21	Arabidopsis thaliana DNA chromosome 4, contin fragment No. 47	EST369413 MAGE resequences, MAGE Homo sapiens cDNA	EST369413 MAGE resequences, MAGE Homo sapiens cDNA	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein,	WR3-SND040-280300-403-607-SN0040 Umms - FNVA	Ovzias latines OIGC7 mRNA for membrane disandal circlese complete cuts	601660352R1 NIH MGC 71 Hamo sapiens cDNA clone IMAGE 30n6085 2	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5	RC-BT091-210199-142 BT091 Homo saplens cDNA	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'	PM-BT103-270499-684 BT103 Homo sapiens cDNA	Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA	Arabidopsis thaliana DNA chromosome 4, contin frament No. 36	Arabidopsis thaliana DNA chromosome 4, contin fragment No. 36	oj94b08.s1 Soares, NFL T GBC S1 Homo saciens cDNA clone IMAGE-1466603 21	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoA, IsoB, IsoC, IsoD, IsoE and IsoF names	om33d02.s1 Scares_NFL_T_GBC_S1 Horno sapiens cDNA clone IMAGE:15428193'
JUS EXOII PIUI	Top Hit Database Source	SWISSPROT	EST HUMAN	N L	EST HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	NT	EST HUMAN	EST_HUMAN		T HIMAN	N	EST HUMAN	EST_HUMAN	П	EST_HUMAN	EST_HUMAN	EST_HUMAN	Þ	N	F	HUMAN		EST_HUMAN
OII	Top Hit Acession No.	Q39102	4.2E-01 AA761653.1	4.2E-01 AE003947.1	4.2E-01 AI280338.1	4.2E-01 AW835527.1	Q04886	4.2E-01 BE073574.1	4.2E-01 AA534093.1	4.2E-01 R13467.1	4.2E-01 BF242055.1	AW854162.1	Ì	l		7.2	4.2E-01 AW957448.1	П	TIM DENREZA	4.2E-01 AW863666 1					3.1	3.1	4.1E-01 Al905949.1	7705283	7	2		Σ.	1.7
	Most Similar (Top) Hit BLAST E Value	4.2E-01 Q39102	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01 AL16154	4.2E-01	4.2E-01	4.2F-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.1E-01 AI905481	4.1E-01 AV70524	4.1E-01	4.1E-01	4.1E-01	4.1E-01 AL161536	4.1E-01 AL161536	4.1E-01 AA90634	4.1E-01	4.1E-01 AA90925
	Expression Signal	1.04	0.89	4.78	1.09	0.96	1	3.63	4.96	3.13	1.5	1.56	9.1	9.1	2.1	5.91	2.1	2.1	1.19	1.48	22	2.04	1.66	1.88	2.4	2.4	1.03	1.52	1.76	1.76	1.13	2.59	1.07
	ORF SEQ ID NO:	21099		23263		23503		,	24273	24350	25484	25518			26219	26233	26739	26740	26844	28084	28528	28799		20835	20844	20845	21356	22434	22633	22634	22985	23852	
	Exon SEQ ID NO:	12691	11800	13472	13499			14438	14487	14557	15422	15450	16024	16024	19461	16083	16543	16543	16655	17842	18276	18517	19353	10994	11003	11003	11496	12543	12836	12836	13186	14077	14107
	Probe SEQ ID NO:	1335	1904	3558	3585	3803	3900	4545	4599	4671	5503	5533	6151	6151	6184	6217	ලෙස	6663	6776	7992	8400	8699	9863 8	1078	1087	1087	1592	2678	2940	2910	3263	4177	4208

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Table 4
Single Exon Probes Expressed in Heart

		_	-	_	_		_		_	_		_	_	_	_											_							
Cirigio Evolis sonos Expressed III Deali	Top Hit Descriptor	9911b03.s1 Scares infant brain 1NIB Homo saniens cDNA clone IMAGE 31814.3	AV747880 NPC Homo sapiens cDNA clone NPCBDF10.5	Bacillus subtilis complete denome (section 21 of 21) from 3000281 to 42/4814	602166590F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE-4207410 K*	Methanococcus jannaschii section 77 of 150 of the complete cenome	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'	Mus musculus signaling intermediate in Toll nathwavenumenthy mensulus signaling intermediate in Toll nathwavenumenthy	Campylobacter Jejuni NCTC11168 complete genome; segment 3/6	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA	Zea mays ZMPMS2 gene for 19 kDa zein protein	VOLTAGE-GATED POTASSIUM CHANNEL PROTFIN KV1 1 /HI IKI) /HBK1)	Homo sapiens DNA for amyloid precursor protein, complete cds	Laqueus rubellus mitochondrion, complete genome	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdofth) mRNA	Ascobolus immersus masc2 gene	Ascobolus immersus masc2 gene	Mus musculus ubiquitin-protein ligase e3 componen n-recognin (Libra) mRNA	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C080	Streptococcus pneumoniae YIIC (yIIC), YIID (yIID), penicillin-binding protein 2x (obp2x), and undersappend.	phosphate-UDP-MunNAc-pentapeptide phospho-MunNAc-pentapeptide transferase (mraY) genes, complete	Outs arise nartial ID2 name for T and promotes dates about 17000 in	Ods aries partial 102 name for T cell receptual della chain (1000) to	MACH IN ASTOCIATION ON CONTROL OF THE CHILD ASTOCIATION OF THE CHILD AS	EST382691 MAGE recentence: MAGE Home coolers could	Synechocystis sp. PCC 9413 transposase gene gamplets adv	Homo seriens chromosome 21 serment Hosp CAO	HYPOTHETICAL 49 7 KD PROTEIN IN GINS STER INTERGENIC BECION	Campylobacter leiuni NCTC11168 complete denome segment 2/6	CM4-HT0136-150999-014-f09 HT0136 Homo saplens cDNA	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
מון דיייייייייייייייייייייייייייייייייייי	Top Hit Datebase Source	EST HUMAN	EST HUMAN	N	EST HUMAN	NT	EST_HUMAN	Ę	TN	EST_HUMAN	N	SWISSPROT	ĮN.	N	N.	N.	N	N	N	Į.	NT		Ŀ			TORPROT	Т	Т		ISSPROT	П	EST_HUMAN	NT
5	Top Hit Acession No.	4.1E-01 R41726.1	4.1E-01 AV747880.1	299124.1	4.1E-01 BF681393.1		4.1E-01 BF574604.1	8755521 NT	4.1E-01 AL139076.2	4.1E-01 BF349382.1		209470	387675.1	8404656 NT	4.0E-01 AF203478.1	6679258 NT	296933.1	296933.1	6678490 NT	4.0E-01 AL163280.2	L163280.2		Eneggina 4		1277511 1	31849	W970610.1	76080.1	L163300.2		Γ	7.7	
	Most Similar (Top) Hit BLAST E Value	4.1E-01	4.1E-01	4.1E-01 Z99124.1	4.1E-01	4.1E-01 U67535.1	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01 X58700.1	4.1E-01 Q09470	4.1E-01 D87675.1	4.0E-01	4.0E-01	4.0E-01	4.0E-01 Z96933.1	4.0E-01 Z96933.1	4.0E-01	4.0E-01	4.0E-01		4 DE-01 A ED 88003	4 0E-01 A 1277511	4.0E-01 A.1277511	4.0E-01 031849	4.0E-0:1 AW970610	4.0E-01 L76080.1	4.0E-01 AL 163300	4.0E-01 P36049	4.0E-01 AL139075.	3.9E-01	3.9E-01
	Expression Signal	0.83	1.26	0.87	4.13	291	1.3	1.23	1.3	1.58	164	279	1.72	1.27	0.98	4.06	1.17	1.17	1.09	2.24	2.24		1.63	3.24	3.24	7.34	1.31	3.24	222	1.33	1.4	1.59	21
	ORF SEQ ID NO:		24247		25650			27323		· •	28349	28121			21079				19931	22865	22666		23330	23451	23452	-	25596					20007	21119
	Exon SEQ ID NO:	14269	14459	15049	15557	16257	16563	17130	17738		_	17880	19702		ì	11374	12709	12709	10110	12866	12866		13551	13668	13668	14598	15517	18766	19567	19327	19387	10196	11262
	Probe SEQ ID NO:	4373	4567	5185	5644	6395	6683	7253	7888	8018	8213	8696	9624	1023	1316	1469	1960	1960	2774	2939	2939		3637	3755	3755	4712	5603	8959	9312	9825	9910	227	1356

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Single Explicased in Hear	rilar Top Hit Acessian Top Hit Database TE No. Source	3.9E-01 AB033019.1 NT Homo saplens mRNA for KIAA1193 protein, partial cds		3.9E-01 X82032.1 NT H.seplens B-m/b dene	3.9E-01 AJ226896.1 NT Sinorhizoblum meliidii edi. svrB2. cvz3 genes and ort3	3.9E-01 BF592611.1 EST HUMAN 7761401.x1 NCI CGAP Bri6 Homo sepiens cDNA clone IMAGE-3330469 2	3.9E-01 BE728667.1 EST HUMAN 1601563948F1 NIH MGC 20 Homo saniens cDNA clane IMA GE-3834800 E	EST HUMAN	3.9E-01 AW195888.1 EST_HUMAN 094821 KIAA0713 PROTEIN:	3.9E-01/Al937337.1 EST HUMAN SW:REX5 HUMAN PARARD RINDING DECH INTO CATALON CA	7	4.1 EST HUMAN	#1 NT	Т	1.1 N	7019488 NT		IN	6678002 NT	Ξ	- N	N.	1 EST_HUMAN	AI807219.1 EST HUMAN	3754095 NT	1.1 EST HUMAN	SWISSPROT	1.1 EST_HUMAN		LS LOUWEN	Proposed National Proposed National Period of Administration of the Administration of th
Siligie Exuli	Acessian Io.	9.1			2.7	1.1						1	7		-	7019488 NT	1.0	7.1	6678002	2	7			_	3754095	=		1.1	Ţ		
	Most Similar (Top) Hit BLAST E Value	Ŀ						3.9E-01 B		3.9E-01 A	3.9E-01 M	3.9E-01 A	3.9E-01 A	3.9E-01	3.9E-01 A	3.8E-01	3.8E-01 A	3.8E-01 AI	3.8E-01	3.8E-01 A.	3.8E-01 A	3.8E-01 A	3.8E-01 AI	3.8E-01 AI	3.8E-01	3.8E-01 BE	3.8E-01 Q	3.8E-01 BE	3.85-01.48	3.8E-01 X6	100
	Expression Signal	3.54	5.98	5.98	3.63	1.47		3.63	1.5	1.4	2.97	2.22	2.49	2.38	1.26	7.44	1.22	2.44	4.41	0.92	2	77.7	0.79	0.91	0.85	96.0	1.62	4.47	3.81	4.83	200
	ORF SEQ ID NO:	22367	22427		22776		24572	25611	27400	27581	27755				25328			22289				23160				24692	25422	26023	26177		07050
	SEQ ID						_	15528	17200	17372	17530	18080	19642	18940	18990	10128											15366	15899	16036		40057
	Probe SEQ ID NO:	2605	2673	2673	3058	3988	4919	5613	7324	7503	7680	8195	9091	9209	9288	154	1827	2524	2591	2972	3010	3438	3494	3506	3841	5048	5445	5994	6053	6438	6090

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Single Exon Probes Expressed in Heart	Similar Top Hit Acession ST E No. Source	AL121154.1	Y18060.1	AJ237934.1 NT	Z	EST HUMAN	EST HUMAN	Т	34.1 EST HUMAN	Z	N	1.1 NT	3.6E-01 X76725.1 NT P.Irregulare (P3804) gene for actin	3.6E-01/AW812033.1 EST_HUMAN RC5-ST0171-181099-011-907 ST0171 Homo sapiens cDNA	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE	3.6E-01 P24206 SWISSPROT ISOASPARTYL PROTEIN CARROXY MFTHYL TRANSFERASE) (L-	Т	Z		3.1 EST HUMAN	TN L.	F	3.1 EST_HUMAN	3.6E-01 Y10196.1 NT Homo saplens PHEX gene	6E-01 R94090.1 EST_HUMAN y774a06.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGF: 275987 5	3.6E-01 AW027174.1 EST HUMAN 015117 FYN BINDING PROTEIN 111.	.2 NT	4504956 NT	4504956 NT	3.6E-01 AI 163204.2 INT Home engines chemical character and the control of the co
Single Exon	Acession o.							7.4	77.7			1.1		33.1						3.1	7.7		3.1 EST			4.1	.2	4504956 NT	4504956 NT	1 -
	Most Similar (Top) Hit BLAST E Vafue	3.7E-01	3.7E-01	L																								3.6E-01	3.6E-01	3.6E-01
	Expression Signal	2.18		1.31	71.17	2.59	2.59	6.05	9.05		1.08	1.04		1.63		2.28	8.9	1.85	1.85	1.16		1.23	7		5.49	1.66	13.42	3.37	3.37	1.4
	ORF SEQ ID NO:		25217				21055	21645		21682				22211		22350		23145	23146	23988	24312	24367	24587	25928		26340	26886	27269	27270	27380
	Exen SEQ ID NO:	19206	19251	19746	10902		11199				11899	12108	12221	12314		12460	15077	13341	13341	14205	14523	14570	14819	15805	16104	16180	16695	17082	17082	17178
	Probe SEQ ID NO:	9634	9701	9964	979	1292	1292	1874	1874	1908	2007	2223	2341	2437		2589	2869	3424	3424	4308	4635	4684	4941	6680	6238	6317	6816	7205	7205	7302

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Top Hit Descriptor	601676418F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE 3958997 5	Arabidopsis thallana mRNA for SigB, complete cds	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete	Homo saplens hHb5 gene for hair kerattin exons 4 to 0	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome	Mus musculus Emri mRNA, complete cds	x60e11.x1 NCI_CGAP_Part Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):	Mus musculus mannose receptor. C type 2 (Mrc2) mRNA	Arabidopsis thallana DNA chromosome 4, contin frament No. 77	Homo sapiens GAP-like protein (I OC51306) mg/mg/mg/mg/mg	Homo sapiens GAP-like protein (1 OC51306) mRNA	601811060R1 NIH MGC 48 Home sanians cDNA clane IMAGE-Ansages 3	601894653F2 NIH MGC 19 Homo sapiens cDNA clone IMAGE:4124244 5	Rattus norvegicus ADP-ribosylation factor-directed GTP as e activation monal commissions and	2708809.51 Stratanene NT2 neumain precurent 037230 Homo aminor anni 1100 1100 1100 1100 1100 1100 1100 1	Elleckodes of the light of the	Danio rerio homeohov minish (howest complete cds	RC5-HT0218-181099-0111-002 HT0218 Home canions ANA	788iE1 fetal brain cDNA Homo saniens cDNA clone 788iE1 V chellor de Dozose	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5	S.scrofa mRNA for CD31 protein (PECAM-1)	Homo sapiens fumor protein p53-binding protein, 2 (TP53RP2), mRNA	Homo saplens tyrosine kinase non-receceptor 1 (TNK1), mRNA	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L	X. Agevis gene for albumin including HP1 enhancer	Carlseus rhodopsin gene for opsin protein	Gailus gallus SPARC gene for osteonectin, promoter and exon 1	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
Top Hit Database Source	EST_HUMAN	뉟	닐	<u> </u>	F	LN	EST HUMAN	Į.	Ā	۲	M	EST HUMAN	EST_HUMAN	ΤN	EST HUMAN	1 1	L	EST HUMAN	EST HUMAN	NT	NT	NT .	NT	SWISSPROT	N	N	LN	NT
Top Hit Acession No.	BE902390.1	3.6E-01 AB004293.1	3.6E-01 AE000856.1	3.6E-01 Y19210.1	3.6E-01 AE000335.1	3.6E-01 U66888.1	3.6E-01 AW180229.1	6678933 NT	AL16158			3.5E-01 BF129786.1	3.5E-01 BF310688.1	3.5E-01 U35776.1	3.5E-01 AA223252.1	105807 4	3.5E-01 AF071253 1	3.5E-01 BE146585.1	V81203.1	M18349.1	K98505.1	11448042 NT	4507610 NT	702294	726825.1	(61084.1	-	
Most Similar (Top) Hit BLAST E Value	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.5E-01		3.5E-01	3.5E-01	3.55-01	3.5E-01	3.5E-01	3.5E-01	3 55-01 105807 1	3.5E-01	3.5E-01	3.5E-01 N81203.1	3.5E-01	3.5E-01 X98505.1	3.5E-01	3.5E-01	3.5E-01 002294	3.5E-01 Z26825.1	3.5E-01	3.5€-01 /	3.5E-01
Expression Signal	1.94	3.69	3.56	1.81	3.05	3.03	1.58	2.18	76.0	1.24	1.24	3.17	1.17	1.05	1.85	980	1.92	1.29	0.84	3.84	3.47	1.88	3.21	1.51	22	2.99	2.34	2.34
ORF SEQ ID NO:	28440	28585	28134							20466	20467	20531	21370	21384	22327		23839	24056	24462	24513			27238	27680	27764	28251	28513	28514
Exon SEQ ID NO:		18326	17890	19761	18886	18983	19704	10174	10596		l	i	11508	11526	12725	12537	14065	14275	14675	14730	15959	16584	17048	17463	17538	18005	18263	18263
Probe SEQ ID NO:	8314	8453	8741.	9044	9127	9281	9889	202	662	. 708	708	763	1603	1622	2563	2672	4165	4379	4790	4849	6199	6704	7171	7612	7688	8116	8386	8386

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		T	T	Т	Т	10	٦		Т	T	T	T	T	0	Т	٦	7	Т	T^-	₽	Т	Т	\top	T	7	1	_
Single Exon Probes Expressed in Heart	Тор Hit Descriptor	Arabidopsis thaliana DNA chromosome 4, confin fragment No. 13	B.taurus atpA1 gene for F(0)F(1) ATP synthase albha-subumit	19564f11.r1 Soares retina N2b4HR Homo sapiens cONA clone IMAGF-219507 5	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5	Homo saplens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes	Isolated from 1.04 cervical carcinoma cell line Desirformance di reconsolutional Desirforma della del	Azotobacter vinelandii nifA gene for NifA profein (nocities social control of the	Synechocystis sp. PCC6803 complete genome 11/07 1314035 1430446	Arabidopsis thaliana DNA chromosome 4 contin frammant No. 28	Homo sapiens chromosome 21 segment HS24C040	Homo sapiens chromosome 21 segment HS21C010	Canis familiaris rod photoreceptor cGMP-cated channel slinha-enhinit (CNCCA) mDNA	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete lods	7n94a01.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232.3' similar to TR:Q9UJ15	not1610 ST NCI CGAP Phet Homo earliers child clare MACE 44 000 47 21	Homo saplens interrin alpha 6 (TCAR) gans axone 42 through 22	MR4-BT0403-230200-202-c01 BT0403 Homo seniens cDNA	hy17d09x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.t3 L1 repetitive element;	qi95c05.x1 NCI_CGAP_Kid3 Hαπο sapiens cDNA clone iMAGE:1867208 3' similar to contains Alu repetitive element:	Sea urchin hsp70 gene II for heat shock protein 70	Arebidopsis theliane DNA chromosome 4 confin frament No on	zn12d11.s1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE 547221 31	Echowins 22 14B 1C 1D 24 2B 2C 34 3B 3C 92 mention DNA	UI-H-811-aei-e-12-0-11 st NCI CCAP Substance continue continue continue de con	DKFZp761A249 r1 761 (synonym: ham/o) Home sanians chiva chem DkFzp761A249 r1 761 (synonym: ham/o) Home sanians chiva chem by the sanians chiva chem	zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3
jle Exon Prol	Top Hit Database Source	12	NT	EST_HUMAN	EST_HUMAN	Ę	LN LN	Į.	LZ.	Z	K	NT	Į	IN	EST HIMAN	EST HUMAN	Z	EST_HUMAN	EST_HUMAN	EST HUMAN	K	N.	EST_HUMAN	ħ	EST HUMAN	ST HUMAN	EST_HUMAN
NIIS	Top Hit Acession No.	3.5E-01 AL161501.2		3.5E-01 H80814.1		3 4E-04 A 1242058 4	_			2	7	3.4E-01 AL163210.2	3.4E-01 U83905.1	3.4E-01 AF106835.1				-	3.4E-01 BE463761.1	3.4E-01 AI240973.1		2	<u>-</u> -		5.1	_	
	Most Similar (Top) Hit BLAST E Value	3.5€-01	3.5E-01	3.5E-01	3.5E-01	2 AE 04	3.45-01	3.46-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.45-01	3.4E-01/	3.4年-01/	3.4E-01	3.4E-01	3.4E-01	3.4E-01 X16544.1	3.4E-01	3.4E-01 /	3.4E-01 L02971.1	3.4E-01 AW20450	3.4E-01	3.4E-01 N95225.1
	Expression Signal	3.34	2.12	2.25	2.25		4 53	1.73	281	1.46	0.81	0.81	5.41	3.48	2.33	1.16	0.78	1.82	0.93	3.57	1.2	2.85	4.71	2.06	257	1.47	1.52
	ORF SEQ ID NO:	29052		24999	25000		20731		22129	22400	22697	22698	22846	23209			24074	24221	. 24494		24614	25469			25724	25786	
	Exen SEQ ID NO:	ı	1	19616	19616	10624	10883	11211	12232	12509	12898	12898	13049	13404	13634	13872	14290	14437	14710	14750	14845	15406	15467	15566	15623	15687	15948
	Probe SEQ ID NO:	8951	9206	9941	9941	69.1	960	1304	2352	2642	2971	2971	3124	3488	3722	3962	4394	4544	4828	4870	4970	.6487	5551	5654	5715	5780	6045

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Probe SEQ ID S	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193	21048	4.82		3.3E-01 BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1588	11492	21352	1.11	3.3E-01	753685	NT	Mus musculus disintegrin 5 (Dtgn5), mRNA
1704	11605		1.05		3.3E-01 AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week I Homo sapiens cDNA 5' end
2355	12235		4.74	3.3E-01	4507834 NT	Ę	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidinè-5- decarboxylase) (UMPS) mRNA
2919	12846	22648	23		3.3E-01 AJ251805.1	Z	Bacteriophage phi-YeO3-12 complete genome
2982	12910		1.12			SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3016	12944	22737	1.01	3.3E-01	2	NT	Streptomyces argillaceus mithramycin blosynthetic genes
3450	13367	23173	1.14		1	N	Homo sapiens MTA1-L1 gene, complete cds
3738	13650	23433	212	3.3E-01 084645		SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3884	13795	23582	1.59		2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3920	13829	23609			3.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4271	14170		2.74		3.3E-01 D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4589	14477		1.48		3.3E-01 Al539114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
5263	15185	24960	2.68		3.3E-01 X89819.1	N TN	R.novegicus mRNA for 3'UTR of ubiquitin-like protein
5263	15185	24961	2.68		3.3E-01 X89819.1	NT	R.narvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	15537	25623		3.3E-01	1	EST_HUMAN	601472768T1 NIH_MGC_68 Hamo sapiens cDNA clone IMAGE:3875753 3'
5622	15537	25624	271	3.3E-01	3.3E-01 BE619650.1	EST HUMAN	601472768T1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3875753 3'
6117	16011	26148	3.64		3.3E-01 AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6117	16011	26149	3.64		3,3E-01 Al628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element,
6575	16433		1.5		3.3E-01 N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6981	16858		19.46		3.3E-01 BF683954.1	EST_HUMAN	602/40372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE-4301800 5
7477	17337	27542	3.26		3.3E-01 N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA done IMAGE:297649 3'
7507	17295		2.81		3.3E-01 BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7739	17589		2.07		3.3E-01 L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
8104	17994			3.3E-01	X63953.1	NT	D.mauritiana Adh gene
8104	17994	28243			3.3E-01 X63953.1	NT	D.maunitiana Adh gene
8389	18265		1.82		3.3E-01 BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213585 5'
8561	18431	28700		١	BE219351.1	EST_HUMAN	hv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

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Single Exon Probes Expressed

	To =	Т	Т	Т	Т	Т	\top	Т	_	Т	Т	Т	7	_	_	Т	7	-	7				т-	7	_	_	_	_		
Top Hit Descriptor	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KE LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)	ob71g02.s1 NCI CGAP GCB1 Homo sepiens cDNA clone IMACE:1336850 31	Rhizobium leguminosarum sym plasmid pRt 5.11 nodX gene	Homo sepiens aldehyde oxidase 1 (AOX1), mRNA	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)	Raftus norvegicus EH domain binding protein Epsin mRNA complete cris	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds	P.vulgaris arc5-1 gene	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTFIN)	S.cerevislae chromosome II reading frame ORF YBR172c	EST369264 MAGE resequences, MAGD Homo sapiens cDNA	EST369264 MAGE resequences, MAGD Homo saniens onna	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen dentivation	601868804F1 NIH MGC 17 Homo sertiens CDNA clane IMAGE-444467	Mus musculus Pbx/knotled 1 homeobox (Planox1) mPNA	Homo saplens promyelocytic leukemia zinc finger protein (DI 75) zong zong har	Humam h NAT allete 3-2 gene for anyamine N-aceth/transferace	Arabidopsis thaliana DNA chromosome 4 contin frament No. 46	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, detta (pseudogene) and beta globin polypeptides, complete cds		Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5	Mouse renin (Ren-1-d) gene, complete cds	Homo sepiens interleukin 12 p40 subunit (IL12B) gene. II 12B-1 allele. complete coll	CM0-HT0569-060300-269-f10 HT0569 Home saniens cDNA	Rat ISO-atrial natriuretic factor gene, complete cds	H.saplens gene fragment for acetylcholine recentor (ACND) alchousts	601897107F1 NIH_MGC_19 Home sapiens cDNA clone IMAGE-4126633 5
Top Hit Database Source	SWISSPROT	EST HUMAN	N	Z	본	Z	N N	Z	뒫	SWISSPROT	N	EST_HUMAN	EST HUMAN	L	EST HUMAN	NT.	N.	LN L	Z	5		Z	П	T_HUMAN			Г			T_HUMAN
Top Hit Acession No.	P47963	AA806621.1	X07990.1	6598319		AF018261.1	П		_			AW957194.1	4.1	5.1	7.1	7710079	2		2			7,5		-						-
Most Similar (Top) Hit BLAST E Value	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.25-01	3.2E-01	3.25-01	3.2E-01	3.2E-01	3.2€-01	3.2E-01	3.25-01	3.2E-01/	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	70 10 0	3.45-01	3.22-01	3.22=-0.1	3.2E-01	3.2E-01 ₽	3.2E-01	3.2E-01	3.2E-01	3.2E-01 BF311635
Expression Signal	3.94	4.79	1.88	1.63	6.05	1.98	2.05	18.99	1.04	6.25	1.22	5.5	5.5	1.16	2.89	2.9	1.55	0.96	0.97	1.35	Š	0.5	3 6	0.80	1.18	0.98	2.82	1.42	13.32	14.29
ORF SEQ ID NO:	28825			28789											21901		22433			23977	24052	20072	71047	1		24771	24913	26819	26946	26951
Exon SEQ ID NO:	18541	l _)	10000	18881	19323	10393	10634	11058	11168	112/4	11638	11645	11645	11698	12003	12368	12542	13470	13779	14193	14274	44202	44500	7702	15081	15000	15146	16631	16751	16754
robe CO CO NO:	8652	8956	8972	9119	9817	\$	2 3	1140	182	200	2	4	144	88	2114	2494	2677	3556	3868	4295	4375	4307			/08b	2133	222	6752	6872	6875
	Exon ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source	Exon ORF SEQ Expression ID NO: Signal Value Top Hit Acession Signal Top Hit Acession Top) Hit Top Hit Acession Source Top Hit Acession Source Top Hit Acession Source Database Source Acession Source Database Source Acession Source Acess	Exon NO: ORF SEQ Signal NO: Expression Signal Value Top Hit No: Top Hit Accession No: Top Hit Accession Source 18541 28826 3.94 3.3E-01 P47963 SWISSPROT SWISSPROT 18763 4.79 3.3E-01 AA8806621.1 EST HUMAN	Exon NO: ORF SEQ Signal NO: Expression Signal Value (Top) Hit No. Top Hit Accession No. Top Hit Accession No. Top Hit Accession No. Top Hit Accession Source 18541 28826 3.94 3.3E-01 P47963 SWISSPROT SWISSPROT 19791 19791 1.88 3.3E-01 AA806621.1 EST HUMAN NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit RLASTE Value Top Hit Accession No. Top Hit Accession Source 18541 28826 3.94 3.3E-01 P479633 SWISSPROT SWISSPROT 18763 4.79 3.3E-01 AA806621.1 EST HUMAN 10000 19791 1.88 3.3E-01 X07990.1 NT 18881 28789 1.63 3.3E-01 6598319 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Hit Nature Top Hit Accession No. Top Hit Source 18541 28825 3.94 3.3E-01 P479633 SWISSPROT SWISSPROT 1.88 18641 28826 3.94 3.3E-01 P479633 SWISSPROT EST HUMAN 1.88 19791 1.88 3.3E-01 AA806621.1 EST HUMAN NT 19881 28789 1.63 3.3E-01 6598319 NT 19323 6.05 3.3E-01 AP000002.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Hash Top Hit Accession Nature Top Hit Accession No: Top Hit Accession No: Top Hit Accession Source 18541 28826 3.94 3.3E-01 P479633 SWISSPROT 18783 4.79 3.3E-01 AA806621.1 EST HUMAN 19791 1.88 3.3E-01 AA806621.1 EST HUMAN 19881 28789 1.63 3.3E-01 AF000002.1 NT 19323 6.05 3.3E-01 AF018261.1 NT 10393 1.38 3.2E-01 AF018261.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit RASTE Value Top Hit Accssion No. Top Hit Accssion Source 1B NO: Signal Value Value No. Source 18541 28826 3.94 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P47963 SWISSPROT 18861 28789 1.88 3.3E-01 AR806621.1 EST_HUMAN 19323 6.05 3.3E-01 AF000002.1 NT 10834 2.06 3.2E-01 AF018261.1 NT 10834 2.05 3.2E-01 AF1618261.2 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Palabase Top Hit Accssion No. Top Hit Accssion Source 18541 28826 3.94 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P47963 SWISSPROT 18764 28826 3.94 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P4806621.1 EST_HUMAN 19323 6.06 3.3E-01 AP000002.1 NT 10393 1.88 3.2E-01 AF018261.1 NT 10634 2.06 3.2E-01 AF018261.1 NT 11059 20902 18.89 3.2E-01 AF047013.1 NT	Exon NO: ORF SEQ ID ID NO: Expression Signal (Top) Hit Top Hit Accssion No: Top Hit Accssion Source Top Hit Accssion Source 1B NO: Signal Signal 1B LASTE No: No: Source 18541 28826 3.94 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P47963 SWISSPROT 18861 28789 1.88 3.3E-01 AR806621.1 EST_HUMAN 19323 6.06 3.3E-01 AP000002.1 NT 10393 1.38 3.2E-01 AF018261.1 NT 11059 20902 18.89 3.2E-01 AF047013.1 NT 11168 27019 1.04 3.2E-01 AF047013.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Palabase Top Hit Accssion No. Top Hit Accssion Source Top Hit Accssion Source 18541 28826 3.94 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P47963 SWISSPROT 18861 28789 1.68 3.3E-01 M500002.1 NT 19323 6.06 3.3E-01 AP000002.1 NT 10834 2.09 3.3E-01 AF018261.1 NT 11059 20902 18.89 3.2E-01 AF047013.1 NT 11168 21019 1.04 3.2E-01 AF047013.1 NT 11174 21130 6.25 3.2E-01 SWISSPROT NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Patch Top Hit Accession No. Top Hit Accession Source Top Hit Accession Source 18541 28825 3.94 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P47963 SWISSPROT 18763 4.79 3.3E-01 P4806621.1 EST_HUMAN 19791 1.88 3.3E-01 AR806621.1 EST_HUMAN 19881 28789 1.63 3.3E-01 AF000002.1 NT 19323 6.05 3.3E-01 AF018261.1 NT NT 10834 2.05 3.2E-01 AF047013.1 NT 11069 20902 18.99 3.2E-01 AF047013.1 NT 11168 27109 1.04 3.2E-01 AF047013.1 NT 11274 21130 6.25 3.2E-01 SWISSPROT R 11638 2150 3.2E-01 23604.1 NT R	Exon NO: ORF 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6.05 3.3E-01 AP000002.1 NT 19324 5.05 4.79 3.3E-01 AP000002.1 NT 19325 6.05 3.3E-01 AP000002.1 NT NT 10834 2.05 3.3E-01 AP018261.2 NT 11083 2.0902 1.04 3.2E-01 AP047043.1 NT 11645 2.151 6.25 3.2E-01 AP047043.1 NT 11645 2.151 3.2E-01 2.36041.1 NT ST HUMAN 11658 2.151 4.1655.1 1.1	Exon NO:- ORF SEQ ID NO:- Expression Signal Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession Source No:- Top Hit Accession No:- Top Hit Accessio	Exon NO:- ORF SEQ ID NO:- Expression Signal (Top) Hit Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession Source No:- 1854 1 28826	Exon NO:- ORF SEQ ID NO:- Expression Signal Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession Source No:- Top Hit Accession No:-	Exon NO:- ORF SEQ ID NO:- Expression Signal Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession Signal Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession Signal Top Hit Accession No:- Top Hit Accession Signal Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession Signal Top Hit Accession No:- Top Hit Accession No:- Source Source No:- Source Source No:- Source Source No:- Source Source No:- Source Source No:- Source Source No:- Source Source No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Acce	Exon NO: CRF SEQ ID ID NO: Expression Signal ID NO: Most Similar No: Top Hit Accession No: Top Hit Access	Exon NO: Signal ID NO: Signal ID NO: Most Similar Signal Accession Top Hit Accession Pathwase Signal Accession Top Hit Accession Pathwase Signal Accession Top 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Source Top Hit Acession Sourc</td> <td>Ekon NO: ORF SEQ Signal Expression (Top) Hit Value Most Similar Part Top Hit Acession Value Top Hit Acession Part Top Hit Acession Source Top Hit Acession Source Source Source Source Source Source Source Source Source Sourc</td> <td>Evon NO: ORF SEQ Signal Expression (Top) Hit Value (Top Hit Acession Value Top Hit Acession Source Top</td> <td>Evon NO: Inc. ORF SEQ Signal Expression Paths (Tφp) Hit Paths Top Hit Acession Paths Top Hit Aces</td> <td>Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Pulse Pulse In No: Top Hit Accession Pulse In No: Top Hit Accession Source Source Top Hit Accession Source Top Hit Accession Sourc</td>	Exon NO: DRF SEQ ID ID NO: Expression Signal (Top) Hit Top Hit Acession No: Top Hit Acession Source Nation Database Nation Database Nation Database Nation Database Nation Database Nation Database Nation Database Nation Database Nation Database Nation Database Nation Database Nation	Exon NO: ORF SEQ ID NO: Expression Signal Most Similar (Top) Hit Value Top Hit Acession No. Top Hit Acession Source Top Hit Acession Source Top Hit Acession Source 18541 28826 3.94 3.3E-01 PA7963 SWISSPROT SOURCE 18763 4.79 3.3E-01 AR806621.1 EST HUMAN INT 19823 4.79 3.3E-01 AR806621.1 EST HUMAN INT 19834 28789 4.79 3.3E-01 AR806221.1 INT 10834 28789 1.68 3.2E-01 AR906022.1 INT INT 10835 1.08 3.2E-01 AR906022.1 INT INT INT 11059 2.0902 18.99 3.2E-01 AR9067194.1 INT INT 11645 2.1513 6.25 3.2E-01 AR957194.1 EST HUMAN INT 11645 2.1514 5.5 3.2E-01 AR957194.1 EST HUMAN INT 12646 2.203 3.2E-01 AR957194.1 EST HUMAN INT INT	Ekon NO: ORF SEQ Inchesion ID NO: Expression Signal ID NO: Most Similar Signal ID NO: Most Similar Signal ID NO: Top Hit Acession Value Top Hit Acession Parket Top Hit Acession Source Top Hit Acession Sourc	Ekon NO: ORF SEQ Signal Expression (Top) Hit Value Most Similar Part Top Hit Acession Value Top Hit Acession Part Top Hit Acession Source Top Hit Acession Source Source Source Source Source Source Source Source Source Sourc	Evon NO: ORF SEQ Signal Expression (Top) Hit Value (Top Hit Acession Value Top Hit Acession Source Top	Evon NO: Inc. ORF SEQ Signal Expression Paths (Tφp) Hit Paths Top Hit Acession Paths Top Hit Aces	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Pulse Pulse In No: Top Hit Accession Pulse In No: Top Hit Accession Source Source Top Hit Accession Source Top Hit Accession Sourc

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID	Exon SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database	Top Hit Database Top Hit Descriptor
	S		•	Value		Source	
6359	16807		1.35	3.2E-01	3.2E-01 AL161574.2	Ę	Arabidopsis thallana DNA chromosome 4, contio fragment No. 70
986	16863	27056	1.5	3.2E-01	3.2E-01 AE002015.1	Z	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome.
7247	17124		2.19	3.2E-01	3.2E-01 M86511.1	뉟	Human monocyte antigen CD14 (CD14) mRNA complete collection
7441	17591	27812	3	3.2E-01	3.2E-01 U44914.1	뉟	Borrelia burgdorferi plasmid co32-2. emC and emD genes complete ado: and united
330	17760		3.25	3.2E-01	3.2E-01 AB011399.1	뉟	Homo sapiens gene for AF-6, complete cals
8058	17949	28199	. 2.7	3.2E-01	T06813.1	EST HUMAN	EST04702 Fetal brain, Stratagene (catter 36206) Home caniens citing Licentification
9152	19662		3.28	3.2E-01	L07288.1	F	Drosophila melanodaster laminin A (I am.A) mRNA ಂಥಾಗಣಿಕ್ಕಾರ್ನೆ
6996	19228		2.97	3.2E-01 083217		SWISSPROT	ELONGATION FACTOR TU (EF-TI)
9801	19313		1.58	3.2E-01	3.2E-01 L39874.1	Z	Homo sapiens deoxicity deaminase gene complete cots
9855	19696	24898	1.67	3.2E-01	3.2E-01 BE385776.1	EST HUMAN	601275480F1 NIH MGC 20 Homo sabiens cDNA clone IMACE 3848748 #
2636	12503	22397	3.73	3.1E-01	R18051.1	EST HIMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to che MA4241 OM PROTEIN (41) MAAN).
2665	12655	22419	3.45	3.1E-01	7661971 NT	NT	Homo saniens KIAA0174 depe product (KIAA0474) DNA
2665	12655	22420	3.45	3.1E-01	7661971 NT	N	Homo sepiens KIAA0174 dene product (KIAA0474), mbNA
2827	12756		1.01	3.1E-01	3.1E-01 AW629036.1	EST HUMAN	hi46h08.x1 Soares NFL T GBC S1 Homp seniens cONA clone MAACE: 20222224 21
3136	13061		2.78	3.1E-01		NT	Mus musculus gene for Ser/Thr kinase KKIAMRE exon 6
3832	13744	23536	1.15	3.1E-01	Ì	F	Daucus carota mRNA for transcription factor F2F (F2F game)
5073	14943	24717	0.99	3.1E-01		L HUMAN	nm61h05.s1 NCI CGAP Br3 Homo sapiens cDNA clone IMA GE-1072784 21
5365	15285	25119	8.66	3.1E-01		Г	Homo sepiens hepatocyte nuclear factor-3 alpha (HNF3A) gene evon 1
5447	15368		45.03	3.1E-01		Ę	Mus musculus mRNA for polycystin
5527	15444	25510	1.94	3.1E-01		Į.	Homo sepiens filamin 2 (FLN2) gene, exons 10 through 22
88	15796	25918	1.34	3.1E-01	9.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sepiens cDNA
99	19438	24861	2.4	3.1E-01	2.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 F:
7023	16900	27092	1.87	3.1E-01		Γ.	yg48f01.s1 Soares infant brain 1NIB Home sapiens cDNA clone IMAGE ਕੁਸਤਾਰ ਕਾ
13	17641	27874	7.76	3.1E-01		П	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5:
	17641	27875	7.76	3.1E-01	3.1E-01 BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_66 Homo sapiens cDNA clone IWAGE:4281611 5
7832	17682	27928	1 06	2 Т.		-	aj61e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700
8211	18095	28348	1.95	3 15 01		NAME OF	ENGREDATE WILL MAY 1-COA LYASE PRECURSOR (HUMAN);
8823	18636	28920	1.99	3.1E-01	7662291 NT	CANO	Homo seniens KIA 40784 generated to the Authority Come IMAGE: 4095814 5
9279	18082	-	6	100			Anolis opalinus Isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene
9315	19007		1.03	3.15-017	3.1E-01 AF294308.1	2 2	Tor mitochondrial product
9457	19089		20.0	9.4E 04.7			Suzzestedion vireum 4US ribosomal protein S11 mRNA, partial cds
			22	V: 15-01/	_		Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene. complete cds

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Homo sepiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,		e), mKNA	Siment 1/2	atriuretic pentide	about the second	Connebacterium sp. Al V-1 ab D-2 mans for policium in the second subunit mKNA, 3' untranslated region	oyyunun kare iyase, complete cos	ouplette outlier	NA close IMA CE:2040724 E	Sanlans CDNA	Organia Company	(mCC40) man and an analysis	(moore) gene, comprese cos	4	(psnΔ) gene nartial cde	complete genome	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clecst9), mRNA	DNA close MACE:3684504 E	BIP complete ode	VD84b10.r1 Scares fetal liver soleen 1NFI S Homo saniens child a close MAA GE 200407 Et	W84b10.r1 Soares fetal liver spleen 1NFI S. Home saniens child close IMA CE. 19410/ 5	Rattus norvedicus mRNA for oluceraldahvie 2 phoenhate debud contract of the management of the manageme	A (Reis) mBMA	late denome	umplete genome	Complete cde	sapiens cDNA	conione cDAIA
Single Exon Propes Expressed in Heart		Homo sepiens transcription factor IGHM e JM10 protein, A4 differentiation-dependen	Wingiplete cds, and L-type calcium channel a>	Homo saniens Xn pseudoautosomel region (PKce), mKNA	xs63f08 xf NCI CGAP Kid11 Homo seriens cDNA class MA CE 277 22 2	Balaenoptera physatus gene encoding atrial natriuretic peptide	Raffus norvenicus Ca2+/celmodulin dena	Connehacterium sp. Al V-1 ah/DC connefactorium in asset it, alpha subunit	PM1-ST0262-261199-001-001 ST0262 Home seriens child	Balaenoptera physal is gene encoding atrial patriaretic parties	601594960F1 NIH MGC 9 Homo saniens china clare (NAA CE:2048724 51	RC3-BT0333-180700-111-803 BT0333 Home seniors CDNA	RC3-BT0333-180700-111-a03 BT0333 Home seriens CDNA	Mus muscullus 129/sv Clara cell 10 kd protein (mCC10)	Mouse cytokeratin 15 gene complete cds	Mus musculus midnolin (Midn-pending) mBNA	Streptococcus pneumoniae strain DBI 5 PsnA (nsnA) gene nartial cds	Thermotoga maritima section 67 of 136 of the complete genome	Mus musculus C-type (calcium dependent (Clecsf9), mRNA	601339079F1 NIH MGC 53 Homo seciens cONA close MAAGE-3684504 F	Aspergillus oryzae bipA gene far ER chaperone BiP completa As	yp84b10.r1 Soares fetal liver soleen 1NFI	yp84b10.r1 Soares fetal liver spleen 1NFI	Rattus norvegicus mRNA for gluseraldehy	Mus musculus ribose 5-phosphate isomerase A (Reia)	Aquifex agolicus section 68 of 109 of the complete genome	Chrysodidymus synuroideus mitochandrian complete genome	Xenopus laevis transcription factor E2F mRNA complete cds	PM1-CT0326-171299-001-f12 CT0326 Homo saplens cDNA	PM1-CT0326-171209-001-f12 CT0326 Light - CT03
gie Exori Proc	Top Hit Database Source	t	LIV	Į.	T	Į.	5	F	HUMAN	Т	EST HUMAN	EST HUMAN	Τ							T HUMAN		EST HUMAN	Т	Т			Ę		EST_HUMAN	FST HIMAN
)IIO	Top Hit Acession No.	2 1E 04 0 E 10 2770 4	AL 1907 / B. I	AJ271735.1	L		3.0E-01 AF237778 1	T	5.1				3.0E-01 BE693575.1	Γ		3947007	AF071810.1	3.0E-01 AE001755.1	9910161 NT	3.0E-01 BE566083.1		3.0E-01 H51029.1		3.0E-01 AJ297631.1	67776		2.9E-01 AF222718.1		_	2.9E-01 AW754239.1
	Most Similar (Top) Hit BLAST E Value	е П	2 OF 04	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01,	3.0E-01	2.9E-01	2,9E-01	2.9E-01	2.9E-01	2.9E-01
	Expression Signal	6.	4.58	11.12	1.89	6.26	0.86	0.98	1.34	1.91	5.34	3.18	3.18	3.51	2.61	2.57	1.35	1.25	4.67	1.27	1.89	2.89	2.89	1.43	2.76	1.6	0.99	1.03	2.29	2.29
	ORF SEQ ID NO:		19866	20037	20960	21256	21873		23488	24089	24981	25147	25148	25368	26171	26358	26451	26693		27007	28034	29074	29075			21762	21989	22873	22939	22940
	Exen SEQ ID NO:	19318	12635	10220	11114	11396	11978	13100	13701	14306	15205	15298	15298	15320	16031	16198	16290	16505	16756	16815	17794	18785	18785	19647	.19690	11871	12088	13072	13137	13137
	Probe SEQ ID NO:	9806	8	254	1204	1491	2089	3175	3789	4412	5283	6379	5379	5401	9809	6335	6429	929	6877	6937	7944	8980	8980	9564	9836	1978	2201	3147	3213	3213

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Single Exon Probes Expressed in Heart

24034 0.98 2.8E-01 ALDZ1127 24038 2.2 2.8E-01 P13615 24352 1.03 2.8E-01 D15050.1 24353 1.03 2.8E-01 D15050.1 24394 2.8 2.8E-01 AF030154 24459 1.54 2.8E-01 BF528188 24459 1.7 2.8E-01 AA249997 25419 2.33 2.8E-01 AB016628
2.33 2.8E-01 AB016625.1
1.34 2.8E-01 bi-528188.1 1.7 2.8E-01 AI272669.1 21.36 2.8E-01 AA349997.1 2.33 2.8E-01 AB016625.1 1.44 2.8E-01 AB016625.1
1.03 2.8E-01 [015050.1 2.8 2.8E-01 [015050.1 1.54 2.8E-01 [BF628180] 1.7 2.8E-01 [AIZ72669]
1.03 1.03 2.8 1.54 1.7
24034 24352 24353 24353 24354 24427 24459 24948 25419 25419

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Table 4
Single Exon Probes Expressed in

	Top Hit Descriptor	9p48h01x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAI PROTEIN I 3 (14) IMANN:	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens CDNA clone Adore Index:1926289 3' similar to gb:X06323_cds1	Homo sapiens lanosterul 14-alpha demothydaca arta-	602022987F1 NCI CGAP BIRIT Home seniors child also MACE 44 F050 - 1	she complete of	Lycobersican esculentum peraddese (TPX4) mBMA	Table (1) All minds, complete cas	601880794F1 NIH MGC 55 Home saplers cPNA class [MA CE: 1100552 2]	601880794F1 NIH MGC 55 Homo seniens cDNA clare NAACE:4109350 5	601852148F1 NIH MGC 56 Homo seniens cDNA clone IMAGE: 402500 5	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7	602137418F1 NIH MGC 83 Homo cardens cONIA aless MA OF Joneses at	Mus musculus DNA for proceedanding Do a rather a	Topic U	Homa saniens CDCA2-hinding professional Linear Leaving III.	October National Color (COC428PB), mRNA	239b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827.3' similar to	(Amont TI-400	Glambia SR2 gene	zd22h10.r1 Soares fetal heart NbHH19W Home servieur CRNA class MACE 244,00-1	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NI ICI COBDOTTEIN PAN	יוא ר'וט]	Feline imminodeficiency view company of the property of the compan	1843-11.x2 More). GGAP_Lu26 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1	TA07E 1	100/3 From Sapiens GUNA	Homo seniens Difference marketing appliens CDNA crone IMAGE;2462828 31	complete cds
Single Exon Probes Expressed in Heart					T	Т	Lycopersicon esculentum peroxic	Homo saplens hypothetical protein (1 OC\$1310) mBNA	Г	Т	Т	Drosophila heteroneura fruitless (Т	Т	Т	T	Rattus norvedicus CDK 104 mRNA	1	T	Glambia SR2 gene	Ţ	GAG POLYPROTEIN (CONTAINS: INNE	Rathis nonedicits vericular mana	Feline immi modeficiency virus om		\top	Т	Homo sanions Difference and trans-	Triticum aestivum (Wcs66) gene, complete cds
gle Exon Pr	Top Hit Database Source	EST HUMAN	EST HIMAN	S L	EST HUMAN	Z	Į.	₽ L	EST HUMAN	EST HUMAN	EST_HUMAN	L Z	EST HUMAN	IZ I	EST HIMAN	L	N FN	EST HIMAN	LN	N.	EST HUMAN	SWISSPROT	TN	L	ENT HIMAN	EST HIMAN	EST HIMAN	L	본
Sin	Top Hit Acession No.	2.8E-01 Al346126.1	2.8E-01 Al346126.1	2.8E-01 U51688.1	2.8E-01 BF347847.1	2.8E-01 AF080592.1	2.8E-01 L13654.1	7706163 NT	2.8E-01 BF241062.1	2.8E-01 BF241062.1	2.8E-01 BF695970.1				39.1	1433629		1.2		Γ	2.7E-01 W58067.1		5.1		2	-	T		
	Most Similar (Top) Hit BLAST E Value	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.7E-01 Y17324.	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01 P03341	2.7E-01 AF04757	2.7E-01 Y13868.	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01 L27516.1
	Expression Signal	1.24	1.24	2.39	7.25	1.35	1.15	2.79	2.27	2.27	3.01	2.62	3.49	6.37	3.11	1.69	2.33	3.14	1.49	1.73	2.96	1.25	2.38	8.78	3.51	1.25	1.88	2.31	0.89
	ORF SEQ ID NO:	26781	26782	26847		27388			28261	28262	28291	28382			25236		20230	20341	20996		21471	21507		22094	22180		23618	23626	24468
	Exon SEQ ID NO:	16593	16593					17639	18014	18014	18041	18134	18466	19150	19219	19851	10411	10533	11147	11509	11600	11639	12712	12197	12283	12883	13838	13851	14681
	Probe SEQ ID NO:	6713	6713	8778	6994	7311	200	7789	8126	8128	8153	8254	8599	9552	9657	9826	468	597	1240	1604	1698	1738	2088	2316	2406	2956	3929	3943	4798

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			Most Similar			On the Charles Expressed in real
ORF SEQ ID NO:		Expression Signal	(Top) Hit BLAST E Value	Top Hit Acesston No.	Top Hit Database Source	Top Hit Descriptor
		3.5	2.7E-01	2.7E-01 AW856131.1	EST HUMAN	RC1-CT0286-230200-016-903 CT0/286 Home capient CDNA
24838	8	3.49	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX A4 (CHOX-1 4)
26192	0	2.25	2.7E-01	2.7E-01 Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
26565	35	2.23	2.7E-01	2.7E-01 AF248054.1	NT	Bos faurus micromolar calcium activated neutral protease 1 (CAPN1) name evens 11,20 and another beautiful
26566	99	2.23	2.7E-01	2.7E-01 AF248054.1	Į	Bos fairus micromolar calcium activated northal access 4 (2012).
27,	27453	10.08	2.7E-01	2.7E-01 083809	SWISSPROT	THREONY - TRNA SYNTHETASE /TUBEONINE TRNA 10.000 (CAPANI) gene, exons 11-20, and partial cds
27.	27454	10.08	2.7E-01	2.7E-01 O83809	SWISSPROT	THREONY TRNA SYNTHETASE (THREONINE TRNA LICASE)
		2.24	2.7E-01	2.7E-01 P37928	SWISSPROT	FIMBRIAE W PROTEIN
27	27888	1.29	2.7E-01	2.7E-01 AF091848.1	¥	Onyctolagus cuniculus calgrandin C mRNA, partial eds
27	27921	1.93	2.7E-01	2.7E-01 AF087434.1	F	Mus musculus transcription factor NE-ATc leaform a Mis AT1 - DNA
28	28322	1.76	2.7E-01	AV705043.1	EST HUMAN	AV705043 ADB Home sapiens CDNA clane ADRCOPAR F
찌	28323	1.76	2.7E-01	2.7E-01 AV705043.1	EST_HUMAN	AV705043 ADB Homo saplens cDNA clone ADBCODO5 5
7	28333	4.09	2.7E-01	2.7E-01 AJ133269.1	ħ	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2).
		1.27	2.7E-01 X95267	X95267.1	LN	G dallus mRNA for remodine recenter time 2
		2.15	2.7E-01	2.7E-01 AF217491.1	Į.	Homo saplens fragile 16D oxido reductase (EOR) name oximia
٦	20224	1.54	2.6E-01 P78411	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX.2
		1.39	2.6E-01 D16459.		F	Bos faurus mRNA for mb-1, complete cds
ام	21133	2.23	2.6E-01	2.8E-01 BE885087.1	EST HUMAN	601510838F1 NIH MGC 71 Home saniens CDNA clone IMACE:301224E E
٦	21188	26.0	2.6E-01		TN	Glycine max pseudogene for Bd 30K
2	21624	8.59	2.6E-01 AL16147	2.2	Ŋ	Arabidopsis thaliana DNA chromosome 4. contig fragment No. 2
۱۳	21625	8.59	2.6E-01		NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
						bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAI PROTEIN 174 (UIIMAN): ALMAAGO
	7	9.9	2.6E-01 AW7331	AW733152.1	EST HUMAN	(MOUSE);
'n	21895	12	2.6E-01 M11844.	1	Ę	Human prealbumin gene, complete cds
1	-	2.68	2.6E-01 Y12996.		¥	B.maritimus rbcl. oene
		9.68	2.6E-01	2.6E-01 BE272440.1	EST HUMAN	601126016F1 NIH MGC 9 Home sanlane CDNA alane 1440F-2006 20 E
	\exists	1.03	2.6E-01		Γ	EST386635 MAGE reseguences. MAGM Homo saniens china
		0.94	2.6E-01 BE21781	6.1	Г	hv30c02.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3174914 3' similar to contains L1.t3 L1 repetitive element
23245	45	1.12	2.6E-01 M22342.		Т	Bacteriphage T2 DNA (adenine-N6)methyltransferace (Aam) anno anno ber
						ייייייייייייייייייייייייייייייייייייי

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Table 4
Single Exon Probes Expressed in Heart

	1																												
	Top Hit Descriptor	Homo sapiens acetylcholinesterase collenen like tril submitte tril	Rattus novegicus mRNA for organic anion transcrete: 3 cm-lot 4	EST371580 MAGE recentlences MACE Home conjune and A	QV1-BT0630-040400-132-e03 BT0630 Home Saniers CNNA	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds, and unknown cene	Gallis gallis mBNA for ekeletel musein beaute.	Gallus gallus mRNA for chalche mania had a complete cds	aa8907 rt Stratanene febal retinn 037202 Long a complete cds	Arabidopsis thallang PSI type III chlorophyll aft-hinding protein (1 p. 2514). East	Ontreetta radicasa metirasa ilto metiria (metirasa il metirasa il metirasa il metirasa il metirasa il metirasa	Vis1e05 rf Scares nacedta Nikolub Location (maux) gene, complete cds; chicroplast gene for chloroplast product	ACYI-COA DEHYDROGENASE MEDILIM CHAIN SPECIFIC VITCOLOSES.	Thermotoga maritima section 123 of 136 of the complete general	Aliques apardinos con los constantes de la constante de la con	ts02e12.x1 NCI_CGAP_Pan1 Homo sepiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1orbring classes at 12.	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT	Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element:	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONI ICLEODDOTTEIN CALLIMARIA.	ye32a07.r1 Sogres fetal liver soleen 1NFI S Homo sarians contact change that the contact of the	602014422F1 NCI CGAP Bm64 Homo saniers CDNA cline MAGE: 146725 5	HYPOTHETICAL 76.2 KD PROTEIN C11C11 02 IN CHRONICE II	RC5-ET0082-310500-021-F10 ET0082 Homo sablens cDNA	RC5-ET0082-310500-021-F10 FT0082 Home saniens conida	VON WILLEBRAND FACTOR PRECIESOR ANAMEN	Human lambda-imminoolohinlin constant region commercial	Mus muscalus ierkv (1k) mRNA	601511052F1 NIH MGC 71 Home sanions COMA circ. MACE COCCOCA 22	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
21 - 100	Top Hit Database Source	뉟	Į.	EST HUMAN	EST HUMAN	Ę	Ę	Ę	EST HUMAN	Į.	<u> </u>	EST HIJMAN	SWISSPROT	NT		EST_HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	SWISSPROT	M	Į.	EST HUMAN	Z
	Top Hit Acession No.	AF229118.1	2.6E-01 AB017446.1	2.6E-01 AW959510.1	2.6E-01 BE080598.1	2.6E-01 AF175293.1	AB021180.1	AB021180.1	2.6E-01 AA457617.1	ļ	03.1	H04858.1	P08503	2.6E-01 AE001811.1		2.6E-01 AI582557.1	Alcoher A	Z.0E-01 A1382337.1	R10365.1	R02411.1	2.6E-01 BF343588.1			39.1			10190655	2.6E-01 BE883491.1	\prod
	Most Similar (Top) Hit BLAST E Value	2.6E-01 AF229	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01 AB021	2.6E-01	2.6E-01	2.6E-01	2.6E-01 AF1427	2.6E-01 H04868	2.6E-01 P08503	2.6E-01		2.6E-01	200	Z.0E-U1	2.6E-01 R10365	2.6E-01 R02411	2.6E-01	2.6E-01 Q10199	2.6E-01	2.6E-01	2.6E-01 Q28295	2.6E-01 X51755.	2.6E-01	2.6E-01	2.6E-01 AF31689
	Expression Signal	1.7	6.0	1	13.13	0.95	0.84	0.84	1.17	1.63	1.28	3.56	0.86	2.03		1.93	6	36.	1.52	1.27	3.01	2.04	4.34	4.34	1.16	93.65	1.98	1.92	2.6
	ORF SEQ ID NO:	:			23742	23935	24072	24073	24134	24224	24292	24554	24696			25777	25778		26588	26656	26925	26973	27112	27113		_			25309
	Exon SEQ ID NO:			13916	13964		14289	14289	14342	14441	14504	14776	14923	19764		15670	15670		16410	16465	16731	16779	16923	16923	17704	18625	18892	19655	19053
	Probe SEQ ID NO:	3591	3651	4010	4062	4259	4393	4393	4448	4548	4616	4896	5051	9200		5763	5763		6552	6585	6852	0000	7046	7046	7854	8812	9136	9328	9395

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Top Hit Acession Signal BLASTE No. Source	0.89 2.5E-01 AB011070.1 NT Mus musculus gene for uncoupling profein 3.5-flanking region and noted E1 1715	0.86 2.5E-01 AW663183.1 EST HUMAN TAR1 repetitive element:	0.86 2.5E-01 AW663183.1 EST HUMAN TAR1 repetitive element:	L	25E-01 AF134119.1 NT	N.	EST HUMAN	2.5E-01 BF038595.1 EST HUMAN	1.1 EST HUMAN	2.5E-01 U89651.2 NT	Z NT	64.1 NT		997.1 EST HUMAN	246.1 EST HIMAN	_	NT.	LN	L L	LN	2.4E-01 AA936316.1 EST HUMAN	24.1 EST HUMAN	2.4E-01 AJ28980.1 NT	2.4E-01 AJ289880.1 NT	2.4E-01 Y17293.1 NT	2.4E-01 AF267753.1 NT	2.4E-01 AF251708.1 NT	2.4E-01 ÁF111168.2 NT	2.4E-01 P45384 SWISSPROT	П
	Most Similar (Top) Hit BLAST E Value																		2.5E-01	2.5E-01	2.5E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01 /	2.4E-01/	2.4E-01	2.4E-01/
	Expression Signal	0.89	0.86	0.86	11.62	1.32	3.73	2.99	2.25	3.95	16.11	18.11	2.04	2.04	1.5	. 1.62	1.68	2.32	2.45	4.2	1.28	1.53	2.38	17.41	17.41	1.04	24.08	1.41	0.88	1.16	2.01
	ORF SEQ ID NO:	24421	24802	24803	24962				26858	27087	27554	27555	27547	27548	27904	28105	28106	28556	29117		25072	20282	20608	21041	21042	21123		21629	21875	- 10000	22005
	Exon SEQ ID NO:	14635	15035			' 1	_1	16463	16667	16897	17351	17351	17341	17341	17664	17860	17861	18300	18851	19729	19581	10482	10757	1199	11190	11268	11/05	11/54	1380	12010	10121
	Probe SEQ ID NO:	4750	5169	5169	5264	9989	9200	6583	6788	7020	7481	7481	7622	7522	7814	8010	8011	8426	9074	9	822	541	8	1282	1282	1362	1808		150 E	27.22	22

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor Source	7h23d04.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW.PRSB_XENLA	Z		P.	NT Onza londistaminata recentor kinace like pertein formits.	NT H septems AGT gene Peet frameant of the and the control (gagpo) genes, complete cds	EST HUMAN	-				I HUMAN		661801 NT Homo saplens HSPC142 protein (HSPC142) mRNA	wc92c11x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 EST HUMAN PROCOLLAGEN ALPHA 2(1) CHAIN PRECEIPSOD (HIMAN)	Т		wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains EST HUMAN MER22 bt TAR1 renetitive element:	Т	Т		NT Pasiatica moselo virus centralir RNA					EST HUMAN RC3-CT0413-100800-023-b06 CT0413 Homo sanions of NA	П	NT aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
Top Hit Acession No.	2.4E-01 BF002171.1	Z36534.1	2.4E-01 X71783.1	2.4E-01 AF030154.1	2.4E-01 U72726.1	2.4E-01 X74209.1	2.4E-01 BE160080.1	D00944.1	2.4E-01 AF091216.1	2.4E-01 AF091216.1		Z.4E-01 BF-39Z336.1	2.4E-01 AF035546.1	766180	2.4E-01 Al698989.1	43001.1	2.4E-01 AJ012585.1	2.4E-01 Al693515.1	203692	2.4E-01 AL161494.2	2.4E-01 AF030199.1	221647.1	2.4E-01 AF217491.1	2.4E-01 AF004213.1	2.4E-01 AJ278191.1	/01507.1	2.4E-01 BF229975.1	2.4E-01 AL163281.2	375898.1
Most Similar (Top) Hit BLAST E Value	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	r T	2.45-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01 L43001.1	2.4E-01	2.4E-01	2.4E-01 Q03692	2.4E-01	2.4E-01	2.4E-01 Z21647.1	2.4E-01	2.4E-01	2.4E-01/	2.4E-01 V01507.1	2.4E-01	2.4E-01	2.3E-01 S75898.1
Expression Signal	0.85	1.63	2.14	6.68	2.82	1.85	0.88	50.15	7.53	7.53	0,70	2 2 2	2.66	2.16	1.79	8.87	1.62	5.72	1.93	3.63	1.99	2.42	1.55	2.39	2.64	1.59	1.26	3.35	6.0
ORF SEQ ID NO:	22111		22491		•	22831		24622	25451	25452	25503	20000	25048	25/14	25966	26371	26931	27511	28056	28285	28347		29109						20153
Exon SEQ ID NO:		l		12618	13020		14700	14856	15389	15389	1.550 R		0,027	2001	15842	16208	16739	17305	17815	18037	18093	18406	18821	19526	18945	19509	19716	19355	10330
Probe SEQ ID NO:	2332	2491	2734	2756	3093	3109	4817	4981	5469	5469	5503	5642	2042	20/6	5937	6346	9860	7617	7965	8149	8209	8534	9030	9162	9222	9439	9650	9865	383

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Most Similar			_	_	-			_	_	_	_	_	٠,						_							-,			_		
SEC ID ORF SEQ Expression Top Hit Acession	bes Expressed in Heart	Top Hit Descriptor	Mycoplasma genitali m section 35 of 51 of the asset of a	Methanococcus lannaschill section 138 of 150 of the conjusted genome	60142073F1 NIH MGC 14 Home sapleme and a language late of the company of the comp	Mus musculus vacuolar protein sorting 4h (vesst) (Vrs.4h) ~DNA	Verelyla naette Umott (twott), two f. / /	Brassica names for Schools charactering and Has (hmsS) genes, complete cds	Mus musculus only sens for a chock siyeuprotein, cuitivar 12	Homo sapiens partial infrom 3 of the wild have AE 4/EET name	601175562F1 NIH MGC 17 Homo saniens cDNA dama IMA CE 2524645 ET	Human erythropoletin gene, complete cds	Marinilabilia agarovorans gvrB gene for DNA grasse subunit B andial ad	no/6d06.s1 NCI_CGAP_Phet Home septembles CDNA clone IMAGE:1100843 3' similar to contains Alu	wh21b07 st Scares placents Nb2HD Home conjust and all the control of the control	y97h10.r1 Soares fetal liver spleen 1NFI S Homo seniens cDNA cland MA CE 130357 3	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic,	Homo sapiens Klaandring (Kitakovica) — Daira	vi 7701. rl Spares placenta NhOHD Homo conjune, DNIA	Mus musculus renin (Ren-1c) dens momente region	Synechocystis sp. PCC6803 comblete nervome 1/27 1.133886	Homo saplens mitogen-activated protein kinase p38delta (PRKM13) DNA	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Human phenyethanolamine N-methyltransferase nene commission	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis	(Lin-1-1) gene, noregene, and sodium phosphate transporter (NPT3) gene, complete cds	Esviralish a cull n-12 Michob Section 130 of 400 of the complete genome	nomo sapiens mkny for KIAA1512 protein, partial cds	MANDENDE XI NCI_CGAP_OVI8 Home sepiens cDNA clone IMAGE:3476699 3' similar to SW;GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS; CORE PROTEIN P15: INNER COAT BROTEIN P19.	SHELL PROTEIN P30; NUCLEOPROTEIN P101;
Exon No: ORF SEQ Expression Signal SEQ ID (Top) Hit Top Hit Aces No: Top Hit Aces No: 10558 4.42 - 2.3E-01 U39713.1 10587 20403 19.84 2.3E-01 U39713.1 11687 20403 19.84 2.3E-01 U39713.1 11689 2.1258 1.5 2.3E-01 U37597.2 11450 2.1258 1.5 2.3E-01 HB231.893.1 11892 2.1258 1.5 2.3E-01 HB231.893.1 12483 2.3E-01 HB231.893.1 1.29 2.3E-01 HB231.893.1 1271 2.127 0.88 2.3E-01 HB01793.1 13244 2.3E-01 HB232.2 1.1 2.3E-01 HB01833.1 13679 2.3E-01 HB01833.1 1.3E-01 HB01833.1 13679 2.3E-01 HB01833.1 1.3E-01 HB01833.1 14284 2.3E-01 HB01833.1 1.42E-01 HB0183.1 14284 2.3E-01 HB0183.1	Jie Exon Prot	Top Hit Database Source	Z	Į.		.4			5	N-	EST HUMAN	N.	¥	EST HUMAN	ST HUMAN	EST HUMAN	5	: 5	T HUMAN						П						EST_HUMAN
Exon No: ORF SEQ DID NO: Expression Signal Did NO: Mos Signal Did NO: Mos Signal Did NO: Mos Signal Did NO: Mos Signal Did NO: Mos Did No: Mos Did	ùis	Top Hit Acession No.			Γ	6677980		80.1	2	53.1	18.1							7662133		-		AF092535.1			5.1	•			-		
Exon ORF SEQ Express SEQ ID NO: Signe NO: 10558 10557 11398 21258 11450 21351 11451 2274 22169 12274 22372 112861 22651 13679 23926 14158 24455 0 14868 24455 0 15169 24942 15169 24944 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24944 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24944 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 24942 15169 15		Most Similar (Top) Hit BLAST E Value	- 2.3E-01	2.3E-01	2.3E-01	2.3E-01	23E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E.01	23F-04	23F-01		. 1	2.3E-01
Exen SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	4.42	19.84	3.35	1.5	0.88	1.38	2.75	1.3	1.56	1.02	0.88	1.29	5.73	1.09	1.11	3.72	0.85	3.35	1.02	2.08	5.1	0.82	0.95	86.0	26.95	26			1.71
		ORF SEQ ID NO:		L				21351	21378		22169	22372	21127	22661	-	23051	23461		23926		24031	24061	24140	24455	24641	24745	24783	24942		,	Z20141
SEQ ID NO: NO: 1494 1494 4349 4386 5332 5546 5536 5332 5546 5536 5332 5546 5536 5332 5546 5535 5332 5546 5535 5332 5546 5535 5332 5546 5535 5332 5546 5535 5332 5546 5535 5332 5546 55332 5546 5546 5546 5546 5546 5546 5546 554		Exon SEQ ID NO:	10558		L			L.	11518	11892	12274	12483	11271	12861	12972	13244	13679	13767	14152	14198	14245	14282	14348	14668	14877	14969	15013	15169		6	125261
		Probe SEQ ID NO:	621	651	918	1494	1546	1586	1614	1999	2396	2615	2794	2934	3045	3324	3766	3856	4253	4300	4349	4386	4454	4826	2005	5101	5146	5246		6230	3337

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Single Exon Probes Expressed in Heart

SEQ ID ID NO: Signal Most Similar Top Hit Acession Top Hit A		_		-, -				_					_							_									
Secondary Seco	Top Hit Descriptor	C.familiaris rom1 gene	as27e12.x1 Barstead aorta HPLRB6 Homo saplens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECTIPEOR (H. MANANA)	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA close IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECI IRSOD ALLIAMAN.	as42f12.xl Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu	Clyping may reciptance produin (M47	Mus muscinus masin XV (Mards) — Dala	601511573E1 NIH MGC 71 Home continue Child Jim Street E.	za12e08.r1 Scares fefal liver sipleen 1NFI S Home constant and a liver constant and a liver sipleen 1NFI S Home constant and a liver sipleen and a	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds	Haemophilus influenzae genes for Hincll restriction-modification system (Hincll methyltransferase (EC	MRQ-HT0559-240400-014-414 HT0559-1.21.4)	Rhizohli m legi milnesenim serial concerni PANA	601846155R2 NIH MCC 50 Long Control of the Copyright of t	Mus muscinis partial mBNA for muscle cont.	Mus musculus partial mRNA for muscle protein 534 (ng534 gene)	Chlamydninia paerimonice AR30 configure 4 - 6 4 - 6 4	Borrella birndonferi 2 0.8 locus ODE A D. 200	HCOEST44 HT29M6 Homo sabiens cDNA clane HOAE44 F	shri1424 seq F Hirman fetal heart I ambda ZAB Error	PM4-SN0012-030400-001-b06 SN0012 Homo sepiens cDNA 5	の21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar th TB:00347E	29Z175 LYSYL OXDASE-RELATED PROTEIN 2. contains PTR5 h2 TAR1 renefition along the contains and the contains are contained by the contains are contained by the contains are contained by the cont	301507202F1 NIH MGC 71 Homo saniens cDNA clone INA CE-3004800 c.	30214445BF1 NIH MGC 48 Homo cardene COMA close MGC 1.3000000 5	Saftus nomenicus mRNA for acid refed in channel	Sattus norveolous mRNA for acid dated for chancel	nac39h12.x1 Lupski_scietic_nerve Homo saplens cDNA clone IMAGE;3395950 3' similar to contains element	with the definent;
Exon NO: ORF SEQ Expression (Top) Hit Acession NO: Top Hit Acession (Top) Hit Top Hit Acession NO: Most Similar Value NO: Most Similar No: Most Similar No: Most Similar No: Top Hit Acession NO:<	Top Hit Database Source	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	L	Ł	T HUMAN	T			HIMAN		T HI IMAN	Vi dini				Т	Π	Т			П	Γ			TOT HIMAN	7
Exon ORF SEQ Expression Mose SEQ ID ID NO: Signal B 15314 25361 4.83 1.87 15533 25617 1.87 1.87 16246 26408 2.62 2.9 16349 26519 1.59 2.3 16544 26741 2.28 2.3 16549 26549 1.37 2.54 17590 27787 2.54 2.54 17590 27811 2.28 4.95 17897 2.8663 2.84 4.95 18898 2.53 2.84 2.84 18970 2.4990 2.05 2.97 19065 2.4995 2.05 2.99 19088 2.69 1.93 19088 4.54 4.54	Top Hit Acesslan No.			AI708840.1	AI718148.1	89.1	6754779	BE888071.1	N80983.1		_	83.1	21.7		Γ			1		9.1						9.1	9.1	=	
Exon SEQ ID ID NO: Signs NO: 15314 25361 25617 15533 25617 156346 26408 16346 26519 16544 26741 26741 26540 17562 27732 17787 17560 27811 17824 18397 28654 24990 24906 19708 19708	Most Similar (Top) Hit BLAST E Value	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	į	2.35-01 /	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01 F	
Exon SEQ ID ORF 15314 15314 16533 16533 16534 16534 16534 16534 1654 1654 1654 1654 1654 1654 1654 165	Expression Signal	4.83	1.87	1.87	3.93	2.62	3.19	1.59	2.9	2.28	1.37	254	226	4.95	2.84	2.84	2.39	2.53	20.46	1.65	207	i c	C0.7	4.88	1.93	2.09	4.54	2.67	
	ORF SEQ ID NO:		·							26741	27732	27787	27811		28663	28664	28830					24000	74990	24905					
Probe SEQ ID NO: 5395 5618 5618 6491 6491 6491 6491 7712 7712 7712 7712 7712 7712 7712 77	Exon SEQ ID NO:	{	- 1		16005	16246	16345	16349	16418	16544	17507	17562	17590	17824	18397	18397	18547	18838	18951	19477	18970	1068K		19708	1988	19088	19088	19310	
	SEQ ID NO:	5395	5618	5618	6111	6384	6487	6491	9290	6664	7657	7712	7740	7974	8525	8525	8658	9144	9232	9258	9266	0324	200	8056	3407	9456	9549	9793	

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	ptor	<u>u</u>	4.0E-4.202004 ET	100000 D	chorto.		ans sucreting milrochoodrial protein mentical at	and an analysis of the state of	ment of mitochordinal protein, partial cds	g protein (hmcC), putative ABC transporter smocin immunity protein (hmcl) genes, complete				0	ASE) (DGK-DELTA) (DAG KINASE DELTA)			0 8 3 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	oc, o, and panda cos	AGE:3223034 a'				has VHs2	To La Calif.	- OONOAK	Clanza			
Outgio Evolutiones Expressed III near	Top Hit Descriptor	Saccharomyces cerevisiae tau 138 (TFC3) gene, complete cds	602152001F1 NIH MGC 81 Homo sabiens CDNA clone IMAGE 1202001 F	Human olfactory recentor (OR17.2) gene partial cds	Archaeoglobus fulgidus section 135 of 172 of the complete general	Canis familiaris keratin (KRT9) gene, complete cds	Glycine max malate dehydrogenase (Mdh-2) gene. nuclear gene encoding milychowdrial acclains	Givolne max malate dehydronensea (Mdh-2) nana mintana anno mandii.	Mus musculus erythrocyte protein band 4.1-like 3 (Ent4.13) mRNA	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds	S. cerevisiae chromosoma II reading frame OBE VBI 035	A.thaliana mRNA for AtRenBP1b protein	Homo sablens o53R2 dene for ribonicileatide reduction	Beta vulgaris mRNA for elongation factor 1-hete	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACY GI YCEROLI KINASE)	Homo sapiens pancreatic polymentide 2 (PDV2) #RNA	RC3-HT0622-040500-013-b11 HT0622 Home sepiess CDNA	Homo sapiens fragile 16D oxido reductase (FOR) gene exms 8 0 and anti-d-d	Human granulin gene	7859e02x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE-3223034 3	Salvelinus alpinus mitochondrion, complete genome	Gallus gallus mRNA for avena, complete cds	Homo sapiens CGL18 protein (LOC51008), mRNA	O.cunniculus germline IqH heavy chain V-H pseudogene allohme VH=2	Mus musculus Major Histocompatibility Locus class (I region	Synechocystis sp. PCC6803 complete genome 7/27 781449 220015	Homo sapiens chromosome 21 segment HS21C013	Homo saplens rac1 gene	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
JIO LAGII L'ION	Top Hit Database Source	FN	EST HUMAN	Z	-N	N FN	L L	IN	N	. 5	Į	Į.	¥	Į		036647 NT	EST HUMAN	F	F	T_HUMAN				F	LN	LN LN	LN LN	TN	T_HUMAN	
	Top Hit Acession No.	2.1E-01 M98261.1	2.1E-01 BF672695.1		2.1E-01 AE000972.1	2.1E-01 AF000949.1	2.1E-01 AF068687.1	2.1E-01 AF068687.1	7305030	2.1E-01 U68399,1			2.1E-01 AB036529.1			1=	2.1E-01 BE180422.1	-		2.1E-01 BE672330.1	5835904 NT	2.0E-01 AB017437.1	7705601 NT		1		2	2	.1	503408
	Most Similar (Top) Hit BLAST E Value	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01 Z35786.1	2.1E-01 X97378.1	2.1E-01	2.1E-01 Z97067.1	2.1E-01 P52824	2.1E-01	2.1E-01	2.1E-01	2.1E-01 L32588.1	2.1E-01	2.1E-01	2.0E-01	2.0E-01	2.0E-01 M77085.1	2.0E-01	2.0E-01 D90905.1	2.0E-01 AL163213	2.0E-01	2.0E-01	2.0E-01
	Expression Signal	0.99	5.99	1.86	1.97	1.74	1.35	1.35	1.21	4.78	5.88	2.36	1.19	2.49	1.49	2.31	2.15	1.6	1.4	1.29	1.29	1.72	2.39	1.19	1.81	1.03	2.57	1.42	1.28	13.51
	ORF SEQ ID NO:		24938	26106		26572	26596	26597		27022	27289	27553	27611	28006	28018		28964			25174		19983		20440	20563	20759	20866	20993	21047	21241
	Exon SEQ ID NO:	15001	15167			16393	16417	16417	16585	16829	17104	17349	17398	17767	17779	18661	18674	19132	19634	19382	19436	10165	10465	10617	10722	10915	11024	1141	11194	11376
	Probe SEQ ID NO:	5134	5243	6123	6385	6535	6559	6223	6705	6951	7224	7479	7547	7917	7929	8849	8862	9522	9730	9905	9979	183	223	684	793	382	1109	1234	1286	1471

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Single Exon Probes Expressed in Heart

		П	1	T	7	7	1	7	1	T	T	_	T	T	T	1	Т	7	7		7	Т	T	7	T	7	T	Т	7	1	7	T	Т	7
	Top Hit Descriptor	Homo saplens mRNA, chromosome 1 specific transcript KIAADRAB	Homo sablens sodium/iodide symbother mRNA partiel cds	Homo saplens 14d32, Jacqed2 dehe complete cde: and information cons	Methanococcus iannaschii sedion 67 of 150 of the complete commen	60144941F1 NIH MGC 65 Home sanians CDNA close INA/OE/sessor c	601449441F1 NIH MGC 65 Homo sapiens CDNA clone INA CE-365232 5	H.sapiens Na+D-ducose cotransport regulator gene	Homo sablens full length insert cDNA YHRSA11	HOMEOBOX PROTEIN GLABRAZ (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP	xp15b02x1 NCI_CGAP_HN9 Homo saplens cDNA_clone IMAGE:2740395 3' similar to contains closes.	MER21 repetitive element:	CED-11 PROTEIN	C.parasitica eapC gene	QV4-EN0032-190500-223-e03 EN0032 Homo sanions CNNA	Homo sapiens gamma-diutamy hydrolasa gana eyyns 8 and 0 and commissional	Homo sapiens hypothetical protein ASH1 (ASH1) mRNA	Homo saplens putative pshHbD pseudonene for hair karalin	Rat SOD-2 dene for manganese-containing supercycle diameters.	Homo saplens dual oxidase-like domains 2 (DLI 10X2) mDNA	Saccharomyces cerevisiae Halfo (HAI 5) mRNA complete and	M.auratus mu class glutathione transferase gene	PM1-CT0247-141099-001-906 CT0247 Homo sapiens cDNA	Andes virus strain Ol23133 glycoprotein G1 and G2 precursor, dene, nartial cris	M.musculus scp2 gene excn 14	Chlamydia trachomatis section 5 of 87 of the complete genome	Homo sapiens filamin 2 (FLN2) mRNA, complete cds	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete ode	Arabidopsis thaliana root gravitropism control protein (PIN2) gene complete cds	Salvelinus pluvius mRNA for transferrin, complete cds	Salvelinus pluvius mRNA for transferrin, complete cds	Pimephales prometas liver ducose-6-phosphate-1-dehydrocepase mRNA activities	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610.31	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
	Top Hit Database Source	N	N.	N-	N-	EST HUMAN	EST HUMAN	N-	F	TOGGGGWG	DAPES WE	EST_HUMAN	SWISSPROT	Ę	EST HUMAN	Т	¥				Ę		T_HUMAN	NT.				LN LN	Ł	¥		Į.	EST_HUMAN	
	Top Hit Acession No.	2.0E-01 AB007974.1				-	_		7.			005.1			1.5	2.0E-01 AF147083.1	22080			1432540			5.1	.1		.1	1	-	.1			2	-	2
	Most Similar (Top) Hit BLAST E Value	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01 X82877.1	2.0E-01	2 0E-01 B46607	100	2.0E-01 /	2.0E-01 P34641	2.0E-01 X83997.1	2.0E-01	2.0E-01	2.0E-01	2.0E-01 Y19216.1	2.0E-01 X56600.1	2.0E-01	2.0E-01 U15300.1	2.0E-01 X61033.1	2.0E-01 A	2.0E-01 AF028026	2.0E-01 X91151.1	2.0E-01 AE001278	2.0E-01 AF148692.	2.0E-01 AF086907	2.0E-01 AF086907	2.0E-01 D89088.1	2.0E-01 D89088.1	2.0E-01 AF206637	2.0E-01 AI023592.	2.0E-01 AF078164
	Expression Signal	2.51	1.59	1.82	1.64	1.33	1.33	1.67	0.95	80		0.89	0.81	0.8	8.47	1.07	6.07	1.1	2.55	2.13	5.29	4.31	3.54	6.95	4.18	4.39	2.07	1.95	1.95	2.7	2.7	1.37	3.22	6.61
	ORF SEQ ID NO:						21619			23166			23346	23628		24519	24618	24687	25089	25491	25705	25900	25962		26839			27857	27858	28350	28351		25202	
	Exon SEQ ID NO:		11442	11590	11624		11743		12789	13359	<u> </u>			l			14847		15263	15428	15603	15780	15839	16517	16651	17299	17542	1/624	17624	18098	18098	19118	19308	19288
	Probe SEQ ID NO:	1534	1538	1688	1723	1847	1847	2299	2861	3442		3520	3646	3945	4464	4859	4972	5041	5342	5510	5694	5874	5934	6637	6772	(91	7697	11/4	41114	8214	8214	9503	9747	9769

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Exon NO: ORF SEQ ID NO: Expression (To Signal ID NO: Control ID NO: Signal ID NO: Most Signal ID NO: A variable ID NO: A variable ID NO: Signal ID NO: A variable ID NO: A va	(Top) Hit Top Hit Acession BLAST E No. 20E-01 11528495 NT 1.9E-01 AF004353.1 NT 1.9E-01 U32581.2 NT 1.9E-01 BE070801.1 ES 1.9E-01 BE070801.1 ES 1.9E-01 BE070801.1 ES 1.9E-01 BE070801.1 ES	Top Hit Database Source	
26163 1.6 20126 6 20392 1.31 20400 5.37 20400 7.32 20400 7.32 20846 9.3 21110 2.3 22109 3.31 222611 3.61 22342 0.96 23457 0.96	AF00435 U32581.2 U32581.2 BE07080		Top Hit Descriptor
20126 6 20392 1.31 20393 1.31 20400 5.37 20400 7.32 20846 9.3 21110 2.3 22109 3.31 222611 3.91 223156 4.68 23457 0.96	AF00435 U32581.2 U32581.2 BE07080	SINT	Mus musculus fructosamine 3 kinase (Fn3k) mRNA
20126 6 20392 1.31 20393 1.31 20400 5.37 20400 7.32 20400 7.32 21110 2.3 22110 3.91 222611 3.91 22611 3.91 22452 3.4 23457 0.96	1.9E-01 AF004353.1 1.9E-01 U32581.2 1.9E-01 BE070801.1 1.9E-01 BE070801.1 1.9E-01 BE070801.1	3NT	Raitus norvegicus And hydrocarbon receptor nuclear translocator 1 (AmH), mDNA
20392 1.31 20393 1.31 20400 5.37 20400 7.32 20400 7.32 20846 9.3 21110 2.3 22109 3.31 22611 3.91 22611 3.91 23072 3.4 23457 0.96	1.9E-01 (U32581.2 1.9E-01 (U32581.2 1.9E-01 (BE070801.1 1.9E-01 (BE070801.1 1.9E-01	N L	Mus musculus pale ear (ep) gene, wild two allele 3' region nartial cals
20393 1.31 20400 5.37 20400 7.32 20400 7.32 20846 9.3 21110 2.3 22109 3.31 22611 3.91 22611 3.91 23072 3.4 23156 4.63 23457 0.96	1.9E-01 U32581.2 1.9E-01 BE070801.1 1.9E-01 BE070801.1 1.9E-01 730518	NT TN	Homo sapiens lambda/lota protein kinase C-interacting protein mRNA complete out
20400 5.37 20400 7.32 20400 7.32 20846 9.3 21110 2.3 22109 3.31 22611 3.91 22611 3.91 23072 3.4 23156 4.63 23457 0.96	1.9E-01 BE070801.1 1.9E-01 BE070801.1 1.9E-01 7305180	N FN	Homo saplens lambda/jota protein kinase C-interacting protein mRNA complete cde
20400 7.32 20846 9.3 21110 2.3 22109 3.31 22611 3.91 23672 3.4 23156 4.63 23457 0.96	BE07080	EST HUMAN	RC3-BT0502-251199-011-d01 BT0502 Home saniens cONA
20846 9.3 21110 2.3 22109 3.31 22611 3.91 23072 3.4 23156 4.63 23457 0.96		EST HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo saniens cDNA
20846 9.3 21110 2.3 22109 3.31 22611 3.91 23612 3.4 23072 3.4 23156 4.63 23457 0.96		TNIC	Mus musculus interleukin 2 receptor gemma chain (197c) mRNA
22109 3.31 22109 3.31 22611 3.91 5.65 23072 3.4 23156 4.63 23432 0.93 23457 0.96	1.9E-01 AA358813.1	EST HUMAN	EST67784 Fetal lung II Homo saniens CDNA 5' and
22109 3.31 22611 3.91 5.55 23072 3.4 23156 4.63 23432 0.93 23457 0.96	1.9E-01 AF061282.1	IN.	Sorghum bicolor 22 kDa kaflrin chisher
22611 3.91 22611 3.91 5.55 23072 3.4 23156 4.63 23432 0.93 23457 0.96	1.9E-01 AF184623.1	N	Plasmodium vivax reticulocyte binding profeip-3 (rhp.2) gene complete od
22611 3.91 5.55 23072 3.4 23156 4.63 23432 0.93 23457 0.96	1.9E-01 8922533 NT	LNE	Homo sepiens hynothetical protein El 19684 (El 19564)
23072 3.4 23156 4.63 23432 0.93 23457 0.96	U66066.1	N-I	Signodan hispidus n53 dene nartiel cde
23072 3.4 23156 4.63 23432 0.93 23457 0.96	1.9E-01 J00922.1	LN	Gallus dallus ovalbumin (V) gene complete cds
23457 4.63 23457 0.93	1.9E-01 D13197.1	M	Mouse gene for immunoalobulin diversity region D1
23432 0.93 23457 0.96	1.9E-01 R16467.1	EST HUMAN	y42710.r1 Soares (et al liver spleen 1NFI S Homo saniens chind chare IMA CE 420647 51
23457 0.96	1.9E-01 AF264017.1	NT	Rettus norvegicus anylacetamide deacetylase gene complete cyle
	1.9E-01 P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
23600 3.02	1.9E-01 AB006784.1	¥	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain complete and
23676 1.89	1.9E-01 AW754106.1	EST HUMAN	CM3-CT0315-271199-045-b11 CT0315 Home sapiens cDNA
23813 1.06		EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo saniens cDNA
24049 0.89	1.9E-01 AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
24338 0.84	1.9E-01 Z93780.1	NT	Fugu rubripes genes encoding carbamovi phosphate synthetase III myosin linht chain MADO
24566 0.86	1.9E-01 AW849203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA
1.04	1.9E-01 AF223642.1	TN	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cols
24605 1.11	1.9E-01 O95239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4
24675 1.03	1.9E-01 AJ251178.1	Т	Phoca vitulina partial aar 28 gene for alpha adresergic recessor 28
14981 24755 0.99	1.9E-01 Z70296.1		S.mansoni elastase HP1 gene
44004	4 00 04 1834400 4		ts93g12x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA
24780	AIOST 198	HOMAN	PLA I ELEI-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);
98.0 801+2	1.9E-01 66/9095 N1		Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA
4.28	1.9E-01 AW130149.1	EST HUMAN	x/29a07.x/ NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:26/19444.3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN):
15386 25446 7.67 1	1.9E-01 AF127937.1	Т	Homo sablens DNA bolymerase ensilon catalyfir submit protein /DOI 54

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Table 4
Single Exon Probes Expressed in Heart

			313				Γ			<u></u>		Γ	Γ	Τ	Τ	Τ	Γ			Γ	Γ				92	\top			Γ	Г	П
leal II heard the coro	Top Hit Descriptor	AU133116 NT2RP4 Homo saniens cDNA close NT2BPA004225 E	yg09a12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13	Architomine the line and the second s	Zea mars oterch homeling are 1771-17	Arabidonale thelines DNA - L.	Homo sanjene mBNA for kTAAAAA	Arabidonsis thelians DMA sets	Arabidoosis thaliana DNA chromosome 4, contig tragment No. 15	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively saliend	Home saniane northal 5 UT4	Discophia majanasata 1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	Architecture Ligaster clausin light chain mkNA, complete cds	Atabidopsis trailana receptor-like kinase LECRK1 (LECRK1) gene, complete cds	mus intescutus prijorip mikina, complete cds	Mus musculus cetg gene for chaperonin containing TCP-1 gamma subunit, partial cds	products	OVZISS Islines tiene for membrane attended emission in it.	wd74f02 x1 NCT CGAP 1 1:24 Home contact the contact of the contact	Dichostelium discoideum plasmid Date	Yeshila nestis nlasmid ACD-4	Mus musculus guennale piralira artifatira ar	Mus musculus guanvale nucleotide hinding protein 1 (Capp.), mRNA	Homo saplens latent transforming growth factor bas kinding scaping 4.1 Tenan	9922d10.x5 NCI_CGAP_Kid3 Home sapiens cDNA clone IMAGE:1761811 3' similar to TR:076936 075936 GAMMA BUTYROBETAINE HYDROXY A s = .		Mus musculus Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, small	OV3-DT0018-081200-036-04 DT0049 U	Aroneidim aceida I EAEV aceida (I EAEVA)	vandpandum adalle LEAT Protein (LEAFYZ) gene, partial cds xi41e03 x1 Soares NET T CBC S1 London	19 : 100 A. 10 A.
	Top Hit Database Source	EST HUMAN	EST LINAAN	TN TN	FZ	FA.	LZ	Ę	L.		L _N	TN	17	- L		-	F	NT	EST HUMAN	NT.	Į.				EST HUMAN		L L	T HIJMAN	Т	T HUMAN	
	Top Hit Acession No.	AU133116.1	1.9E-01 R43212 1		5	57.2		Γ				90.1	T		\ <u>.</u>		4502532 NT	1.8E-01 AB021490.2				6753947 NT	6753947 NT	4505036 NT	1.8E-01 AI733708.1		1.8E-01 AB051897.1		9.1		1.8E-01 AW995178.1 E
	Most Similar (Top) Hit BLAST E Value	1.9E-01 AU133	1.9E-01	1.9E-01	1.9E-01 AF0727	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01 AJ2432	1.9E-01	1.9E-01	1.8E-01	1 8F-01		1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01		1.8E-01	1.8E-01 AW9357	1.8E-01	1.8E-01 A	1.8E-01
	Expression Signal	2.26	1.7	1.43	3.06	1.62	12.89	2.16	2.16	1.75	2.61	1.67	126	2.28	122		2.41	2.15	0.85	121	5.28	1.29	1.29	0.92	8:		1.6	2.99	1.61	1.09	1.28
	ORF SEQ ID NO:		24863	26446	26476	26735	27109	28176	28177	28271	29060		-	19811	20041		20145	20493	20735	20832	21024	21252	21253				21644			22595	22803
	Exon SEQ ID NO:	15503	15119		16310	16538			17930	18025	18768	19146	19546	10016	12663		10322	10661	10889	10990	11174	11392	11392	11700	11720		11769	12527	12796	12800	13012
	Probe SEQ ID NO:	5588	6162	6423	6449	6658	7041	8038	8038	8137	8961	9546	9880	28	260		366	EZ/	986	1075	1267	1487	1487	1803	1823		1873	2660	2868	2873	3085
					_						1		_		نـــا							_	<u> </u>						_		_

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Pube	Ewan			Most Similar	;		Topos rypressed in nealt
SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3570	13484	23275	1.07	1.8E-01	1.8E-01 H03369.1	EST HUMAN	1945e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element:
3570			1.07	1.8E-01	1.8E-01 H03369.1	EST HIMAN	1/45e01.s1 Soares placenta Nb2HP Homo sapiens oDNA clone IMAGE:151704 3' similar to contains Alu
4154		23828	0.8		1.8E-01 AJ271735.1	LN LN	Home canions Vancardonit
4238			1.13	1.8E-01	1.8E-01 D37954.1	Į.	Bovine NB25 mRNA for MHC class II Par A PORS
4466	14350	24141	5.12		1.8E-01 AL161556.2	Į.	Arabidoosis thaliana DNA chromosome 4 continued to 50
							Coing Hagineri No. 36
4663		24339	2.36	1.8E-01	1.8E-01 AB051897.1	Ł	Mus musculus Scya6, Scya16-ps, Scya16 genes for small inducible cytokine A6 precursor, small inducible cytokine A0 precursor, small
4700	14586	24377	0.93	1.8E-01	1.8E-01 X92179.1	L.	Striberge in mPNIA for along a selection of the complete cds
4977	14852	24618	1.11	1.8E-01	1.8E-01 AW814270 1	FST HIMAN	MR3-ST0203-161200-142 -06 CT2020-1
5027	14900	24670	4.17	1.8E-01	1.8E-01 AF181258.1	L	Mesoricotis ametrs No terrental
5053	_	24697	1.28	1.8E-01		EST HUMAN	fig7ent v1 NCI CGAD 1 may un
5117	_		1.03	1.8E-01		N	Homo Seriens his H1 nene 51 1 TR
5549			1.41	1.8E-01	1.8E-01 AL161594.2	TN.	Arabidonsis thaliana DNA chromonana 4
5922		25952	1.28	1.8E-01	1.8E-01 Q9QY14	SWISSPROT	FORKHEAD BOX DROTTEIN ES
5948			2.5	1.8E-01		EST HIMAN	W62h02 1 Sparse multiple colored and most in
6179		26214	1.38	1.8E-01	=	- L	Citrullus languis mRNA for unun commission de la company d
6179	ı	26215	1.38	1.8E-01	\ <u>\-</u>	L	Citullus langua mRNA for users complete cds
7382	17251	27456	1.72	1.8E-01		N	Human celliller DNAd-uman celliller
7396	17314	27521	122	1.8E-01	9626232 NT	N	Bacterionhare Ike commissionance
7933	17783	28022	1.19	1.8E-01	1.8E-01 X63440.1	μ	M.musculus mRNA for P19-proteins shows between
8033	17925	28172	3.19	1.8E-01	1.8E-01 X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
8065	17956	28205	6.65	1.8E-01	1.8E-01 U38906.1	Ę	Barteriurhane ritintourese
8118	16065	26214	2.9	1.8E-01	-	Ę	Citrillis langues mRNA for many
8118	16065	26215	2.9	1.8E-01	-	Į.	Circulate analyse ment of many complete cds
8119	18007	28254	3.88	1.8E-01	-	NT	Dichostellin discaldente inhamm (Dodas)
8381	18258	28507	2.64	1.8E-01	1.8E-01 M59257.1	LN L	Human carcinoembronic antigen (CEA) game, complete cas
8758	17907	28152	3.98	1.8E-01 X57033.1			B taurus mRNA for priaseitim channel
8976	18781	29073	2.83	1.8E-01	8394421		Raffus nonyaricus Thombowns recented (The Co.
9169	18912	25344	1.65	1.8E-01	1.8E-01 BF348623.1	T HUMAN	602019928F1 NCI CGAP Ring? Home scalars and 1
9625	19200		2.05	1.8E-01 Q96682			DNA TERMINAL PROTEIN (BELL ETT PROTEIN/JPTP DESCENA
						1	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ. ID NO:	Expression · Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94			T_HUMAN	унч8h10_r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9776	19294		1.63		1.8E-01 Y11114.1		E.dispar mRNA for hexokinase (hxk1)
563	10503	20309	1.8		4.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5
788	10717	20559	2.04		-		P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
945	_				1.7E-01 P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1042	L	20802	1.6		1.7E-01 AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1042	10960		1.6		1.7E-01 AF081810.1	IN	Lymantria dispar nucleopolyhedrovirus, complete genome
1938	11833		3.8		1.7E-01 AF255051.1	L	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2829	12758	22548	1.93		1.7E-01 AF000716.1	Ż	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
	1						Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease
2829			1.93		_		regulatory protein (hapR) gene, complete ods, and YRAL VIBCO gene, partial cds
2896	12823		1.74		.1	EST_HUMAN	EST41651 Endometrial fumor Homo sapiens cDNA 5 end
2967	12894		1.35		1	NT	Naja naja atra ctv-1 gene, exons 1-3
2987	12894		1.35		1.7E-01 AJ238736.1	NT	Naja naja atra ctv-1 gene, exons 1-3
3067			1.80		1.7E-01 AF081514.1	TN	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3401	13318	23119	1.96	_	1.7E-01 AJ269505.1	IN	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3557					1.7E-01 AJ224877.1	N	Homo sapiens hap1 gene, complete CDS
	1						Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron
3859		23562		$oldsymbol{\perp}$	1.7E-01 AJZ35377.1	Z	Software general clubs condition DNA
4459	14353		1.88		1./E-U1 A32836.1	Z	Sullstand glogala apria repount
4732	14617	24403	4.1		1.7E-01 Al247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains OFR.b1 OFR repetitive element;
4986	14861		1.16		1.7E-01 U28376.1	IN	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5067	7 14937	1	1.18		1,7E-01 AF072725.1	N	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5321	<u> </u>	1 25046	1.76		1.7E-01 AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5321	<u> </u>		1.76		1.7E-01 AA470686.1	EST HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5820					1.7E-01 H72118.1	EST HUMAN	ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6112	ſ				1.7E-01 AF026552.3	N	Mesocricetus auratus oviduciin precursor (OVI) gene, complete cds
	1						

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Probe SEQ ID 8 NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9807	19319		2.47		1.6E-01 AF287344.1	, LN	Fuchsia hybrid cultivar Qiu 94208 ribosomal protain S10 gene, partial cds; nuclear gene for mitochondrial product
9827	19328	25208	127	1.6E-01	9506522 NT	Ę	Rattus norvegicus chondroitin suifate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
248	10214	20030	1.87	1.5E-01	1.5E-01 BE710087.1	EST_HUMAN	L3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20031	1.87	1.5E-01	1.5E-01 BE710087.1	EST_HUMAN	L3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
572	12640		2.28		1.5E-01 AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	10697		1.4		1.5E-01 AL163284.2	님	Homo sapiens chromosome 21 segment HS21C084
1076	10992	20834			1.5E-01 AJ009735.1	NT ·	Opprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1081	10997		1.87	1.5E-01	1.5E-01 AJ251885.1	F	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1097	11013		1.82		1.5E-01 L36125.1	F	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1198	11108		1.36		1.5E-01 AW195516.1	EST_HUMAN	xn39d11.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2696086 3'
1254	11161	21010	2.81	1.5E-01	1.5E-01 D26535.1	M	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1254	11161	21011	2.81	1.5E-01	1.5E-01 D26535.1	TN.	Human gene for dihydrolipoamide succinytransferase, complete cds (exon 1-15)
1466	11371	21238	1.49	1.5E-01	1.5E-01 AF117340.1	M	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
1866	11762		1.54	1.5E-01	1.5E-01 AW 444451.1	EST_HUMAN	UFH-Bi3-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2679	12544		1.12		1.5E-01 BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA done IMAGE:4247537 5
2999	12927	22719	0.89	1.5E-01	1.5E-01 M81441.1	TN	Bos faurus factor V variant 2 (factor V) mRNA, complete cds
3308	13229	23034	4.22		1 5E-01 AA935049 1	FST HIMAN	oo88d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 RETINOL-BINDING PROTFIN I CFI I II AR HI IMANY
3322	13242				1.5E-01 Z23104.1	LN LN	L. stagnalis mRNA for G protein-coupled receptor
3322	13242	23049	78'0	1.5E-01	1.5E-01 Z23104.1	N _T	L. stagnalis mRNA for G protein-caupled receptor
3380	13298	23097	96.0		1.5E-01 AW612237.1	EST_HUMAN	Int29f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2856539 3' similar to contains element MER16 repetitive element;
3696	13610	23394	1.34	1.5E-01	1.5E-01 U09964.1	TN	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.5E-01	7108358INT	TN	Homo saplens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	13703	23490	2.35		1.5E-01 AW665983.1	EST HUMAN	hi10f06.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:29814113'
3806	13718	23506	0.8		1.5E-01 AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3806	13718	23207	8.0		1.5E-01 AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3964	13871		96'0	1.5E-01	1.5E-01 AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4006	13912		76.0		1.5E-01 Z12628.1	LN	B.napus mitochondrian DNA for ORF158
4091	13991	23768	8.36		1.5E-01 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4623	14511	24301	1.34	1.5E-01	1.5E-01 BF687665.1	EST HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5' .

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Table 4
Single Exon Probes Expressed in Heart

		T	T	T	T	T	T	T		T	T	T	T	T	T	T	T	T	g	7	Τ	П	Т	Ť	T	T	7	T	7	7	T	\top
man rypressed in real	Top Hit Descriptor	602083269F1 NIH MGC 81 Homo sapiens cDNA clone IMAGE:4247537 5	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA	CM0-HT0565-280200-245-b10 HT0565 Homo saniens cDNA	Arabidopsis thaliana DNA chromosome 4. confin fragment No. 60	Arabidopsis thaliana AP2 domain containing protein RAP2 12 mRNA martial calc	THROMBOSPONDIN 1 PRECURSOR	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)	IL3-CT0219-160200-064-F10 CT0219 Homo saplens cDNA	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds	Mus musculus DNA methyltransferase 2 (Dnmtz). mRNA	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA	Mus musculus genomic fragment 279 Kb. chromosome 7	801564322F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE 3833981 5	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA	Influenza B virus (B/Nanchand/480/04) NB professione complete also	Archaeoglobie faligidie gegener Et 4120 eff. To protein gene, complete cus, and neuramindase gene, partial co	Homo sabiens chromosome 5 open reading frame 3 (CSORES), mbNA	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE	AMELOGENIN	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TAI B INTERCENIC BECION JOBES	EST382376 MAGE reseguences. MAGK Homo saniens cDNA	Homo sapiens HARP (HARP) dene, extra 17 and complete cds	wr52c08.x1 NCI CGAP Uti Homo seniens cDNA clone IMAGE 22c01310 2	UI-HF-BNO-akk-d-05-0-UI TI NIH MGC 50 Home sanions china clare MAA Clare MAA Clare MAA	UI-HF-BN0-akk-d-05-0-UI-r1 NIH MGC 50 Homo sapiens cDNA clone IMA CE: 2077-409 5	0085g12.s1 NCI_CGAP_Kid5 Home sepiens cDNA clone IMAGE:153030 3' similar to gb:M26062	C16800 Clontesh himan and and and many (#572) Home confers the confers of the con	Pandasianodon digas growth hormone (GH) mRNA complete ada	Homo sapiens mRNA for ASK1, complete cds
מו דווסאין סופ	Top Hit Database	EST HUMAN	EST HUMAN	EST HUMAN	IN	L	SWISSPROT		SWISSPROI	EST_HUMAN	NT	NT	NT	N	N	EST HUMAN	1	LN	MT	L L	TOGGGGWG	SWISSPROT	SWISSPROT	EST HUMAN	Į.	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	N I	NT
5	Top Hit Acession No.	1.5E-01 BF695381.1	1.5E-01 BE173796.1	1.5E-01 BE173796.1	1.5E-01 AL161560.2	1.5E-01 AF003105.1	P07996	7	15186	1.5E-01 AW850754.1	U65016.1	1	6753659 NT	6753659 NT	1.5E-01 AJ276505.1		6396	12	į	7236				295.1	12	-		1.1	7.1			
	Most Similar (Top) Hit BLAST E Value	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01 P07996	10 04	1.0E-01 P15186	1.5E-01	1.5E-01 U65016.1	1.5E-01 U65016.	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01 AF13490	1.5F-01	1.5E-01	4 5E 04 DARGE	1.5E-01 028462	1.5E-01 P30143	1.5E-01	1.5E-01 AF21084;	1.5E-01 AI973157	1.5E-01 AW50061	1.5E-01 AW50061	1.5E-01 AA97031	1.5E-01 C16800.1	1.5E-01 L27835.1	1.5E-01 D84476.1
	Expression Signal	2.18	1.08	1.08	1.3	0.94	202	70 7	70.0	4.06	6.77	6.77	1.9	1.9	1.87	2.44	1.86	1.78	1.86	5.13	7	2.09	1.4	5.63	1.71	1.88	1.68	1.68	1.22	11.77	1.88	1.44
	ORF SEQ ID NO:	22435	24361	24362	24576		24833						25660	25661	25694	25774		25845	25948		25971	26000	26067	24866		26396	26507	26508	28856		26983	27064
	Exen SEQ ID NO:	12544	14566	14566	14808	<u>.</u>	15139	45,488	1	91501	15345	15345	15564		15593		15691	15734	19455	15840	15847	15876	15935	15123	16148	16236	16340	16340	18865	16774	16790	16873
	Probe SEQ ID NO:	4645	4680	4680	4929	5072	5216	F268	000		424	6424	2652	5652	5684	5760	5785	5828	2567	5935	5942	5972	6031	6166	6284	6374	6481	6481	6786	6895	6912	9669

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Table 4
Single Exon Probes Expressed in H

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens adaptor-related protein complex 1 heta 1 suhimit (ADTEA)	Za59e06.s1 Scares fetal liver spleen 1NFLS Homo saplens CDNA clone IMAGE:296866 3' similar to	AV754819 TP Homo serviers CDNA closs TDAA I IDAA E	Acbenser transmontano utellonenia mBNA portici de	Aplysia californica carboxpentidase D mRNA Ammieto da	Aplysia californica carboxopetidase D mRNA complete cds	P Jeniusculus mRNA for Integrin beta subunit	wk53h12x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone INAGE:2419175 3' similær to gb:M27508 BETA GALACTOSIDASE-RELATED PROTFIN PRECI IPSOP ALL INAAAA.	wk53h12.x1 NCI_CGAP_P722 Homo saplens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA	Danio ratio transcription factor Book (B. 2) - Busy	Claurens minutes and come	Clavinens in intrinses not come	Homo saniens chromosome 24 comment 11024 com	Homo saniens chromosome 24 comment 1504 Comment	Site scrafe CVDR4 areas for learned and services of the scrafe CVDR4 areas for learned and services of the scrafe CVDR4 areas for learned and services of the scrafe CVDR4 areas for learned and services of the services of t	Il R-Chinnal nagano pae not chinnal il	wt5208 x4 NCL CGAB 114 U	602128753E1 NIH MCC FE U.	V087604.r1 Scares fetal liver sulcen 1NEI'S LOWA GIONE IMAGE: 4285549 5	AV741272 CB Homo seniens cDNA clone CRDA CDNA FI	Campylobacter jeluni NCTC1168 complete general 112	Sus scrofa mRNA for sortium inclide exmander	Rettus norvegicus pyridayal kinasa mRNA complete odo	Homo sapiens T cell recentor hata focus TCRB//8560 to TCBB//25545	Xenopus laevis mRNA for DNA (cutosing 6.) moth the control of the	Nd54c01.s1 Spares fefal liver spleon ANEI s U	Mus musculus grawth differentiation forths (Autor) Days	Thermotoga marijima section 22 of 136 of the	U-H-Bit-eaf-a 09-04 154 NOI COAD Site u	In/22d07.s1 NCI CGAP GCR4 Home serions - DNA -1 111.05	GLYCEROL-3-PHOSPHATE ACYI TRANSFERASE BRECI IBSCH 70747
gle Exon Pr	Top Hit Database Source	Z	FST HIMAN	EST HUMAN	Z	E	¥	Z.	EST_HUMAN	FST HIMAN	L L	Z	Ę	ځا	F	5	EST HIMANI	EST HIMAN	EST HIMAN	EST HUMAN	EST HUMAN	₽ FN	Ę	N.	F	N	EST HUMAN	٧.	Z	EST HUMAN	EST HUMAN	SWISSPROT
	Top Hit Acession No.	4501972 NT	1.5E-01 N74226.1	AV754819.1			1.5E-01 AF007570.1	.1	1.9	6.1	-				Γ			T	T	1.5E-01 R83077.1				Γ			T91864.1	TN 0868299	1.4E-01 AE001710.1	41.1	5.1	
	Most Similar (Top) Hit BLAST E Vatue	1.5E-01	1.5E-01	1.5年之	1.5E-01	1.5E-01	1.5E-01	1.5E-01 X98852	1.5E-01 AI81404	1.5E-01 AI81404	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01/	1.5E-01/	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.4色-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01 AW 1357	1.4E-01 AA72061	1.4E-01 P30706
	Expression Signal	1.71	2.48	2.98	6.6	7.02	7.02	286	2.45	2.45	1.54	1.35	1.35	5.15	5,15	1.74	1.73	2.17	20.02	4.14	2.14	3.99	3.01	1.58	1.96	2.57	1.62	1.43	1.53	0.94	10.35	0.97
	ORF SEQ ID NO:	27200	27335					27955	27998	27999	28031	28103	28104	28334	28335		28555	26396				25133	25179		-				21487			22199
	Exon SEQ:ID NO:	17007	17142	Ш		- 1	_l	17710	17758	17758	17789	17859	17859	18084	18084	18219	18299	16236	19547	19565	19588	19497	19402	19432	10260	10818	11145	11615	11618	11759	11837	12303
	Probe SEQ ID NO:	7130	7265	7306	7438	7706	7706	7860	7908	7908	7939	6008	8008	8199	8199	8342	8425	8506	6606	9531	9621	9726	8832	3972	236	892	1238	174	1717	1883	1942	2426

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Table 4

Single Exon Probes Expressed in Heart	Top Hit Descriptor	wm74d01.x1 NCL CGAP Utz Homo sapiens cDNA clone IMAGE:2441665.3	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE-41467 5'	yg97a03.r1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGF-41467 5	to 56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570.31	b56c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570.31	Thermotoga maritima section 22 of 136 of the complete genome	450b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA done IMAGE:453673 3' similar to gb:X01057_ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains Alu repetitive element:	QV3-SN0022-100500-186-h09 SN0022 Homo seniens cPNA	Homo sapiens chromosome 21 segment HS210084	Lycopersicon esculentum genomic RAPD band 26	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone (MAGE:117812 3'	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrocenase, complete cde	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydronenase, complete cds	hr67c02x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5'	AU117147 HEMBA1 Homo saplens cDNA clone HEMBA1000769 51	xb71d12x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE-2581751 31	601193523F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3537581 5	QV1-UM0036-080300-103-d09 UM0036 Hamo sapiens cDNA	UI-H-BI0-eat-c-09-0-UI:s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone_IMAGE:2710289_3*	AV659047 GLC Homo saplens cDNA clone GLCFSH063'	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 57	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains	Homo saplens PHEX gene	Homo sapiens PHEX gene	Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finner protein (DNZ1) remes complete and	099903.s1 NCI CGAP GCR1 Homo saniens cDNA cione IMACE (1920)28.4.9	1/70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE-1540ag 5	C.perfringens ORF for putative membrane transport protein
jle Exon Probe	Top Hit Database Source	EST_HUMAN w	EST_HUMAN X	П	Т	Г	TN T	gi gk EST HUMAN re	Т		N L	EST HUMAN YE	N E	N LN		EST_HUMAN A	EST HUMAN A	EST_HUMAN X	EST_HUMAN 60	EST_HUMAN Q	EST_HUMAN UI	EST_HUMAN A	EST_HUMAN E	EST_HUMAN 60	bz NAMIH TRE	Т	¥	Į.	T HUMAN	HUMAN	
Sing	Top Hit Acession No.	1.4E-01 AI933496.1	1.4E-01 R59232.1	1.4E-01 R59232.1	1.4E-01 AI699094.1	1.4E-01 AI699094.1	1.4E-01 AE001710.1	AA776287.1	1.4E-01 AW866022.1	1.4E-01 AL163284.2	1.4E-01 AJ005180.1	T90677.1	1.4E-01 AB004556.1	1.4E-01 AB004556.1	1.4E-01 BE326891.1	47.1	AU117147.1	AW082796.1	1.4E-01 BE266536.1	1.4E-01 BF378533.1	1.4E-01 AW015373.1	1.4E-01 AV659047.1		1.4E-01 BF310959.1	1.4E-01 W93411.1		-	1.4E-01 AF121361.1		Γ	
	Most Similar (Top) Hit BLAST E Value	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01 AA7762	1.4E-01	1.4E-01	1.4E-01	1.4E-01 T90677.	1.4E-01	1.4E-01	1.4E-01	1.4E-01 AU1171	1.4E-01 AU1171	1.4E-01 AW082	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01 Y10196.	1.4E-01 Y10196.	1.4E-01	1.4E-01	1.4E-01 R53400	1.4E-01 X66092.
	Expression Signal	3.07	1	1	8.38	8.38	3.16	0.8	0.91	1	0.81	. 4.5	4.29	4.29	2.72	5.64	5.64	3.07	1.56	1.89	1.62	1.33	4.48	8.05	38	1.56	1.56	2.03	2.02	3.28	1.89
	ORF SEQ ID NO:	22517	23524	23525	23762	23763	23817			24759	24784	24944	24963	24964	25823	25934	25935	25985		26009			27236	27377	27410	27461	27462	26639		28352	28751
	Exan SEQ ID NO:	12624	13735	13735	13985	13985	14044	14210	14904	14984	15014	15171	15189	15189	15710	15809	15809	15863	15874	15887	16233	16814	17044	17176	17211	17256	17256	16449	17982	18100	18480
	Probe SEQ ID NO:	2762	3823	3823	4083	4083	4144	4313	2032	5116	5147	5248	5267	5267	5805	2903	5903	5958	5969	5982	8371	8838	7167	200	7343	7387	7387	7436	8091	8216	8613

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Table 4
Single Exon Probes Expressed in Heart

ingle Exoli Flobes Expressed in Realt	Top Hit Descriptor	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds	M.musculus p16K gene for 16 kDa protein	Ephydatia fluviatilis mRNA for aldolase, partial cds	P.salina plastid gene secY	Rattus norvegicus desmin (Des), mRNA	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycinamide ribonucleotide	Synechocystis sp. PCC6803 complete genome 23/27 2868767_3nnaper	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABI	601465575F1 NIH MGC 67 Homo sapiens cDNA clone IMAGE 3868795 5	Homo sapiens ephrin-B3 (EFNB3), mRNA	Mus musculus mRNA for prolidase, complete cds	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA	Homo sapiens G protein-coupled receptor 50 (GPR60) mRNA	Homo sapiens gene for NBS1, complete cds	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK	Human calicivirus HU/NLY/Girlinaton/83/UK RNA for cansid protain (CBE)	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4	Rattus norvegicus A-kinase anchor protein mRNA, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'	Homo sapiens adapter protein CMS mRNA, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Rhodopseudomonas acidophila pucB5, pucA5, pucA6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151	RC4-ST0173-191099-032-d12 ST0173 Hamo sapiens cDNA	Archaeoglobus fulgidus section 91 of 172 of the complete genome	
III GIE EXUI	ion Top Hit Database Source	Ā	ΤN	Ϋ́	۲	1968117 NT	EST_HUMAN	L	 	SWISSPROT	EST HUMAN	1425031 NT	N	EST HUMAN	4758467 NT	4758467 NT	ΙΝ	TN	L	LN LN	F	N	Ā	EST_HUMAN	NT	۲	Ä	EST HUMAN	Z	
7	Top Hit Acession No.	U28760.1	X52102.1	1.4E-01 AB000890.1	X74773.1	119681	1.4E-01 BE513802.1	4F083221 1	364004.1	210447	BE782738.1	114250		1.4E-01 AW377998.1	47584	47584	4B013139.1	1.3E-01 AJ277606.1	1.3E-01 AJ277606.1	(53330.1	1.3E-01 AF139518.1	4L117078.1	1.3E-01 AL115265.1	1V712467.1	1F146277.1	4L117078.1	\J243578.1	1.3E-01 AW812104.1	1.3E-01 AE001016.1	
	Most Similar (Top) Hit BLAST E Value	1.4E-01 U28760.	1.4E-01 X52102.1	1.4E-01	1.4E-01 X74773.1	1.4E-01	1.4E-01	1 4F-01 AF08322	1.4E-01 D64004.	1.4E-01 P10447	1.4E-01 BE78273	1.4E-01	1.4E-01 D82983.1	1.4E-01	1.3E-01	1.3E-01	1.3E-01 AB01313	1.3E-01	1.3E-01	1.3E-01 X53330.1	1.3E-01	1.3E-01 AL117078	1.3E-01	1.3E-01 AV71246	1.3E-01 AF14627	1.3È-01 AL117078	1.3E-01 AJ243578	1.3E-01	1.3E-01	
	Expression Signal	2.23	3.02	1.48	2.32	1.89	1.82		229	3.28	1.41	1.42	3.41	1.77	2.69	2.69	1.86	0.89	0.80	1.09	1,83	1.55	2.23	1.07	1.36	2.56	1.29	1.17	2.99	
	ORF SEQ ID NO:	28158		25138	25277									•	20098	20099	20271	20369	20370	20603	20852	20771		20952		21689				
	Exon SEQ ID NO:	17913	18626	19517	19065	19073	19734	19156	19163	19754	19282	19332	19566	19398	10281	10281	10460	10557	10557	10753	10802	10928	11026	11107	11331	11811	12012	12129	12210	
	Probe SEQ ID NO:	8764	8813	9365	9413	9427	9470	9560	9573	9646	9762	9831	9850	9926	319	319	518	620	620	826	876	1010	1111	1197	1426	1918	2124	2245	2329	

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Single Exon Probes Expressed in Heart	Top Hit Descriptor Source	NT Bowne branched chain alpha-keto acid dihydrolipov/ transacylase mRNA complete refe	F	Ŋ	N.	¥	Į,		N.	Ż	1 EST HUMAN QV3-DT0018-081299-036-a03 DT0018 Homo sepiens cDNA	N	EST HUMAN	EST HUMAN	EST HUMAN	N.	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN.	LN.	EST_HUMAN	EST_HUMAN	EST_HUMAN				T_HUMAN		EST_HUMAN 60218701571 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'			T_HUMAN	
Single Exon P	Top Hit Acession Detabase	•	<u>-:</u>	1.		Ξ.	Ξ.	6978840 NT						Γ	EST	호	Γ				T.		EST		7.1		.1			11423294 NT	+		8923919 NT	1	
	Most Similar (Top) Hit BLAST E Value	35 1.3E-01 M21572.1	1.3E-01 AP00000	1.3E-01 AP00000								1.3E-01 AF026805.1	1.3E-01 AW273741.1											9 1.3E-01 BF679819.1			1.3E-01								
	Expression Signal	2 0.95	1.18	1.18	8 0.78		3 0.86	1 0.85	1.7	1.15	3.44	1.89	16.36	0.85	0.85	1.65	3 2.16	0.81	3.17	0.86	1.21	1.21	6.0					2.04		1.34		4.54			7 7
	ORF SEQ ID NO:	23122	5 23362	5 23363	L	23362		23431					23770	23870	23871			24202			24718	24719			25013		25936				26744			27031	27767
	Exon SEQ ID NO:	13321	13575										13993		14092		14328		15075	14783				1	_1		_1	1			_1		_1	_1	17261
	Probe SEQ ID NO:	3404	3661	3661	2998	3714	3714	3734	3906	4046	4068	4075	4093	4192	4192	4218	4433	4525	4771	4903	5074	5074	5173	6173	5292	5428	5904	5956	6305	6649	9999	6858	9889	0960	7452

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8029	17921		2.88	1.3E-01	1.3E-01 BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo saplens cDNA
8444		28577	1.83	1.3E-01	1.3E-01 AF119117.1	Ā	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8576			5.13	1.3E-01	6671745 NT	ᅜ	Mus musculus cofflin 2, muscle (Cfi2), mRNA
8873			3.72	1.3E-01	1.3E-01 BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
9261		25320	1.97	1.3E-01	1.3E-01 BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5
9399			3.18		1.3E-01 AJ242790.1	7	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
9757	19279		1.56	1.3E-01	1.3E-01 AB026829.1	N	Ephydalia fluvialilis mRNA for sALK-8, complete cds
9784	19297		1.32		1.3E-01 AW001114.1	EST HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:060287 060287 KIAA0539 PROTEIN
9945	19414		1.26	1.3E-01	1.3E-01 BF571764.1	EST HUMAN	602078440F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4253049 57
378	10362	20185	7.21	1.2E-01	_	EST HUMAN	#39b02.x1 NCI_CGAP_Bm23 Homo saplens cDNA clone IMAGE:2098539 3' similar to gb:U06760_ma1 ANNEXIN V (HUMAN);
418	9985		1.55	1.2E-01	1.2E-01 U66912.1	Ŋ	Dictyostellum discoldeum ORF DG1016 gene. partial cds.
535			2.63	1.2E-01	1.2E-01 AF039442.1	Į.	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355		21117	2.78	1.2E-01	1.2E-01 AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sepiens cDNA clone NT2RM4001691 3'
1355		21118	2.78	1.2E-01	1.2E-01 AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1361	11267		3.94	1.2E-01	1.2E-01 AV735249.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cdAAJB11 5'
1490	11395		1.13	1.2E-01	1.2E-01 AA897474.1	EST_HUMAN	a48e09.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16871 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR
1613	11517	21377	1.17	1.2E-01 Q14934	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-AT24) (NF-AT24)
1631	11535	21396	2.62	1.2E-01	1.2E-01 AI285402.1	EST_HUMAN	qt69f09.x1 NCI_CGAP_Eso2 Hamo sapiens cDNA clone IMAGE:1960553 3'
1730	11631		29.48	1.2E-01		Г	H.sapiens DNA for endogenous retroviral like element
1877	1173		1.43	1.2E-01	1.2E-01 AW449368.1	EST_HUMAN	UI-H-Bi3-aki-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo saplens cDNA clone IMAGE:2734554 31
2134	12022	21919	2.1	1.2E-01	1.2E-01 BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5
240	12124	22025	1.01	1.2E-01		Ŋ	Homo sapiens chromosome 21 segment HS21C013
2546	12420	22310	2.02	1.2E-01	AW996556.1	EST HUMAN	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
							1s18g07.x1 NCI_CGAP_Pan1 Homo sapiens dDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN_11 contains element PTRs panelitius
2697	12561	22451	0.86	1.2E-01	1.2E-01 AI623388.1	EST_HUMAN	element;
2812	12741	22537	1.5	1.2E-01	1.2E-01 U18018.1	IN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2872	12799	22594	1.96	1.2E-01	AI720470.1	EST HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN):
2904	12831	22628	2.89	1.2E-01	1.2E-01 M16364.1	П	Human creatine kinase-B mRNA, complete cds

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יינים ביינים בארונים ב	Top Hit Descriptor	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	QV1-BT0259-261099-021-d05 BT0259 Homo saniens cDNA	Methanococcus jannaschii section 142 of 150 of the complete ganoma	Bacillus subtilis complete genome (section 15 of 21): from 27g5131 to 3013540	Wheat mRNA for a group 3 late embryogenesis abundant protein (I FA)	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 301354n	601810786R1 NIH MGC 46 Homo sapiens cDNA clone IMAGE ANSARR 3'	P.clarkii mRNA; repeat region (ID 2MRT7)	P. clarkii mRNA; repeat region (ID 2MRT7)	HEMOLYSIN PRECURSOR	HYPOTHETICAL 52.4 KD PROTEIN C12810 08C IN CHROMOSOME I	HYPOTHETICAL 52.4 KD PROTEIN C12810 OBC IN CHROMOSOME 1	UI-HF-BK0-agh-d-01-0-UI-1 NIH MGC 36 Home septiens cDNA clone IMAGE-2052647 E	2008d02.r1 Soares, parathyroid fumor NbHPA Homo seniens CDNA clane IMAGE 224600 F	Homo sapiens gene encoding plakophilin (exons 1-13)	601493518F1 NIH MGC 70 Homo septens cDNA dome IMAGE: 3805R13 S	ILO-CT0031-221099-113-e04 CT0031 Home saniens cTNA	Mouse galactosyltransferase mRNA, complete cds	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:	xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional	regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds	Haemophilus influenzae Rd section 29 of 163 of the complete genome	S.cerevisiae HXT5 gene	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5	Yeast MPT5 gene for suppressor protein, complete cds	601655578R1 NIH MGC 65 Homo sepiens cDNA clone IMAGE:3846283 3'	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
21 1100- 216	Top Hit Database Source	L	EST HUMAN	IN	N.	Z	LN LN	N	EST HUMAN	LN PA	Į.	SWISSPROT	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	۲	EST HUMAN	EST HUMAN	₽ F	EST_HUMAN	EST_HUMAN	EST_HUMAN		Į.	NT	NT	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	NT
	Top Hit Acession No.	1.2E-01 X56882.1	1.2E-01 AW370668.1	1.2E-01 U67600.1	1.2E-01 Z99118.1	1.2E-01 X56882.1	1.2E-01 X56882.1	1.2E-01 Z99118.1	1.2E-01 BF128551.1	1.2E-01 Z54255.1	Z54255.1	P16466	Q10441	Q10441	1.2E-01 AW 401836.1	W33035.1	298266.1	BE620945.1	AW845275.1	M26925.1	1.2E-01 BE007072.1	A1913753.1	1.2E-01 AW083652.1		1.1			4V710857.1		3E962324.2	.1	1.2E-01 AF190493.1
	Most Similar (Top) Hit BLAST E Value	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01 Z54255.1	1.2E-01 P16466	1.2E-01 Q10441	1.2E-01 Q10441	1.2E-01	1.2E-01 W33035.	1.2E-01 Z98266.1	1.2E-01 BE62094	1.2E-01 AW8452	1.2E-01 M26925.1	1.2E-01	1.2E-01 AI913753	1.2E-01	L.	1.2E-01	1.2E-01 U32714.1	1.2E-01 X77961.1	1.2E-01 AV710857	1.2E-01 D26184.1	1.2E-01 BE962324	1.2E-01 BF314481	1.2E-01/
	Expression Signal	86.0	2	76.0	0.79	1.14	1.14	1.2	0.88	2.2	2.2	1.04	1.47	1.47	2.47	2.63	1.9	1.69	2.19	1.56	121	2.46	9.72	C	3.86	22/	1.5	1.51	2.95	3.35	1.93	2.6
	ORF SEQ ID NO:		22923				23199			23766	23767			24808		24947		25776	25824	25858		26715			1		27546	27819				28715
	Exon SEQ ID NO:	12901	13117	13143	13350	13393	13393	13350	13617	13990	13990	14886	16040	15040	15062	15174	15218	15669	15711	15745	16487	16522	16772	46700	78701	ומאלמו	17340	17597	18140	18291	18360	18447
	Probe SEQ ID NO:	2974	3192	3219	3433	3477	3477	3554	3704	4090	4090	5012	5174	5174	5199	5251	5297	5762	5806	5839	6607	6642	6893	700	40804	7045	7521	1/4/	8280	8417	8487	8579

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Table 4
Single Exon Probes Expressed in Heart

				_			_		_						_	_	_	_					_	_		_		_	_		
onige Extra Flobes Expressed in Hear	Top Hit Descriptor	Rabbit divoden esspoiated profein phosphatasa requilatory sulkimit (PC4) mBN 4	AV658033 GLC Homo sapiens cDNA clone Gl CFIR12.3*	Homo sapiens Xq pseudoautosomal region: segment 2/2	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)	Homo saplens colon cancer antigen NY-CO-45 mBNA restrained.	R.norvegicus NF68 gene for 68kDa neurofilament	QV4-BT0234-111199-031-010 BT0234 Homo saniens cDNA	gn20g05x1 NCI CGAP Lu5 Homo saniens cDNA clone IMAGE-1808840 3	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds	CYCLIN T	601900763F1 NIH MGC 19 Homo saplens cDNA clone IMAGF 41301103 5	th 18d08.x1 NCI_CGAP_Brin25 Homo sapiens cDNA clone IMAGE:2187983 3'	Inm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059820 3' similar to gb:X06985_ma1 HEME OXYGENASE 1 (HUMAN):	602128847F1 NIH MGC 56 Homo saniens cDNA clare MACE 428847F1 NIH MGC 56 Homo saniens	Arabidopsis thaliana DNA chromosome 4 contingramment No. 60	EST384142 MAGE reseguences, MAGI Homo saplens chivid	Synechocystis sp. PCC6803 complete genome 23/27 2868767-300065	AU140363 PLACE2 Homo sapiens cDNA clone PI ACE 2007 51	Mus musculus pre T-cell antigen receptor alpha (Pipra) mRNA	Rattus norvegicus Procollagen II alpha 1 (Col2a1) mRNA	RC0-ST0379-210100-032-g04 ST0379 Hano saplens cDNA	interleukin-12 p35 subunit [mice, Genomic, 700 nt. seament 4 of 51	HSC1RF022 normalized infant brain cDNA Homo sabiens cDNA clone c-1 m2 3'	Mus musculus calcium channel voltace-dependent T frae alcha 10 eukunit	601308679F1 NIH MGC 44 Homo sapiens cDNA cione IMAGE-2627ARR F	C.reinhardtil nuclear gene on linkage group XIX	A.Immercus gene for transposase	G.gallus gene encoding non-histone chromosomal protein HMG-14b exms 4 and 5	MR3-ST0290-290100-025-907 ST0290 Homo saplens cDNA	MR3-ST0290-290100-025-907 ST0290 Homo sapiens cDNA
gie Exon Pio	Top Hit Database Source	L N	EST HUMAN	NT	TOBBBON	NT	N.	EST HUMAN	EST HUMAN	IN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Į.	EST HUMAN	LN N	EST HUMAN	F	N	EST_HUMAN	TN	EST_HUMAN	N F	EST_HUMAN	NT	IN.	M	7	1 1
	Top Hit Acession No.	M65109.1	1.2E-01 AV658033.1	1.2E-01 AJ271736.1	004012	1.2E-01 AF039442.1	X53981.1	BE061418.1	1.2E-01 AI299903.1	L10187.1	096433	1.2E-01 BF314481.1	1.1E-01 AI561003.1	1.1E-01 AA569006.1	1.1E-01 BF697308.1		1.1E-01 AW972158.1	J64004.1	1.1E-01 AU140363.1	6755215 NT	6978676 NT	19.1			6753231 NT	_				2.1	2.1
	Most Similar (Top) Hit BLAST E Value	1.2E-01 M65109.	1.2E-01	1.2E-01	1 2E-01 004912	1.2E-01	1.2E-01 X53981.1	1.2E-01 BE06141	1.2E-01	1.2E-01 L10187.1	1.2E-01	1.2E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01 D64004.1	1.1E-01	1.1E-01	1.1E-01	1.1E-01/	1.1E-01 S82418.1	1.1E-01 F03265.1	1.1E-01	1.1E-01 BE393186	1.1E-01 X62135.1	1.1E-01 Y07695.1	1.1E-01 X52708.1	1.1E-01 AW81941	1.1E-01 AW81941
	Expression Signal	2.02	222	2.78	2.58	7.69	1.41	2.36	3.68	2.07	4.72	2.18	0.95	3.38	1.53	1.29	4.08	1.72	2.47	2.25	1.17	1.17	1.84	0.8	1.39	3	1.54	0.94	123	1.31	1.31
	ORF SEQ ID NO:				24897				25231				20301	20344	20789		20899	20980	21267				22546	22717		23092	23123	23246	23348	23698	23699
[Exan SEQ ID NO:	18612		19043	19693		19230	19706	19281	19295	19636	19424	10493	10535	10956	10985	12686	11137	11408	12150	12653	12394	12754	12925	13221	13293	13322	13450	13562	13925	13925
	Probe SEQ ID NO:	8798	9032	9383	9458	9567	9671	9739	9761	9782	9786	888	225	286	1038	1089	1143	1229	1504	2266	2492	2520 2520	2825	2997	3239	3374	3405	3534	3648	4021	4021

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Table 4
Single Exon Probes Expressed in Heart

			_									_																
Onigne Lyon riouses Expressed in Real	Top Hit Descriptor	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREBARP and tensecin X / TNX), sense	Drosophila melanoaster klarsicht brotein (klar) mRNA complete ode	ILS-UM0070-020500-068-a08 UM0070 Homo sepiens cDNA	Fugu rubitpes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds	Tapa-1≕integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 71	A.immersus gene for transposase	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311/34	nx78a03.s1 NCI_CGAP_Ewt Home sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element MER35 repetitive element.	S.bombe ste8 dene encoding protein kinasa	Providencia retigeri penicillin G amidase cene	Homo saplens LGMD2B gene	PM3-FT0024-130600-004-f12 FT0024 Homo seniems CDNA	RC3-CT0254-280999-011-a01 CT0254 Home sapiens cDNA	AF035746 Human salivary gland cell line HSG Homo saniens CDNA clone R1 43	ACETYL-COENZYME A SYNTHETASE (ACETATE—COA I ICASE) (ACYI -ACTIVATING ENZYAJE)	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA complete rds	Homo saplens phosphatidylinositol glycan, class B (PIGB), mRNA	602/40976F1 NIH_MGC_46 Homo saplens cDNA clone IMAGE-4302019 5	602140976F1 NIH MGC 46 Homo septens cDNA clone IMA CF 4302010 5	TRAB PROTEIN	ah31b06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483	CHRUMOGRANIN A PRECURSOR (HUMAN);	phodato of NCI CGAD This Users active	Histories 15 name	PM4-ST0270-001-00 ST0270 Uses series	DKFZp547P194 r1 547 (synonym: Mpr1) Homo saniens cDNA close DKFZxE47P544 g:	Pediococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds
ואום באחוו רוט	Top Hit Database Source	F	LN L	EST HUMAN	N	¥	NT.	LN LN	EST HUMAN	N	N.	NT	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	Į.	님	EST_HUMAN	EST HUMAN	SWISSPROT	144711111 1101	EST HIMAN	EST HIMAN	TN	FST HIMAN	EST HUMAN	IN
5	Top Hit Acession No.	1.1E-01 AF030001.1	1.1E-01 AF157066.1	1.1E-01 AW802056.1	1.1E-01 AF064564.2	S44957.1	1.1E-01 Y07695.1	1.1E-01 D90908.1	1.1E-01 AA747216.1	1.1E-01 X68851.1	1.1E-01 M86533.1	1.1É-01 AJ007973.1	1.1E-01 BE769152.1	1.1E-01 AW853699.1	1.1E-01 AF035746.1	069635	1.1E-01 AF032922.1	11432372 NT	1.1E-01 BF684628.1	1.1E-01 BF684628.1	P41067	4 412 04 4 4 78 0 7 0 4 4	1.1E-01 AA493574 1	1.1E-01 AA493574 1	1.1E-01 X91233.1	1.1E-01 AW817918.1	1.1E-01 AL134349.1	
	Most Similar (Top) Hit BLAST E Value	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1Ë-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01 069635	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01 P41067	10,11	1.1E-01	1.1E-04	1.1E-01	1.1E-01	1.15-01	1.1E-01
	Expression Signal	0.87	7.93	0.8	0.91	2.02	1.26	1.25	1.43	1.62	4.73	1.46	1.79	7.01	1.39	3.48	2.9	2.21	7.05	7.05	1.74	3.07	1.57	1.57	122	1.24	1.78	2.19
	ORF SEQ ID NO:			23867	24150	24214	24397	24487		25551	25570	25681	25697	25708	25903	26012		26198	26474	26475	26550	26570	26845	26846	26872		26934	27186
	Exan SEQ ID NO:	13930	14059	14089	14360	14432	14611	14702	15399	15478	15494	15581	15596	15606	15782	15890	15931	16052	16309	18309	16372	16390	16656	16656	16682	16705	16741	16995
	Probe SEQ ID NO:	4027	4159	4189	4466	4539	4725	4819	5479	6562	5579	5672	6687	2692	5876	6985	6027	8998	8448	\$ 8	6513	6531	11119	11119	6803	8826	6862	7118

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					•		onigo Evolutiones Expressed III Dealt
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7228	17105	27294	2.24	1.1E-01	AA192153.1	EST HUMAN	zp93b12,r1 Strategene muscle 937209 Homo seniens CDNA clone MACE 627743 gr
7228	17105	27295	2.24	1.1E-01		EST_HUMAN	과정3b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE 627743 중
7287	17163	27362	2.48	1.1E-01	1.1E-01 T72675.1	EST HUMAN	9d19h03.s1 Scares fetal liver spleen 1NFLS Homo sapiens CDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE HETA 2 (12) MAAAN
7467	17327		. 2.08	1.1E-01	1.1E-01 BF085149.1	EST HUMAN	MR2-GN0027-040900-005-e08 GN0027 Homo saniens cDNA
7861	17711		1.23	1.1E-01	1.1E-01 R80590.1	EST HUMAN	W96a09.s1 Soares placenta Nb2HP Homo santens cDNA cleme IMAGE: 447064 3
8181	12925	22717	1.94	1.1E-01	1.1E-01 F03265.1	EST HUMAN	HSC1RF022 normalized infant brain cDNA Homo saniens cDNA Arms 2-1470 2-
8294	18173		3.88	1.1E-01	2.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
8402	18278	28530	2.93	1.1E-01		EST HUMAN	M35f12.rf Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element contains TAR1 renefitive element
8519	18391	28655	1.95	1.1E-01 X70058.1		IN IN	M.muscalus cytokine dene
8539	18411	28676	3.21	1.1E-01 Z11910.1		N.	Z.mobilis tot and lip genes encoviim tRNA graning transcurption does and DNA in
8539	18411	28677	3.21	1.1E-01 Z11910.1		L L	Zmobilis tat and lid denes encoding 18NA disapline denes and DNA ligase
8626	18491	28763	2.79	1.1E-01 P17437		SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
9241	18956		3.19	1.1E-01	1.1E-01 BE767023.1	EST HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo saniens CDNA
9485	19507		2.06	1.1E-01	1.1E-01 BE974556.1	EST HUMAN	601680551R2 NIH MGC 83 Homo sapiens cDNA clone IMAGE 3050604 31
9833	19372	25192	2.14	1.1E-01	1.1E-01 BF239753.1	EST HUMAN	601906350F1 NIH MGC 54 Homo sapiens cDNA clane IMAGE 4134085 51
183	11094		4.08	1.0E-01 O62855		SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) // VSOSOMAL DNASE III
1251	11158	21007	1.89	1.0E-01	1.0E-01 Al985499.1	EST HUMAN	ws08d01x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7:8
1370	11276	21132	2.88	1.0E-01	1.0E-01 AL161504.2	Z	Arabidopsis thaliana DNA chromosome 4, conting fragment No. 16
2439	12316	22213	-	1.0E-01	5.1	EST HUMAN	Ui-H-Bi3-alo-d-07-0-Ui.s1 NCI CGAP Sub5 Homo saniens cDNA clone IMAGE-2726/20 21
3468	13384	23189	0.98	1.0E-01	1	EST_HUMAN	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5
3658	13572	23359	1.01	1.0E-01	.1	EST HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3871	13782	23574	2.44	1.0E-01	1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4307	14204	23987	1.5	1.0E-01	2	NT	Chlamydophila pneumoniae AR39, section 91 of 94 of the complete genome
4455	14349		1.17	1.0E-01	1.0E-01 AI792349.1	EST HUMAN	en32c04.y5 Gessler Wilms tumor Home seniens cDNA clone IMAGE-17mage Er
4613	14501	24289	1.26	1.0E-01 U50450.1		NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA complete c4s
4838	14719	24502	2.06	1.0E-01	1.0E-01 AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sabiens CONA
5158	15025	24792	0.87	1.0E-01 D49683.1		N	Mouse FTZ-F1 gene
5188	15051	24815	1.44	1.0E-01 E	1.	EST_HUMAN	UI-H-BW1-aoa-e-12-0-UI.s1 NCI CGAP Sub7 Homo saplens cDNA clone (MAGE-2084022 2)
9280	15182		9.16	1.0E-01 W86490.1		EST_HUMAN	zh6Zh04.s1 Soares fetal liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE-416Rd5 3
5670	15580	25680	11.21	1.0E-01/	1.0E-01 AF274875.1		Hamo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete ods

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Table 4
Single Exon Probes Expressed in Heart

		T	T	T	Т	T	T	Т	T	Т	Т	Т	Т	Т	T	Т	Т	Т	Т	Т	Т	Т	T	Т	Т	Т	7	Т	Т	T	Т	_	Т
Single Exoli Flobes Explessed in Real	Top Hit Descriptor	yd34h06.r1 Sœres placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element,	M.musculus whn gene	Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds	Human pro-elpha-1 (V) collagen mRNA, complete cds	Hellcobacter pylori, strain J99 section 62 of 132 of the complete genome	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5	Homo sapiens mRNA for KIAA1579 protein, partial cds	Homo sapiens mRNA for KIAA 1579 protein, partial cds	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE;4106089 5	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 51	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA	Drosophila melanogaster ftz gene	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA complete cde	601065554F1 NIH MGC 10 Homo sapiens cDNA clone IMAGE:3451033 F	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cde	Zea mays mRNA for Toc342 protein (toc348 gene)	Bacillus halodurans genomic DNA, section 1/14.	Drosophilla melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA,	601070219F1 NIH MGC 12 Homo cambras aDNA dona NAAOE 2 Accorde El	601070219F1 NIH MGC 12 Home sanians cDNA done INAGE: 3400303 3	AV730747 HTF Homo sepiens cDNA clane HTFRNIDA R	Homo saciens neurextu III-alcha dene nartial cots	7477c12.X1 NCI CGAP Lu24 Homo sabiens cDNA clone MAACE 2778008 3	Aspergillus terreus BSD mRNA for blasticidin S deaminase complete cde	Mus musculus phospholipid transfer protein (Pito), mRNA	O.sativa RAmy3C gene for alpha-amylase	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA	Daticus cardia leuroamhdrovanldin diowyrenese 2 (1 mm) menia 1 mm 1 mm
אום בעמוז בומר	Top Hit Database Source	EST HUMAN	IN	N	N.	TN	EST_HUMAN	FN	Z	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N F	ᅜ	N E	EST HUMAN	N	ΙN	NT	Ę	T HIMAN	Т	Т	Т	T HUMAN	Г		F		
	Top Hit Acession No.	1.0E-01 R23821.1	1.0E-01 Y12488.1	1.0E-01 AF102855.2	M76729.1		1.0E-01 BF240154.1	1.0E-01 AB046799.1		1.0E-01 BE792750.1	AÚ159127.1	BF242946.1	3.1	3.1	1.0E-01 BE537719.1	7662165 NT			9.1		1.0E-01 AJ271049.1	7.1	+		T	Γ			Γ	6755111 NT		503224	Į.
	Most Similar (Top) Hit BLAST E Value	1.0E-01	1.0E-01	1.0E-01	1.0E-01 M76729.	1.0E-01 AE00150	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01 AU15912	1.0E-01 BF24294	1.0E-01 BF24294	1.0E-01 BE79054	1.0E-01	1.0E-01	1.0E-01 X00854.1	1.0E-01 U52691.1	1.0E-01 BE53771	1.0E-01 U66834.1	1.0E-01	1.0E-01 AP00150	0 0E-02 AE274008	9.9E-02	9.9E-02 E	9.9E-02	9.9E-02	9.9E-02	9.9E-02 D83710.1	9.9E-02	9.8E-02 X56338.1	9.8E-02	9.8E-02 AF184274
	Expression Signal	1.88	2,45	1.16	1.8	2.73	1.84	9.08	9.08	1.26	2.02	2.9	2.9	4.43	2.5	1.34	2.03	2.57	2.46	8.59	1.28	4.16	00.	4-	1.44	0.92	1.15	22.55	7.96	1.5	1.58	1.53	3.28
	ORF SEQ ID NO:			27376			27724	27788		28007		28520	28521	28803							25187		22505	22511	22512	22675	22952	24260	24862	27440		21482	22827
	Exon SEQ ID NO:	16072			17333	17293	17501	17563	17563	17768	17941	18269	18269	18521	19285	19085	19098	19688	19285	18664	19360	.19363	12814	12619	12619	12877	13153	14472	15118	17236	10492	11612	13032
	Probe SEQ ID NO:	6187	6549	7299	7473	7505	7651	77.13	7713	7918	8050	8393	8393	8703	9226	9453	9469	9735	9765	9818	9871	9877	2752	2757	2757	2950	3229	4582	6161	7332	551	171	3106

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor		- Cons	FIRST COSTON	ing invAGE;3884Z87 5		Tromo septens riprobless growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA	SCUNA	COPROTEIN A33)	S CLIVA	VIII 239,111 IO 3213410	ion of MA June 1140 Francisco	wx78b06x1 NCI_CGAP_Ov38 Homo saplens CDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1 PEPTIDYI -PROI YI CISTPANS ISOMEDASC A AUTINANA	JIMPAN);		4 clone IMAGE:1678485 3	4 clone IMAGE: 16/8485 3	* Z C	CONA	MACE: 2000 ASE EL	10 10 10 10 10 10 10 10 10 10 10 10 10 1	te IMAGE:3919363 5'	the, exons 1 to 55	the, exons 1 to 55	Insposase (in S-5 copy)	unsposase (in S-5 copy)	PRECURSOR (CD55)	Segment 102/182	lone IMAGE:745392 3'	INA clone IMAGE Ages 2	HIMAGE:3832008 F	CDNA	
Single Exon Probes Expressed in Heart	τ	Leptosphaeria macufans befa-fullullin mRNA	Leptosphaeria macrifans beta-fribillin mBNA complete cus	601460793F1 NIH MGC 66 Home senions of NIA Alexanders	Aloe arborescens mRNA for NADP-mails enzume complete and		NVI-HT0518 070300 005 -01 UT0518 U	CELL SHIREACE A33 ANTICEN DESCRIBEOR CON MORPHINE	EST366546 MAGE resentiences MAGO Licenter Child	Bacillus subtilis complete genome (section 18 of 21): from 2007773 1. 8232333	W41c03.s1 Weizmann Olfactory Epithellium Homo semions cDNA Apro 1440E-054708 at	W41c03.s1 Weizmann Olfachov Enithelium Home senione, DNA -1 ILAN CE. 234/88 3	wx78b06x1 NCI_CGAP_0v38 Homo saplens cDNA clone IM PEPTIDYI -PROI Y CIS.TRANS ISOMEDASE A ULI MARAN	Mus musculus ligatin (I oth) mRNA partial calc	oz47d11 x1 Scarpe NHHMD; S1 Home Series DNA	0247d11x1 Scares NHHMP1 S1 Home capters conv. Const. 144 Scares NHHMP1 S1 Home capters conv.	Profeus mirabilis fimhrial phason strain L1/220	EST378303 MAGE resemiences MACI Homo conjunctions	RC5-BT0254-031099-011-an3 BT0254 Homo september 2010A	1601498088F1 NIH MGC 70 Homo sanians CONA close IMA CE 200815E EI	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5	601434080F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3919363 5	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 conv)	Antirhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CDES)	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392.3	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE-ARRES 2	601563355F1 NIH MGC 20 Homo sapiens cDNA clome IMAGE:383290R &	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA	Venbergien ergilant im selven lest manes
gie Exon Pro	Top Hit Database Source	¥	Į	EST HUMAN	N-	1	EST HIMAN		EST HUMAN	N	EST HUMAN	EST HUMAN	EST HUMAN	N	EST HUMAN	Τ	T	EST HUMAN	EST HUMAN		HUMAN	T_HUMAN					SWISSPROT	Γ			EST_HUMAN		Ż
iio	Top Hit Acession No.	9.8E-02 AF257329.1	9.8E-02 AF257329.1		9.7E-02 AB005808.1	AECOTAC	3E168660 1 ES	٠ı	NW954476.1	299119.1			_		-			-	-	Γ	-	1	_	_		_			.1		.1	-	
	Most Similar (Top) Hit BLAST E Value	9.8E-02/	9.8E-02/	9.8E-02 BF03742	9.7E-02/	0 75 00	9.7E-02 BE16866	9.7E-02 Q99795	9.7E-02 AW95447	9.7E-02 Z99119.1	9.7E-02 N22798.1	9.7E-02 N22798.1	9.7E-02 Al953984.	9.7E-02 U58337.1	9.6E-02 AI080721	9.6E-02 A1080721	9.6E-02 Z32686.2	9.6E-02 AW96623	9.6E-02	9.6E-02	9.6E-02 AV687898,	9.6E-02 BE894895	9.6E-02 AJ243211	9.6E-02 AJ243211.	9.6E-02 AB013985	9.6E-02 AB013985.	9.6E-02 P08174	9.6E-02 Z79702.1	9.6E-02 AA625755	9.6E-02 H14599.1	9.6E-02 BE728219.	9.5E-02 AW992398	9.5E-02 U63374.1
	Expression Signal	6.67	29'9	2.1	1.16	80 0	2.37	3.56	1.39	4.27	1.59	1.59	1.32	1.97	127	127	6.02	96.0	0.8	2.72	1.51	<u>48</u> .	1.75	1.75	1.59	1.59	3.29	6.51	1.8	1.38	1.26	2.25	0.87
	ORF SEQ ID NO:	23805	23806	28148			22004		25669	26345	26731	26732	27207		21753	21754	23921	24579	24738		27580		27855	27826	27933	27934	7/380	28260	29056		25212	23694	24704
	Exon SEQ ID NO:	14031	14031	17904	11235	11471	12100	13811	15572	16184	16535	16535	17014	18403	11862	11862	14147	14810	14963	15621	17371	17527	1/622	7,077	200	17689	P .	18013	18/64	19312	19344	13918	14932
	Probe SEQ ID NO:	4131	4131	8755	1328	1567	2214	3901	5661	6321	9992	6655	7137	8531	1969	1969	4248	4932	5093	5713	7502	7/9/	7/1/2	7/1/7	3 6	7005	000/	8125	/cgg	86/6	8848	4012	2005

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														genes															and partial	erie, par usi	Detai, o-			
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Trimeresurus flavoviridis DNA for phospholipase 42 intilhifation and a second s	Arabidopsis thaliana DNA chromosome 4 continutrament No. 38	601453642F1 NIH MGC 66 Homo saniens cDNA clone 1848 CE-3867243 E	601453642F1 NIH MGC 66 Homo serviens cDNA clore IMACE: 3657243 5	601453642F1 NIH MGC 68 Homo samiens con a chara MAGE secretary	601453642F1 NIH MGC 66 Home serviens cDNA clara NA CE 28 57243 5	602150882F1 NIH MGC 81 Home saniens cDNA clane IMAGE 4204047 E	Cavia porcellus 3beta-hydropysteroid sulfotransferase mBMA completed	Cavia porcellus 3beta-hidroxisteroid suffortansferase mRNA complete cds	M.capricolum DNA for CONTIG MC073	Mus musculus coding region determinant-binding protein (Crdbb), mRNA	Acineibbacter so own Own Own at the state of the Carte of	Human BRCA1 Rho7 and vall genes committee of the section of the se	Raftus norvenicus calcium channel alabe of cubinett (2000).	Human penhRGT-1 hataing CABA transmotor miblin	Homo seniens BAI1-associated protein 3 (BAIAD3) BAIA	Homo sabiens nasonhanggal enlithelium sna-the and an 4 (NESCA)	602133086F1 NIH MGC 84 Homo capiene chiva Anna Harana H	601286082F1 NIH MGC 44 Homo seniens cDNA clama IVA GE 2607552 5	601286082F1 NIH MGC 44 Homp saniens cDNA cline IMAGE:3607862 E	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5	601655988R1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3855981 3'	HYPOTHETICAL PROTEIN KIAA0032	HYPOTHETICAL PROTEIN KIAA0032	Ul-H-BI1-afx-h-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE-2723553 31	Photobacterium damselae subsp. damselae partial ovrB gene for DNA grazae R submit	hd28h12x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE: 2910887 3	Mus musculus major histocompatibility locus class II region: Fas-binding profession Dayx (DAXX) grand purities	cds; Bing1 (BING1), tapasin (tapasin), RaiGDS-like factor (RLF). KE2 (KE2) BING4 (BING4). Nets. 3	galactosyl transferase (beta1,3-galactosyl tr>	Molluscum contagiosum virus subtype 1, complete genome	Molluscum contagiosum virus subtype 1, complete genome	Molluscum contagiosum virus subtype 1, complete genome
Jie Exon Proi	Top Hit Database Source	NT	Ę	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	노	NT	N P	NT	Į L	L	LX	LN	٦	12	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN		EST_HUMAN						N
S IIO	Top Hit Acession No.	AB003473.1	AL161538.2	9.5E-02 BF035861.1				<u>~</u>				6753517 NT					4809280	6912525 NT	9.3E-02 BF575511.1		İ	1.1	.2			7.1	.1	1.1			3.1			
	Most Similar (Top) Hit BLAST E Value	9.5E-02 AB00347;	9.5E-02 AL181538	9.5E-02	9.6E-02 BF03586	9.5E-02 BF03586	9.5E-02 BF03586	9.4E-02 BF67106	9.4E-02 U55944.1	9.4E-02 U55944.1	9.4E-02 Z33059.1	9.4E-02	9.4E-02 Z46863.1	9.4E-02 L78833.1	9.4E-02 U31815.1	9.4E-02 U27699.1	9.3E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02 AV732224	9.3E-02 BE962631	9.3E-02 Q15034	9.3E-02 Q15034	9.3E-02 AW 20611	9.3E-02 AJ249850	9.3E-02 AW 468850		1	9.3E-02 AF100956.	9.2E-02 U60315.1	9.2E-02 U60315.1	9.2E-02 U60315.1
	Expression Signal	3.72	7.48	2.59	2.59	3.29	3.29	3.86	0.86	0.86	4.34	0.89	2.62	2.69	3.36	1.42	1.83	5.39	2.03	3.51	3.51	1.88	2.24	3.52	3.52	3.74	1.85	8.62			1.95	4.32	4.32	4.32
	ORF SEQ ID NO:	26348		26666	26667	28206	28207	21565				24621		26505		25182			22946	23738	23739		27665	27949	27950	1			•	,	00000	20008	20009	lorooz
	Exon SEQ ID NO:	16186				17957	17957	11690	11717	. 11717	13716	14855	16876	16338	19603	19411	12887	12921	13142	13962	13962	14516	17450	17705	17705	1//63	19527	19555		7000	19002	18101	76101	1/8/1
	Probe SEQ ID NO:	6323	6467	6288	6288	9086	8066	1792	1820	1820	3804	4980	6669	8304	9083	9943	2960	2993	3218	4060	4060	4628	1,599	G20	(822	/813	88	9704		9000		87	87 5	1077

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Table 4
Single Exon Probes Expressed in Heart

Olligie Lyon Flobes Explessed in nean	Most Similar (Top) Hit Acession (Top) Hit Acession Signal BLASTE No. Source Source	2.2 9.2E-02 R54156.1 EST HUMAN 1998107.11 Soares infant brain 1MiB Homo sanions cDNA clone MACE: 44.620 El	4.53 9.2E-02 Q28631 SWISSPROT	1.16 9.2E-02 AA534354.1 EST HUMAN	5755215 NT	1.34 9.2E-02 U92048.1 NT Human herpesvirus 1 strain KOS-63. latency-associated transcript premater readon	1.02 9.2E-02 BE299722.1 EST HUMAN	1.86 9.2E-02 X96402.1 NT	· 1.86 9.2E-02 T49920.1 EST HUMAN	2.07 9.2E-02 X95256.1 NT	2.77 9.1E-02 X77665.1 NT	1.01 9.1E-02 P78985 SWISSPROT		1.81 9.1E-02 AL161554.2 NT	1.73 9.1E-02 AF129768 1 NT	11.89 9.1E-02 AW160658.1	1.65 9.1E-02 T02984.1 EST HUMAN	9633494 NT	T HUMAN	9.1E-02 AJ291390.1 NT	3.36 9.0E-02 P15328 SWISSPROT	6.45 9.0E-02 BE220482.1 FST HIIMAN	1.11 9.0E-02 AF138522.1 NT	1.11 9.0E-02 AF138522.1 NT	0.92 9.0E-02 AF279135.1 NT	0.8 9.0E-02 S68757.1 NT	0.8 9.0E-02 S68757.1 NT	1.2 9.0E-02 P55268 SWISSPROT
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-	ORF SEQ ID ID NO:	67		88 22986	53	45		31 24213	50 26746	35 26823		45 22139	32	79 24058	25 25487	34 26393		15	22	84	59 20490	21379						24001
	Probe Exon SEQ ID SEQ ID NO: NO:	2180 12067	3142 13067					4538 14431			417 9984			4383 14279	5507 15425	6372 16234	7958 17808	9021 18815	9256 19692	9785 19548	727 10659	1617 11521			- 1	ı		4321 14218
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Single Exon Probes Expressed in H

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| Top Hit Descriptor | Plasmodium falciparum P-type ATPase 3 gene | REGULATORY PROTEIN ZESTE | za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:552171 S52171 smail G protein - human : | Homo saplens chromosome 16 coen reading frame 5 (C16orfs) mRNA | 602129030F2 NIH MGC 56 Homo sapiens cDNA clone IMAGE-4285951 F | 802129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5 | PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA | Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds | zw03d04.s1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:768199.3'

 | Ul-H-BI3-alo-f-08-0-Ul.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'

 | Ul-H-Bl3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGF:3068294.37 | Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
 | FOLD BIFUNCTIONAL PROTEIN (INCLUDES: METHYLENETETRAHYDROFOLATE
DEHYDROGENASE: METHFNY TETRAHYDROFOLATE CYCLOLYDROLAGE 1 | H. Sapiens flow-sorted chromosome 6 Hindlill frament SCRAADRER | EST180187 Liver, hepatocellular carcinoma Homo saniens cDNA 5' ond | 602129682F1 NIH MGC 56 Homo segiens cDNA clone IMAGE-4286480 S | PROBABLE DNA LIGASE (POLYDEOXYRIBONICI FOTIDE SYNTHASE (ATE)

 | EST11595 Uterus Homo sapiens cDNA 5' end | TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFIL135) (TAFII135) (TAFII-130) | Homo sapiens paired box gene 6 (anitidia, keratifis) (PAX6) isoform h mBNA | या99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE ਜ਼ੁਲਾਤਕ ਕਾ
 | 601191770F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3535648 5 | 601191770F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3535648 5 | DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 F | S.cerevislae chromosome XIV reading frame ORF YNL285w | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes. controleid cits: and biglycan (BGN) | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete citis, and nissma membrane celetium ATDoor in forms. |
| Top Hit
Database
Source | Ę | SWISSPROT | EST HUMAN | 1. | EST HUMAN | EST_HUMAN | EST_HUMAN | NT | EST_HUMAN

 | EST_HUMAN

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 | SWISSPROT | LN L | EST HUMAN | EST HUMAN | SWISSPROT

 | EST_HUMAN | SWISSPROT | NT | EST_HUMAN
 | EST_HUMAN | EST_HUMAN | EST HUMAN | NT | Ł | L |
| Top Hit Acession
No. | X65740.2 | Q24597 | W56037.1 | 11431759 | BF701593.1 | BF701593.1 | BE153572.1 | AF286055.1 | AA424887.1

 | AW 452122.1

 | AW 452122.1 | 11433478
 | P47259 | Z79021.1 | AA309319.1 | BF696918.1 | 027474

 | AA299128.1 | 000268 | 4580423 | AA151872.1
 | BE264455.1 | BE264455.1 | AL040129.1 | | | 8.7E-02 U82695.2 |
| Most Similar
(Top) Hit
BLAST E
Value | 9.0E-02 | 9.0E-02 | 9.0E-02 | 9.0E-02 | 8.9E-02 | 8.9E-02 | 8.9E-02 | 8.9È-02 | 8.9E-02

 | 8.9E-02

 | 8.9E-02 | 8.9E-02
 | 8.9E-02 | 8.9E-02 | 8.9E-02 | 8.9E-02 | 8.8E-02

 | 8.8E-02 | 8.8E-02 | 8.8E-02 | 8.8E-02
 | 8.8E-02 | 8.8E-02 | 8.8E-02 | 8.8E-02 | 8.7E-02 | 8.7E-02 |
| Expression
Signal | 1.79 | 1.06 | 8.02 | 15.35 | 2.15 | 2.15 | 1.41 | 1.71 | 0.92

 | 3.3

 | 3.3 | 3.13
 | 1.56 | 1.83 | 5.28 | 4.03 | 1.25

 | 96'0 | 3.24 | 1.13 | 1.83
 | 3.19 | 3.19 | 10.63 | 1.38 | 3.02 | 3.02 |
| ORF SEQ
ID NO: | 24248 | | 25653 | | 21189 | | | | 24208

 |

 | | 25568
 | 26290 | | 27088 | | 21113

 | 23532 | | | 27260
 | 28596 | 28597 | 28722 | 25332 | 23337 | 23338 |
| Exon
SEQ ID
NO: | 14460 | 15009 | 15560 | 19428 | | | | | _1

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 | | -1
 | 16135 | 16320 | 16875 | 18949 | 11257

 | 13740 | 13856 | 14104 | 17072
 | 18334 | 18334 | 18453 | 19001 | 13550 | 13550 |
| Probe
SEQ ID
NO: | 4568 | 5142 | 5647 | 2962 | 1419 | 1419 | 2338 | 4104 | 4534

 | 2269

 | 2269 | 9299
 | 6270 | 6460 | 8669 | 9228 | 1351

 | 3828 | 3948 | 4205 | 7195
 | 8461 | 8461 | 8585 | 9302 | 3636 | 3636 |
| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source | Exon ORF SEQ Expression (Top) Hit Top Hit Acession NO: Signal Value 1460 24248 1.79 9.0E-02 X65740.2 NT Plasmodium falciparum P-type ATPase 3 den | Exon ORF SEQ Expression Signal (Top) Hit Accession Signal Top Hit Accession No. Top Hit Accession Source Top Hit Accession Source Top Hit Accession Source Top Hit Accession No. Top Hit Accession Source Top Hit Accession No. Top Hit Accession No. Top Hit Accession Source Top Hit Accession No. Top Hit Ac | Exon ORF SEQ ID NO: Signal 1709 Most Similar Signal NO: Top Hit Acession Signal No: Top Hit Acession No: Top Hit A | Exon No: Signal NO: Signal NO: Signal NO: NO: NO: NO: NO: NO: NO: NO: NO: NO: | Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit Top Hit Acession No. Top Hit Acession No. | Exon No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Source No:- Source No:- Signal No:- Source No | Exon No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Signal No:- Source No | Exon No:- ORF SEQ ID NO:- Expression Signal (Top) Hit Top Hit Accession No:- Top Hit Accession No:- <t< td=""><td>Exon No:- ORF SEQ ID NO:- Expression Signal Top) Hit Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:- Top Hit Accession No:-
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8.9E-02 (24445272) SWISSPROT 15485 25560 3.3 8.9E-02 (2444527) SWISSPROT 16491 25608 3.13 8.9E-02 (27474) SWISSPROT 16875 27113 1.25 8.9E-02 (27474) SWISSPROT</td><td>Exon ORF SEQ Expression Signal Most Similar Acession Signal Most Similar Acession Signal Top Hit Acession Source Source Source Source Source Alue Top Hit Acession Source Source Source Source Source Source Source Source Source 15009 Value No. ELAST E Source Source Source Source Source Source Source Source 15009 Value Source Source Source Source Source Source Source 15009 NT Top Hit Acession Source Source Source Source Source Source Source 15009 NT Top Hit Acession Source Source Source Source Source Source Source Source Source 15009 NT Top Hit Acession Source Sour</td><td>Exon No:- CAF SEQ Breasston Signal Figh Hit Top Hit Acession Source Source National SEQ ID ID NO:- Most Similar Signal Top Hit Acession Database Source Source Source Source Source Source Source Source Source Source Source Source Source 15:06 Top Hit Top Hit Top Hit Acession Database Source Source Source Source Source Source Source Source Source Source Source 16:06 Top Hit Top Hit Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source 16:06 Top Hit Acession Source Sour</td><td>Exon No:- Signal N</td><td>Exon
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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Wost SimilarTop Hit AcessionTop Hit AcessionTop Hit DescriptorBLAST ENo.Source	2/108a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417194 5' similar to contains element MER12 repetitive element.	Т	8.7E-02 AE000895.1 NT complete cenome	5.1 EST HUMAN	5.1 EST HUMAN	Т	NT NT	X17116.1 NT	79057 NT	-N	EST_HUMAN	L	NT NT	LN	8.6E-02 Y10826.1 NT Homo sepiens LCN1b gene	N.		5730066 NT	8.6E-02 5730066 NT Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA	8.6E-02 AF206551.1 NT Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product	8 6E-02 AF206551.1 NT Lacerta media cytrochrome c cythonis 4 const.	2	EST HUMAN	LN L	Bacillus stearothermophilus BsrF1 methylase (FIM) and BsrF1 restriction endonuclease (FIR) genes, complete	<u> </u>	SWISSPROT	85.1 NT
eiBuic		_	7:	5.1	5.1	5.1		+		79057	17	2		2.1					142	5730066 NT	τ.	•	Ī						-
	₽	8.7E-02 W	8.7E-02 AF	8.7E-02 AE	8.7E-02 AA	8.7E-02 AA	8.7E-02 LO	8.7E-02 AJ	8.7E-02 X1	8.7E-02	8.6E-02 AJ	8.6E-02 BE	8.6E-02 LO	8.6E-02 AF	8.6E-02 U6	8.6E-02 Y1	8.6E-02 JOC	8.6E-02 JO	8.6E-02	8.6E-02	8.6E-02 AF	8.6E-02 AF	8.6E-02 BF	8.6E-02 BF.	8.6E-02 AE	8.6E-02 AE	8.5E-02 AE	8.5E-02 PO	8.5E-02 AF
	Expression Signal	0.82	1.22	1.06	5.41	5.41	2.58	1.77	2.58	1.81	7.05	2.22	2.94	3.07	0.87	4.38	1.51	1.51	1.26	1.26	1.98	188	3.63	3.63	4.71	1.73	2.87	1.8	6.34
	ORF SEQ ID NO:	23578	24286	•	24951	24952		28770			20991	21986	22876		24060	25718	25867	25868	26695	26696	28441	28442	28710	28711	28131	28958	22124		25665
	Exen SEQ ID NO:	13790	14497	14906	15177	15177	17985	18496	18994	19105	11139	12084	13076	13507	14281	15616	15752	15752	16508	16508	18192	18192	18442	18442	17887	18670	12227	15419	15570
	Probe SEQ ID NO:	3879	4609	5034	5255	6255	8094	8631	9293	9484	1232	2197	3151	3593	4385	5708	5846	5846	6628	6628	8315	8315	8574	8574	8738	8858	2347	5500	5668

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	T	T	T	T	T	T	T	T	\top	Ţ	T	T	T	7	1	Ţ	T	T	Т	T	T	T	T	T	Τ	٦	7	T	T	T
Top Hit Descriptor	Mus musculus zinc transporter (ZnT-3) gene, complete cds	601439576F1 NIH_MGC_72 Homo sapiens cDIVA clone IMAGE:3924523 5	Bos faurus connective tissue growth factor precursor (CTGF) gene, complete cols	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA	Beet necrotic yellow vein virus RNA-2	601115055F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:3355508 ST	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdci and mdcM nenes) commiste ada	Homo sadens extracellular alvontratin facilità premient montre della del	Homo sablens chromosome 21 segment HS21 Cnn2	EST366723 MAGE resequences, MAGC Homo saniens cinna	Wolluscum contagiosum virus surbkne 1, commiste cenoma	Human gene for dihydrolipoamide succinvitransferase, complete cds (exp. 1.15)	Human gene for dihydrolipoamide succinytransferase, complete cds (exp. 1-15)	PM3-BT0347-170200-001-b08 BT0347 Homo seniens cDNA	Synechocystis sp. PCC6803 complete gename, 17/27, 2137259-2267259	Synechocystis sp. PCC6803 complete gename. 17/27, 2137259-2267259	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619.57	Dictyoselium discadeum cyclic nucleotide phosphodiesterase gene, complete cds	Thermoplasma acidophilum complete genome; segment 5/5	EST378191 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL 2) mRNA	M.musculus gene for gelatinase B	Herpesvirus sainlit transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene,s	Company and singli nuclear RIVAS (URIVAS)	Homo sepiens ABCA1 (ABCA1) gene, complete cos	Botvits cinetea strain T4 cDNA library under conditions of nitrogen dendications	H. saplens AGT gene, intron 4	H.sepiens AGT gene, Inton 4
Top Hit Database Source	N	EST HUMAN	N.	EST_HUMAN	F	EST_HUMAN	TN	TN	F	L	N	EST HUMAN	N	TN.	N	EST_HUMAN	12	בּוֹ			Ę	ST HUMAN	בא	۲۲	Į,					NT
Top Hit Acession No.		0.1	5.1	26.1					3.1	1	22								1.1		NL445067.1	1W965118.1								
Most Similar (Top) Hit BLAST E Value	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.1E-02	8.1E-02	8.1E-02/	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02/	8.0E-02/	8.0E-02	8.0E-02.	8.0F-0218	8.0E-02/	8.0E-02/	8.0E-02	8.0E-02	8.0E-02 X74208.1
Expression Signal	2.82	1.43	3.14	3.13	5.33	2.11	4.13	1.84	1.72	1.65	3.38	3.28	1.33	10.54	10.54	3.9	1.01	1.01	4.08	0.81	1.01	0.84	1.06	5.62	0.87	3.35	1.63	3.65	1.49	1.49
ORF SEQ ID NO:	24655			27164					21247		28894	19784	20690	21440	21441	21632	22103	22104		20833	22591	23440			24499	25581	25581	26798	27471	27472
Exa SEQ ID NO:				_				19480	11384	17553	18604		10844	12701	12701	11757			[ı	1	13887	14595	14716	15506	15506	16607	17268	17268
Probe SEQ ID NO:	5014	5271	6188	7094	7536	7628	9314	9706	1479	7703	8789	5	920	1671	1671	1861	2323	2323	2421	2790	282	3745	3980	4709	4834	5591	6261	6727	7401	7401
	Exon ORF SEQ Expression (Top) Hit Acession ID NO: Signal Value Source Source	Exon ORF SEQ ID NO: Expression Signal (Top) Hit Acession No: Top Hit Acession No: Top Hit Acession Source Top Hit Acession Source Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Database Source Source Source 14888 24655 2.82 8.2E-02 U76009.1 NT Mus musculus zinc transporter (ZnT-3) gene.	Exon SEQ ID NO: ORF SEQ Signal NO: Expression Signal Value (Top) Hit PLASTE Value Top Hit Acession No. Top Hit Acession No. Top Hit Acession Source 14888 24655 2.82 8.2E-02 U76009.1 NT 15193 24968 1.43 8.2E-02 BE897030.1 FST HUMAN	Exon ORF SEQ ID Expression ID NO: Crop) Hit Signal Top Hit Acession (Top) Hit Top Hit Acession Signal Top Hit Acession No: Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Source Source 14888 24656 2.82 8.2E-02 U76009.1 NT 15193 24988 1.43 8.2E-02 BE897030.1 EST HUMAN 16073 26222 3.14 8.2E-02 AF309555.1 NT	Exon ORF SEQ ID NO: Expression ID NO: Top Hit Acession Signal ID NO: Top Hit Acession Signal ID NO: Top Hit Acession ID No: Top Hit Acession ID Actabase No: Top Hit Acession ID Actabase No: Top Hit Acession ID Actabase	Exon ORF SEQ ID ID NO: Expression Signal No: (Top) Hit Top Hit Acession Signal No: Top Hit Acession No: Top Hit Ac	Exon ORF SEQ ID ID NO: Expression Signal Ansatz (Top) Hit Top Hit Acession Signal Ansatz Top Hit Acession No: Database No: Source	Exon ORF SEQ ID ID NO: Expression Signal ID NO: (Top) Hit Signal Signal ID NO: Top Hit Acession Patabase ID NO: Top Hit Acession ID NO: Top Hit Acession ID NO: Top Hit Acession ID Adabase	Exon ORF SEQ ID ID NO: Expression Signal ID NO: (Top) Hit Signal ID NO: Top Hit Acession No: Top Hit Acession No: Top Hit Acession Database No: 14888 24656 2.82 8.2E-02 ID 176008.1 NT 15/33 24656 3.14 8.2E-02 ID 24730955.1 NT 16971 27764 3.13 8.2E-02 AF30955.1 NT 17387 27598 5.33 8.2E-02 AW875126.1 EST HUMAN 17479 27759 2.11 8.2E-02 AW875126.1 INT 16006 25336 4.13 8.2E-02 AE00246.2 NT 19480 1.84 8.2E-02 AE002246.2 NT	Exon ORF SEQ ID Expression ID NO: Signal Signal Most Similar Top Hit Acession Signal Top Hit Acession No: Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Source Native Source 14888 24656 2.82 8.2E-02 U76009.1 NT 15193 24988 1.43 8.2E-02 U76009.1 NT 16073 26222 3.14 8.2E-02 BE897030.1 EST HUMAN 16073 26222 3.13 8.2E-02 AF309555.1 NT 17387 27598 5.33 8.2E-02 AF309555.1 NT 17479 27699 2.11 8.2E-02 AF30955.1 NT 19006 25336 4.13 8.2E-02 AF30955.1 NT 19480 1.84 8.2E-02 AF205368.1 NT 11384 21247 1.72 8.1E-02 AF275386.1 NT	Exon ORF SEQ ID NO: Expression Signal (Top) Hit PLASTE Top Hit Acession No. Top Hit Acession Source Top Hit Acession Source 14888 24656 2.82 8.2E-02 U76008.1 NT 15193 24988 1.43 8.2E-02 U76008.1 NT 16073 26222 3.14 8.2E-02 RE897030.1 EST HUMAN 16971 27164 3.13 8.2E-02 AW875126.1 EST HUMAN 17387 27598 5.33 8.2E-02 X04197.1 NT 19006 25336 4.13 8.2E-02 AE002246.2 NT 19480 1.84 8.2E-02 AE002246.2 NT 11384 21247 1.72 8.1E-02 AF275366.1 NT 17553 8.1E-02 AF275366.1 NT NT	Exon ORF SEQ ID NO: Expression Signal (Top) Hit PLASTE Top Hit Acession No. Top Hit Acession Source 14888 24656 2.82 8.2E-02 3.14 BE897030.1 8.2E-02 BE897030.1 NT 1593 24988 1.43 8.2E-02 3.14 BE897030.1 BE2-02 BE897030.1 NT 16973 25222 3.14 8.2E-02 3.13 BE807030.1 BE2-02 BE897030.1 NT 16974 27164 3.13 8.2E-02 3.33 BAR-02 BE2-02 BE2-02 BE2-02 BE2-02 BE2-02 BE2-02 BE2-02 BE2-02 BE2-03 BE2-02 BE2-02 BE2-02 BE2-02 BE2-03 BE2-02 BE3-03	Exon SEQ ID 10 NO: CRF SEQ Signal Signal NO: Most Similar Signal Signal NO: Top Hit Acession NO: Top Hit Acession No:	Exon ORF SEQ ID NO: Expression Signal (Top) Hit PLASTE Value Top Hit Acession ID NO: Top Hit Acession Source Top Hit Acession Source 14888 24656 2.82 8.2E-02 U76008.1 NT 15193 24988 1.43 8.2E-02 BE897030.1 EST HUMAN 16073 26222 3.14 8.2E-02 BR895030.1 EST HUMAN 16971 27164 3.13 8.2E-02 AW875126.1 EST HUMAN 17387 27598 5.33 8.2E-02 AW875126.1 INT 17479 27699 2.11 8.2E-02 ARW875126.1 INT 19006 25336 4.13 8.2E-02 AR9017138.1 INT 19480 1.84 8.1E-02 AR002246.2 INT 17553 1.65 8.1E-02 AY005150.1 INT 12657 19784 3.38 8.1E-02 AY005150.1 INT 12667 19784 3.28 8.0E-02 AW9954683.1 EST HUMAN 108	Exon ORF SEQ ID ID NO: Expression Signal (Top) Hit Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession Source No: Top Hit Acession No: Top Hit Acessi	Exon ORF SEQ ID ID NO: Expression Signal Signal (Top) Hit Top Hit Acession No: Top Hit Acessi	Exon ORF SEQ ID ID NO: Expression Signal Signal (Top) Hit Top Hit Acession No: Top Hit Acessi	Exon ORF SEQ ID NO: Expression Signal (Top) Hit PLAST E Value Top Hit Acession No. Top Hit Acession Source 14888 24656 2.82 8.2E-02 U76008.1 NT 15193 24958 1.43 8.2E-02 D76008.1 NT 16073 26222 3.14 8.2E-02 AR9375126.1 EST HUMAN 16073 26222 3.13 8.2E-02 AW875126.1 EST HUMAN 17387 27598 5.33 8.2E-02 AW875126.1 EST HUMAN 17479 27769 5.31 8.2E-02 AW875126.1 INT 16006 25336 4.13 8.2E-02 AW875126.1 INT 11384 2.124 8.2E-02 AR02246.2 INT 11384 2.124 8.1E-02 AR05516.1 INT 1255 1.65 8.1E-02 AV055150.1 INT 1266 1.244 1.054 8.0E-02 AV055150.1 INT 12701 27441 10.54 8.0E-02	Exon ORF SEQ ID NO: Expression Signal (Top) Hit PLASTE Value Top Hit Acession No. Top Hit Acession Source Top Hit Acession Source 14888 24656 2.82 8.2E-02 U76008.1 NT 16973 26222 3.14 8.2E-02 AR9375126.1 EST HUMAN 16977 27764 3.13 8.2E-02 AW875126.1 EST HUMAN 17387 27758 5.33 8.2E-02 AW875126.1 EST HUMAN 16976 25336 4.13 8.2E-02 AW875126.1 EST HUMAN 16900 25336 4.13 8.2E-02 AW875126.1 INT 17479 27769 5.33 8.2E-02 AW875126.1 INT 16900 25336 4.13 8.2E-02 AR902246.2 INT 1753 1.65 8.1E-02 AR002246.2 INT 1753 1.65 8.1E-02 AR90556.1 INT 12701 2744 1.054 8.0E-02 AR90556.2 INT 12704	Exon SEQ ID ORF SEQ Signal ID NO: Signal Signal ID NO: Top Hit Acession Signal Signal ID NO: Top Hit Acession Signal PLAST E No. Top Hit Acession Source Native Top Hit Acession Source Source Top Hit Acession Source Source Top Hit Acession Source Source Top Hit Acession Source Source Native Top Hit Acession Source Native Top Hit Acession Source Source Native Top Hit Acession Source Source Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Top Hit Acession Source Native Native Native Top Hit Acession Source Native Native Native Native Native Native Native Nati	Exon SEQ ID CRF SEQ Signal ID NO: Signal Signal ID NO: CTOP) Hit Signal Signal ID NO: Top Hit Acession Value Source Source Source Source Top Hit Acession Value Signal ID NO: Top Hit Acession Signal S	Exon SEQ ID NO: Signal Signal (Top) Hit Top Hit Acession Signal (Top) Hit Top Hit Acession Signal Most Similar Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit Acession Signal Top Hit 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Signal (Top) Hit Top Hit Acession Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: Signal ID NO: ID NO: Signal ID NO: Signal ID NO: ID NO: Signal ID NO:	Exon SEQ ID ID NO: Signal NO: Si	Exon DRF SEQ ID CNF SEQ ID (Top) Hit SEQ ID (Top) Hit SEQ ID (Top) Hit SEQ ID (Top) Hit SEQ ID (Top) Hit Secure Source 14888 Top Hit Acession Source Source Source 14888 Top Hit Acession Source Source Source 14888 Top Hit Acession Detabase Source Source 1532 Top Hit Acession ID NOT ID N	Exon No:- CAPE SEQ ID (Top) Hit Top Hit Acession No:- Moet Simal Plast EQ ID (Top) Hit Top Hit Acession No:- Moet Simal Plast ID No:- Moet Simal Plast ID No:- Top Hit Acession Source Source No:- Top Hit Acession ID No:- Top Hit Acession Source Source Source No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- Top Hit Acession ID No:- No:- Source Source ID No:- Source ID No:- Source ID No:- Ace No:-	Exon NO: ORF SEQ Signal NO: Most Similar Signal No: Most Similar Value Top Hit Acession Value Top Hit Acession Value Top Hit Acession No: Top Hit Acession Signal No: Top Hit Acession Value Top Hit Acession Signal No: Top Hit Acession Value Top Hit Acession Signal No: Top Hit Acession Value Database Source 16193 24656 2.82 8.2E-02 BES97030.1 EST HUMAN 16971 27164 3.13 8.2E-02 AW975128.1 EST HUMAN 17387 27788 5.33 8.2E-02 AW975128.1 EST HUMAN 19006 25336 4.13 8.2E-02 AR977138.1 NT 19480 21247 1.72 8.1E-02 AV965465.2 NT 17553 28894 3.38 8.1E-02 AV965465.1 NT 17553 28894 3.38 8.1E-02 AV965465.1 NT 17561 27441 10.54 8.0E-02 AV966465.1 NT 17201 27441 10.54 8.0E-02 BE067219.1 EST HUMAN 12204 22103 1.01 8.0E-02 BE067219.1 EST HUMAN	Exon NO: ORF SEQ Signal Expression (Top) Hit PASTE (Top) Hit No. Top Hit Acession Value Top Hit Acession Source Top Hit Acession Top Hit Database 14888 24655 2.82 8.2E-02 U76006.1 NT 16133 24656 2.82 8.2E-02 U76006.1 NT 16133 24656 2.14 8.2E-02 AN987128.1 EST HUMAN 16977 27164 3.13 8.2E-02 AN987128.1 EST HUMAN 17397 277896 5.33 8.2E-02 AN98718.1 EST HUMAN 19006 25336 4.13 8.2E-02 AR002246.2 NT 11384 21247 1.72 8.1E-02 AE002246.2 NT 11860 25336 4.13 8.2E-02 AE002246.2 </td <td>Exon NO: ORF SEQ Signal Expression (Top) Hit Value (Top) Hit No: Top Hit Acesston (Top) Hit Value Top Hit Acesston No: Top Hit Detabase Source 14888 24656 2.82 8.2E-02 8.2E-02 8.2E-02 8.2E-02 1438 1.43 8.2E-02 8.2E-02 17409 8.2E-02 1760965.1 NT 17387 NT 17387 NT 17389 NT 17289 NT 1728</td>	Exon NO: ORF SEQ Signal Expression (Top) Hit Value (Top) Hit No: Top Hit Acesston (Top) Hit Value Top Hit Acesston No: Top Hit Detabase Source 14888 24656 2.82 8.2E-02 8.2E-02 8.2E-02 8.2E-02 1438 1.43 8.2E-02 8.2E-02 17409 8.2E-02 1760965.1 NT 17387 NT 17387 NT 17389 NT 17289 NT 1728

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Table 4
Single Exon Probes Expressed in Heart

ייים יייים בייים Dore SEQ Expression (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession BLASTE No. Signal Value Source		25300 2.94 8.0E-02/AJ005375.1 NT	1.47 8.0E-02 4503034 NT	3.04 8.0E-02/AJ278435.1 NT	21913 3.98 7.9E-02 BE250008.1 EST HUMAN	22673 6.43 7.9E-02 AI582029.1 EST HUMAN	23471 3.31 7.9E-02 6681044 NT	23472 3.31 7.9E-02 6681044 NT	24269 1.06 7.9E-02 BF348454.1 EST HUMAN	1.16 7.9E-02 AB008019.1 NT	26756 3.25 7.9E-02 U27832.1 NT	27838 5.68 7.9E-02 A1081644.1 EST HUMAN	27839 5.68 7.9E-02.A[081644.1 FST HI IMAN	20947 1.43 7.8E-02 AI793275.1 EST HUMAN	20948 1.43 7.8E-02.AI783275.1 FST HIMAN	24371 0.81 7.8E-02 BE836331.1 EST HUMAN	2.71 7.8E-02 BE250048.1 EST_HUMAN	24825 1.04 7.8E-02 AI418520.1 EST_HUMAN	27306 2.06 7.8E-02.AF233437.1 NT	27307 2.06 7.8E-02.AF233437.1 NT	27513 1.27 7.8E-02 AA468354.1 EST HUMAN	21139 1 7.7E-02 AF181897.1 NT	2.09 7.7E-02 AJ238093.1 NT	26682 4.4 7.7E-02 AA402949.1 EST HUMAN		
		28310	25300			21913	22673	23471	23472	24269		26756	27838	27839	20947	20948	24371		24825	27306	27307	27513	21139		26682	
	Exon SEQ ID NO:	_	19023	13887	19854	12015	12875	13688	13688	14483	14592	16562	17612	17612	11102	11102	14574	13603	15060	17113	17113	17307	12693	13454	16495	
	Probe SEQ ID NO:	8172	9344	9891	6966	2127	2948	3776	3776	4595	4706	2899	7762	7762	1192	1192	4688	5019	5197	7236	7236	7389	1378	3538	6615	

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Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7660	17510	27736	4.62	7.7E-02	P38080	SWISSPROT	PROBABLE SERINFITHREONINE PROTEIN KINASE VERAGO
8376	18253	28504	5.24	7.7E-02		N FN	Homo sapiens KIAA0628 rene modust (KIAA0828) mRNA
9535	19561		2	7.7E-02	-	TN	Homo saciens interferon regulatory factor 7 (1957)
3341	13261	23067	2.67	7.6E-02	BE51443	EST HUMAN	601316426F1 NIH MGC 8 Home seniors CONA Alone MA CC 262 1000 E1
3362	13281		0.94	7.6E-02	7.6E-02 AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sepiens cDNA 5' end similar to similar to professional and
3512	13428	23229	0.93	7.6E-02	-	Ę	Homo saplens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf17 gene, C11orf17
4765			0.96	7.6E-02	4	EST HIMAN	8422-CT0347-410300-014-205-CT0347-U
2383	17311	27518	1.34	7.6E-02	Γ	LN	Homo sabiene SCI nene irvite
7695	17545		1.34	7.6E-02		ż	Campylobacter jellinj NCTC14188 complete annother actions the
8927	18735	. 29028	2.45	7.6E-02		EST HUMAN	QV3-BN0046-150400-151-904 BN0046 Home seniors cinna
787	10698	20535	1.13	7.5E-02	5902093 NT	Į L	Homo saplens solute cerrier family 6 (neurotrenemittee frameworks, alucia)
787	10698	20536	1.13	7.50.00		<u> </u>	MRNA (SECOND), MRNA
1878	1	24840	2 2	7.05-02		2	Homo sabiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
7407	1	21048	0.87	/.5E-02	2	LN	Homo sapiens chromosome 21 segment HS21C078
7	150	24085	0.84	7.5E-02	7.5E-02 AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, infron 1 and exon 2
6855	16734	26927	1.19	7.5E-02	7.5E-02 AI864367.1	EST HUMAN	W52b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOI ASE (HI IMAN)
6953	16831	27024	121	7.5E-02	3.1	EST HUMAN	AU16913 HEMBA1 Home saniens child class Levie Augusta et
469	10412	20231	123	7.4E-02		EST HUMAN	RC5-LT0054-260/00-011-H09-LT0054-H00-conjunction ADMA
144 4	11349		1.08	7.4E-02	Γ	NT.	Equine herpesvirus 4 strain NS80567, complete genome
2536	- 1		0.93	7.4E-02	6755069 NT	7	Mus musculus paired-like homeodomain transcription factor 1 (Pitv1) mRNA
3545	- [23255	0.89	7.4E-02	1,1	EST_HUMAN	W43h01x1 Sogres NFL T GBC S1 Hamp sapiens cDNA clame IMACE: 726226 21
4806	- [24282	3.38	7.4E-02	7.4E-02 L78810.1	LN	Homo sapiens ADP/ATP carrier protein (ANT-2) dena completa cels
4687	- 1	24370	2.66	7.4E-02	6978442 NT	7	Rattus norvegicus Activin receptor like kinase 1 (Acard.) minus
4858	ı	24518	1.7	7.4E-02	6678492 NT	ラ	Mus musculus ublaulutin c-terminal harirdase related advanced of 124-7
5913	15819		1.75	7.4E-02	7.4E-02 R17477.1	EST HUMAN	7914906.11 Sogres infant brein 1NIB Homo seniens CONA class 144.05.13
6612	16492	26678	1.4	7.4E-02	-	EST HUMAN	601493366F1 NIH MGC 69 Home sanians CDNA clone INACE 306554 F
6950	16828	27021	1.37	7.4E-02		N	Human periodic trotonhan protein 2 (BNIP2) against 145 to 3
9271	18975	-	2.08	7.4E-02	525893	5	Homo sapiena histone deacendase 5 (NV.CO. o) TONA
9527	19674		2.82	7.4E-02	7.4E-02 AW379431.1	T HUMAN	CM4-HT0243-081199-037-d11 HT0243 Home sanions CNA
8298	19235	25242	1.81	7.4E-02	-	Т	601453813F1 NIH MGC 66 Homo Saniens CDNA June MAGE:3857728 F
<u>\$</u>	10405	20222	96.0	7.3E-02	7.3E-02 BE964961.2	П	601658738R1 NIH MGC 69 Homo seniens cDNA clone MACE: 388-200 3
						1	S BOZDOOC TOURIL DIGIT OF THE TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR

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Table 4
Single Exon Probes Expressed in Heart

TIBALLII DOSSOLITO CORRESPONDE	Most Similar Top Hit Acession (Top) Hit Top Hit Acession Signal BLAST E No. Source Source	0.96 7.3E-02 BE964961.2 EST HUMAN 601658738R1 NIH MGC 69 Homo sapiens cDNA clone IMAGE 3888206 31	Γ	7.3E-02 AW900281.1 EST HUMAN	Ŋ	Z	2.44 7.3E-02 P05143 SWISSPROT PROLINE-RICH PROTEIN MP-3	2.44 7.3E-02 P05143 SWISSPROT PROLINE-RICH PROTEIN MP-3	7662107 NT	2.78 7.3E-02 AA779977.1 EST_HUMAN gb:L02428 26S PROTEASE SUBUNIT 4 (HUMAN):	0.94 7.2E-02 AE000882.1 NT genome Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete	0.94 7.2E-02 AE000882.1 NT denome thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete	Z	7.2E-02 AL163301.2 NT	Z	2.1 EST HIMAN	1 EST HUMAN	466563 NT	-N	7.2E-02 U67531.1 NT	7.2E-02 P11120 SWISSPROT	7.2E-02 BF216086.1	7.2E-02 5834897 NT	EST_HUMAN	4.23 7.2E-02 L14561.1 NT partial cds plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products,	2.64 7.2E-02 AW873187.1 EST HUMAN ATYPICAL PKC SPECIFIC BINDING PROTEIN .	
	ORF SEQ ID NO:			5 21237	1]		5 26438	,	25910	19911			21229		23511		24268		_		26272		27608	27697	27818	28016
	Exon SEQ ID NO:				12705				16628	15788	10093			11365	12377	13722	14148			_ {		- 1	_{	17396	17476	17596	17776
	Probe SEQ ID NO:	461	699	1465	1801	4927	6413	6413	6749	8548	114	114	1460	1460	2502	3810	4249	4594	4897	5230	5231	6252	6281	7546	7625	7746	7926

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Γ						
	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
16855	27048	1.37	6.9E-02	6.9E-02 BE567435.1	EST HUMAN	601340661F1 NIH MGC 53 Homo sapiens cDNA clone IMAGE:3683030 5'
16855	27049	1.37	6.9E-02		EST HUMAN	601340661F1 NIH MGC 53 Homo sapiens cDNA clone IMAGE:3883030 5
18939		3.95		6.9E-02 X74315.1	IN IN	X.laevis XFD2 mRNA for fork head protein
19045		1.5	6.9E-02 P44621		SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
19180		2.19		6.9E-02 AF195953.1	N	Homo saplens membrane-bound aminopeptidase P (XNPEP2) gene, complete ods
11736	21610	1.11	6.8E-02	6.8E-02 AA496759.1	EST HUMAN	ae30f02.r1 Gessler Wilms turnor Homo saptens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN):
11736	21611	1.11	6.8E-02	6.8E-02 AA496759.1	EST HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECLIRSOR (HI IMAN)
11761	21635	3.91	6.8E-02	6.8E-02 AF156673.1	N	Homo sapiens putative hepatic transcription factor (WBSCR14) gene complete cuts
12989	22780	1.23	6.8E-02	6.8E-02 AA781996.1	EST HUMAN	ai75a06.s1 Soares testis NHT Homo sapiens cDNA clone 1376676.3
12989	22781	1.23	6.8E-02	6.8E-02 AA781996.1	EST HUMAN	ai75a06.s1 Soares testis NHT Homo saniens CDNA clone 1376676.3
12989	22782	1.23	6.8E-02	6.8E-02 AA781996.1	EST HUMAN	ai75a06.s1 Soares testis NHT Homo sapiens cDNA clone 1376626.3
14347		0.92	6.8E-02	6.8E-02 BE141076.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
16178	26337	7.71	6.8E-02	6.8E-02 AL163268.2	F	Homo sapiens chromosome 21 segment HS21C068
16701	26894	6.12	6.8E-02	6.8E-02 AJ248287.1	E	Pyrococcus abyssi complete genome; segment 5/6
16701	26895	6.12	6.8E-02	6.8E-02 AJ248287.1	F	Pyrococcus abyssi complete genome; segment 5/6
.19719		1.37	6.8E-02		EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo saplens cDNA clone FB4A8 3'end similar to I INE.1
18895		2.98	6.8E-02	6.8E-02 AA758014.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705.31
19284		2.97	6.8E-02	910585	Ā	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
11416		2.17	6.7E-02	.1	TN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
11747	21622	2.5	6.7E-02		EST_HUMAN	4979e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 31
13570	23356	3.52	6.7E-02 P17278	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
11233	21089	1.05	6.6F-02	6.6F-02 A1735509 1	NAMIN TRA	at12e09.X1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW+1N1 NYCCO DARAR (INE 4 DEVEDCE TRANSCOURT ACT IN STATE OF TRANSCOURT
11253	21109	1.5	6.6E-02	2	NT	Drosobila melanorasher caciin mRNA complete cde
12021	21918	3.07	6.6E-02	-	N	Mus musculus Cabn12 gene for calpain 12 exons 1.21 three alternative francishs.
13058		1.32	6.6E-02 Q13585		SWISSPROT	MELATONIN-RELATED RECEPTOR (Hg)
13335	23139	8.61	6.6E-02	6.6E-02 R64306.1	EST HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGF-139579 3'
13349	23154	2.19	6.6E-02	7108357 NT		Homo sepiens mesothelin (MSLN), transcript variant 1, mRNA
13349	23155	2.19	6.6E-02	7108357 NT		Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
13896	23673	1.59	6.6E-02,	25.1	NT	Homo sepiens TESTIN 2 and TESTIN 3 genes, complete cds. alternatively spliced
14784	24558	8.4	6.6E-02 Q61703			INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
14784	24559	8.4	6.6E-02 Q61703		SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Amsacta albistriga nucleopolyhedrovirus AcORF17 homolog gene, complete cds	Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome	P. vulgaris mRNA for chalcone synthase	qh41d01x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds	Homo sapiens EWS, gar22, rrp22 and bam22 genes	MR1-SN0064-010600-006-a12 SN0064 Homo sepiens cDNA	Mus musculus DIPB gene (Dipb), mRNA	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene. 5' flanking region	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'	Homo sepiens E2F-like protein (LOC51270), mRNA	Xenopus laevis alpha(E)-catenin mRNA, complete cds	Aquifex aeolicus section 96 of 109 of the complete genome	246h12.s1 Soares ovary tumor NbHOT Homo sepiens cDNA clone IMAGE:756743 3' similar to gb:M26038 HLA CLASS II HISTOCOMPATIBII ITY ANTIGEN DR.5 RETA CHAIN 44114AANY	z32g05.s1 Soares NHHMPu S1 Homo seniens cDNA clone IMAGE-6654443	Rabbit microsomal epoxide hydrolase	Nectria haematococca kinesin related protein 2 (KRP2) gene. complete cds	A.carterae precursor of peridinin-chlorophylla-protein (PCP) gene	Mus musculus histone deacetylase 5 (Hdac5), mRNA	Mus musculus histone deacetylase 5 (Hdac5), mRNA	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249.3' similar to contains LTR8.b3 LTR8 repetitive element :	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene complete cus	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene complete cds	601680425R2 NIH MGC 83 Homo saplens cDNA clone IMAGE:3950503 3'	Mus musculus chaperonin subunit 6a (zeta) (Oct6a), mRNA	K1419.seq.F Human fetal heart, Lambda ZAP Express Homo saplens cDNA 5'	Homo sapiens mRNA for KIAA0554 protein, partial cds	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
-	Top Hit Database Source	N An	IV	N-	EST_HUMAN qh		N FN	EST_HUMAN MI	NT MI	NT . Ra	EST_HUMAN 60		NT	NT Aq	Zw EST HUMAN HL	Т	Г		NT A.c			qei	Τ	NT	EST HUMAN 60	NT	EST_HUMAN K1	Π	υΗ ΙΗ)
	Top Hit Acession No.	_	5.1		1	_	6.6E-02 Y07848.1	6.6E-02 BF374248.1	937991	6.6E-02 AF167430.1	6.5E-02 BF027639.1	8009	6.5E-02 U47624.1	6.5E-02 AE000764.1	6.5E-02 AA443991.1	5		7		6996923 NT	6996923 NT	6.4E-02 AI191956.1	6.4E-02 AF052733.1	Ĺ	6.4E-02 BE974448.1	753323	6.4E-02 AA093305.1	6.4E-02 AB011126.1	
	Most Similar (Top) Hit BLAST E Value	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.4E-02 X94549.1	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02 U91328.1
	Expression Signal	1.34	0.84	3.09	2.93	1.48	1.37	6.28	2.08	1.46	1.91	1.75	4.17	2.16	1.76	5.61	3.53	3.73	1.63	1.35	8.78	4.1	7.58	7.58	5.23	2.57	4.12	2.02	1.86
	ORF SEQ ID NO:	24800	24817				27894	28457				20743	21131	21474	25383	28173		 -	20307	22708		25094	25727	25728	26210		27099	27668	29049
	Exon SEQ ID NO:						17656		19175	19366	10506		11275	11603	15333	17927	18823	18051			15044	15267	15625	15625	16062	16732	16911	17454	18754
	Probe SEQ ID NO:	5167	5190	2968	6209	6635	7806	8330	9593	9882	567	971	1369	1702	5413	8035	9034	9393	561	4802	5180	5346	5718	5718	6026	6853	7034	7603	8946

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Table 4
Single Exon Probes Expressed

		y y			VG23,			T		1	RNA,						ē	T	1	1	T		T	7		T	Met,	7
Single Exon Probes Expressed in Heart	Tap Hit Descriptor	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HI A-H) nene RoBei nene and codition about the terminal contractions of the contraction of the contractions of the contractio	Homo sepiens minip 58 (MI ICSE) page model and analysis of the complete cds	Drosophija melanogaster mRNA for mod/mdd4151 4 projein	Mus musculus major histocompatibility locus class III regions Hec70t gene, partial cds; smRNP, G7A, NG23, MutS homolog Ci CP NG24 NG25 and NG26	HEAT SHOCK PROTEIN 20 HOMO! On	Henstitis G virus RNA for notwardein (NSSA region), spetial edg. China and	601873316F1 NIH MGC 54 Home saniers CINA class (MAACE-1007200 E)	TRANSCRIPTIONAL REGULATORY PROTEIN ALCO ALCUMATE BEGLI LATORY BEGLIA CONTRACTOR DE COLOR DE C	Arabidopsis thaliana DNA chromosome 4, contin frament No. 68	Rettus norvegious differentation-associated Ne-dependent inorganic phosphate cotransporter (DNPI) mRNA,	Mainpiere das 55 KD BO DENTEIN /S IOCHEN SWINDOWN TO THE COMMISSION OF THE COMMISSIO	AV705704 ADB Homo contact AND Alone APPRAGO F	Mus musculus shows cell defined forther manufactory. 200 July 1	Wetarthzium anisonilae mRNA for Chamothach (Abha 2001), mrinh	Aquifex aeolicus section 82 of 109 of the complete neuma	7137h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homesapiens cDNA clone IMAGE:3523815.3' similar to TR:09Y456 09Y4S6 HYPOTHETICAL 30 3 KD POTTEIN 191.	Human mRNA, Xq terminal portion	Arabidopsis thaliana K+ inward rectifying channel protein (AHKCA) gans committee and	Homo saplens mRNA for KIAA1464 protein, partial cds	H.sapiens mRNA for B-HLH DNA binding protein	L3-HT0618-110500-136-C06 HT0618 Home services ADMA	Sjaponicum mRNA for serine-enzyme	Homo sapiens chromosome 21 segment HS21Chn7	Thermotoga maritima section 89 of 136 of the complete genome	EST380924 MAGE reseguences. MAGJ Homo saniens china	Mesocestoldes cort mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gin, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2	278c04.r1 Stratagene HeLa cell s3 937216 Homo saniens chNA close INA CE 202340.51
gle Exon Prol	Top Hit Database Source	ħ	Ŀ	IN	, ,	SWISSPROT	Ę	EST HUMAN	SWISSPROT	Ę	FV	SWISSER	EST HIMAN	L	NT	LN	EST HUMAN	NT	NT	NI	E	EST HUMAN	u	FN.	N.	EST_HUMAN	Ŋ	HUMAN
Sir	Top Hit Acession No.	6.4E-02 U9132B.1	-		6.3E-02 AF109905.1		6.3E-02 AB010162.1			72.2	,		4.4	7898	6.2E-02 AJ242735.1					1.1		2.5		2	-		6.0E-02 AB031289.1	-
	Most Similar (Top) Hit BLAST E Value	6.4E-02	6.4E-02	6.4E-02	6.3E-02	6.3E-02 P37092	6.3E-02	6.3E-02	6.3E-02 P15276	6.2E-02	6.25-02	6.2E-02 O62191	6.2E-02/	6.2E-02	6.2E-02/	6.2E-02	6.2E-02	6.1E-02 D16471.1	6.1E-02 U73325.1	6.1E-02 AB040897	6.1E-02 X99268.1	6.1E-02 E	6.1E-02 X70969.1	6.1E-02 AL163207	6.0E-02 AE001777	6.0E-02 A	6.0E-02	6.0E-02 AA188730
	Expression Signal	1.86	3.65	2.27	2.43	2.09	3.14	3.29	1.49	3.37	1 11	5.41	122	1.21	1.84	3.53	1.98	4.53	2.65	1.01	3.46	5.44	71.17	3.6	1.41	1.57	1.61	1.22
	ORF SEQ ID NO:	29050		25295	21490		27825	25741	-	23831	 			27525	28827		25265	20038		24785	26877	28248			20997	22399		19892
	Exen SEQ ID NO:	18754	19635	19017	11621	13467	17602	15637	19039	14057	14142	14373	14687	17319	18544	19752	19142	10222	13819	15017	16688	18002	19670	19296	11148	12508	12607	10076
	Probe SEQ ID NO:	8946	9289	9337	1720	3552	7752	8038	9373	4157	4243	4479	4803	7459	8655	9129	9541	256	3909	5150	6809	8112	9088	9783	1241	2641	2745	2906

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Single Exon Probes Expressed in Heart

		_	- 1	-		_		_	_	_	_		_	_		_											_						_
Single Exon Flobes Expressed in Hear	Top Hit Descriptor	2078c04.r1 Stratagene Hella cell s3 937216 Homo conjens cDNA class NII OF Granding Fi	EST84266 Colon adenocarcinoma IV Homo sariens cDNA 5 and circilor to the contract of the contr	EST84266 Colon adenocarcinoma IV Home saniens cDNA K, and similar to the signature of the saniens cDNA K, and similar to	601658150R1 NIH MGC 68 Home seniens cDNA clare IMA CE 3926050 21	Streptococcus oneumoniae part, narE and transmoses general ODE DATA	RC3-BT0253-011199-013-504 BT0253 Home caniens child	Homo saplens stimulated trans-acting factor (50 kDa) (STAE50) mPNA	Homo sapiens stimulated trans-action factor (50 kDa) (27 new)	601815274F2 NIH MGC 56 Hamp saniens cDNA clone IMACE: 4040226 F1	df58b08.x1 Soares testis NHT Homo sanians CDNA close IMACE: 475,4400	Is78a06.x/ NCI CGAP GC6 Homo saniens cDNA close IMAGE 2222222 21	Is78a06.x1 NCI CGAP GC8 Homo saniens cDNA clone IMAGE:2237362.3	Acibenser baeri partial IGLV gene for Imminordohilin licht chair verinkly sonice.	Acidenser baeri parrial (GLV gene for Imminophalin light chair waitatie	Homo sapiens DNA-dependent protein kinase catalytic subunit-interaction protein 2 (kilb2)	wf69h03.xt Soeres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:060298	RC1-DT0001-290100-012-410 DT0061 Home seniors 20NA	Mismiscille p83 thror elegence and a squalist COVA	Saccharomyces cerevisies and in transity and 11, partal ods; alternatively spliced	Mile missiline includes added to the control of the	Mus musculus follistationlike (Fstf) mRNA	Homo sapiens ninein (LOC51199) mRNA	Gallus gallus HKC9 telomere junction	Thiobacillus ferrooxidans mer cenes and I IRF-1	Populus trichocarpa CCoβOMT1 gene expn 1 th expn 5	Thermotoga maritima section 87 of 136 of the complete genome	WXZ4c02x1 NCI CGAP Kid11 Home saniens cDNA clone IMACE 25544578 21	Wx24c02.x1 NCI CGAP Kid11 Homo sepiens cDNA clone IMA CE: 3544578 57	ch56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697.3' similar to gb:M13142 COAGULATION FACTOR X1 PRFCI IRSOR (HI IMAN).	ph56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo septems CDNA clone IMAGE:1848697.3' similar to ab M13142 COACI II ATION EACTOD VI DEFINED ATION EAC	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA complete colo	one condition to a milk that the
פופ באטוו רוט	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT.	EST HUMAN	N	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN LN	LN.	NT	EST HIMAN	EST HUMAN	LN	L N	Ę	k	Z	LN	NT	LN	NT	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	NT	
	Top Hit Acession No.	AA188730.1	AA372376.1	6.0E-02 AA372376.1	BE964443.2	6.0E-02 Z67739.2	6.0E-02 AW370211.1	5174698 NT	5174698 NT	6.0E-02 BF382349.1	AI204275.1	AI623167.1		AJ245365.1	AJ245365.1	11431702 NT	A1809273.1	AW934719.1	5.9E-02 AF190269 1	5.9E-02 AF006304 1	QUESO NIT	TN 058970	11433356 NT	33.1	+	5.8E-02 AJ223621.1		5.8E-02 AW051927.1	5.8E-02 AW051927.1	A1247505.1	5.1	24.1	İ
	Most Similar (Top) Hit BLAST E Value	6.0E-02 AA188	6.0E-02 AA372	6.0E-02	6.0E-02 BE964	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02 AI2042	6.0E-02 AI6231	6.0E-02	6.0E-02 AJ2453	6.0E-02 AJ2453	6.0E-02	6.0E-02 A18092	5.9E-02 AW934	5.9E-02	5.9E-02	5 9F-02	5.9E-02	5.9E-02	5.9E-02 AJ2407	5.8E-02 D90110	5.8E-02	5.8E-02 AE0017	5.8E-02	5.8E-02	6.8E-02 AI24750	5.8E-02 AI24750	5.8E-02	
	Expression Signal	1.22	1.2	1.2	6.0	1.17	3.46	2.86	2.86	1.97	2.05	1.19	1.19	1.79	1.79	1.95	1.84	3.42	2.59	0.88	1.87	2.72	3.15	1.99	4.35	1.1	1.44	4.36	4.36	4.21	4.21	2.04	
	ORF SEQ ID NO:	19893	22921	22922		24551		24848	24849	26284	26562		27407	27486		25294		20011	22681	24443	27077		28509				23314	23931	23932	24132	24133		:
	Exon SEQ ID NO:	10076	13116	13116	13497	14773	15235			16130	16383		17208			19016	19256	10198	12882	14655	16885		18260	18655	10841		╛	14156	14156	14341	14341	14365	
	Probe SEQ ID NO:	2906	3191	3191	3583	4893	5314	6172	6172	6265	6524	7340	7340	7411	7411	9336	9715	229	2955	4770	7008	8165	8383	8845	917	2830	3613	4257	4257	4447	4447	4471	

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Table 4
Single Exon Probes Expressed in Heart

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Oligie Lyon riones Expressed in near	Top Hit Descriptor	Mus musculus tuftelin 1 (Tuft1), mRNA	Homo sapiens ell'4E-transporter (4E-T), mRNA	Homo sapiens elF4E-transporter (4E-T), mRNA	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), dibracid debiatrorenae (dhaK), dib	ninaso (unary, gr)caro denyunogenase (unary, utansonputuna activator (unary, 1,3-propanedio) dehydrogenase (dhaT), glycerol dehydratase (dhaB),>	Oryza sativa rbbi3-1 gene for putative Bowman Birk tryosin inhibitor	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds	Mus musculus p-glycoprotein (mdrla) gene, exons 1 and 2	Neurospora crassa ubiquinol-cytochrome c oxddoreductase subunit VIII (OCR8) mRNA. complete crts	Rana catesbiana heat shock protein 30 (HSP30) mRNA, complete cds	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA	ye37f12.r1 Strategene lung (#8372f0) Homo sepiens cDNA clone IMAGE:119961 6' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN):	Pseudomonas putida ttgS gene	Drosophila melanogaster laminin B2 gene, complete cds	Drosophila melanogaster laminin B2 gene, complete cds	Pseudomonas putida ttgS gene	Arabidopsis thallana eli5 gene, exons 1-11	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds	Helicobacter pylori 26695 section 5 of 134 of the complete genome	Helicobacter pylori 26695 section 5 of 134 of the complete genome	Lymphocystis disease virus 1, complete genome	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]	Podospora anserina mitochondrial epsilon-sen DNA	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Human steroid hormone receptor Ner-I mRNA, complete cds	Drosophila melanogaster filament protein homolog (sep1) gene, complete cds
ופ רעמון גומס	Top Hit Database Source				N FZ	03	<u> </u>		1-	×	NT.	IN	N N	1	EST_HUMAN O		NT P	N	Z			NT TN		H			d LN		H . LN			N _T
3110	Top Hit Acession No.	6755902 NT	10947034 NT	10947034 NT					<u></u>					1	l		6.3E-02 AJZ76408.1			.1	5.1		7.	.1	9695413 NT			5031908 NT	.1	.1		
	Most Similar (Top) Hit BLAST E Value	5.5E-02	5.5E-02	5.5E-02	5.5E-02 U69492.1		5.5E-02 U09771.1	5.4E-02/	5.4E-02	5.4E-02 U53528.1	5.4E-02 M96761.1	5.4E-02 U20790.1	5.4E-02 U44894.1	5.3E-02/	5.3E-02	5.3E-02 T94759.1	5.3E-02	5.3E-02 M58417.1	5.3E-02 M58417.1	5.3E-02 /	5.3E-02	5.3E-02 M80463.1	5.3E-02 AE000527	5.3E-02 AE000527	5.3E-02	5.3E-02 S78221.1	5.3E-02 X03127.1	5.2E-02	5.2E-02 AJ277661	5.2E-02 AJ277661	5.2E-02 U07132.1	5.2E-02 L33246.1
	Expression Signal	1.58	1.3	1.3	1.48		11.56	0.95	6.34	0.92	7	1.79	1.55	1.62	1.62	18.21	3.14	3.91	3.91	4.59	1.22	7.26	1.76	1.76	3.87	1.94	1.78	439.66	2.34	2.34	3.35	1.04
	ORF SEQ ID NO:	26388	27632	27633	27689		28508			24563	24751	28223		20797	20798	21255	22222	22638	22639	22834	24185	24662	24955	24956	26145		27349		22793	22794	23854	24311
	Exen SEQ ID NO:	16228	17417	17417	17470		18259	12914	15078	14787	14976	17974	19552	10955	10955	11394	12324	12839	12839	13038	14399	14894	15180	15180	16009	16216	17153	12123	13003	13003	14081	14521
	Probe SEQ ID NO:	6365	7566	7566	7619		8382	2986	3375	4908	5108	8083	9323	1037	1037	1489	2447	2912	2912	3113	4506	5021	9228	5258	6115	6353	7276	2239	3076	3076	4181	4633

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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	wi80e04.x1 NCI_GGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element ;	Homo sapiens chromosome 21 segment HS21C004	Turnip mosaic virus genomic RNA for Capsid protein, complete cds	Turnip mosaic virus genomic RNA for Capsid protein, complete cds	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	DKFZp547D073_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D073 5'	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA	Spodoptera littoralis mRNA for 3-dehydroecdysone 3beta-reductase	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)	Homo sapiens ES18 mRNA, partial cds	Homo sapiens ES18 mRNA, partial cds	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds	Mus musculus fatty acid amide hydrolase gene, exon 10	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-	Oncologies canically IDP-alternated from Aline 102 PEP IDE P-C]	Mire miscribe Line Station of The Journal of Colors of Mire Mire Mire Station of The Station of Colors of	Antherage permit period clock profein homolog mRNA Ammeter Ac	Homo sapiens ubiquitous tetratricopedide containing protein RoXaN mRNA partial cal	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) INF-1)	Mus musculus Fas-interacting serine/threonine kinase 3 (Fists) mRNA, complete cds	Methanococcus jannaschii seotion 142 of 150 of the complete ganome	NO-ON-TRANSIENT A PROTEIN	Chicken 28-kDa vítamin D-dependent calctum-binding protein (CaBP-28) mRNA, complete cds	Homo sapiens ABCA1 (ABCA1) gene, complete cds	Homo sapiens ABCA1 (ABCA1) gene, complete cds	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)	zq48a12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Atu repetitive element contains element MSR1 repetitive element	zf78a03.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:728428 3'
gie Exon Pioi	Top Hit Database Source	EST_HUMAN	LN	NT	IN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	LN L	SWISSPROT	F	E	Ŋ	NT	LN.	CWICEDDOT	MT	TN	LN L	NT	SWISSPROT	ĮN	N	SWISSPROT	2	N	LN	SWISSPROT	EST_HUMAN	EST_HUMAN
IIIO	Top Hit Acession No.	A1830965.1	5.2E-02 AL163204.2	D10927.1	D10927.1	203030	AL134071.1	5.1E-02 BE957423.2	6.1E-02 BF378625.1	5.1E-02 AJ131966.1	5.1E-02 AF012898.1	P40603	AF083930.1	5.1E-02 AF083930.1	5.1E-02 AF062467.1	5.0E-02 AF098004.1	299104.1	000840	J72742 1	TANSBAN NT		5.0E-02 AF188530.1	25616	5.0E-02 AF305238.1	J67600.1	204047	M14230.1	4.9E-02 AF275948.1	4.9E-02 AF275948.1	54258	4.9E-02 AA188940.1	VA400914.1
	Most Similar (Top) Hit BLAST E Value	5.2E-02 A183096	5.2E-02	5.2E-02 D10927.	5.2E-02 D10927.	5.2E-02 Q03030	5.1E-02 AL13407	5.1E-02	6.1E-02	5.1E-02/	5.1E-02	5.1E-02 P40603	5.1E-02 AF08393	5.1E-02	5.1E-02	5.0E-02	5.0E-02 Z99104.1	5 0E-02 D02840	5.0E-02 U72742	5.05.00	5.0E-02 U12769	5.0E-02/	5.0E-02 P35616	6.0E-02	5.0E-02 U67600.	5.0E-02 Q04047	4.9E-02 M14230.	4.9E-02/	4.9E-02	4.9E-02 P54258	4.9E-02	4.9E-02 AA40091
	Expression Signal	1.73	2.23	2.03	2.03	1.63	1.02	1.12	1.65	1.43	6.22	2.36	2.42	2.42	1.81	1.98	7.11	4.97	1.64	1 17	5.53	0.88	10.61	1.32	2.47	2.81	28.95	2.57	2.57	1.87	0.87	1.19
	ORF SEQ ID NO:			27677	27678					26930		27944		28340			20942	24726	20742		23330	24548	26477	27954	28886			20143	20144	22972		23262
	Exon SEQ ID NO:	15622	16647	17461	17461	19157	12194	14854	15108	16738	17495	17699	18088	18088	19159	10418	11096	11842	10894	13217	13543	14770	16311	17708	18597	19593	10188	10321	10321	13174	13438	13459
	Probe SEQ ID NO:	5714	6768	7610	7610	9561	2313	4979	8609	6829	7645	7849	8204	8204	9569	474	1186	1947	2788	3295	3629	4830	6450	7858	8782	9606	218	365	365	3251	3522	3543

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Single Extended Expressed in real	Top Hit Descriptor	zt78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'	xg56g10.x1 NCL_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'	xg56g10x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:26323386 3'	Rat elastase II gene, exon 6	Rat elastase II gene, exon 6	Homo sapiens prepro placental TGF-beta gene, complete cds	Homo sapiens CS box-containing WD protein (LOC55884), mRNA	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds	Human mRNA, Xq terminal portion	Human mRNA, Xq terminal portion	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds	zo49b02.s1 Soares, senescent fibroblasts, NbHSF Homo septens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA	S.scrofa gene for skeletal muscle ryanodine receptor	Streptococcus constellatus D-alanine: D-alanine ligase gene, partial cds	MR2-ST0129-221099-012-b02 ST0129 Homo seplens cDNA	Rattus norvegicus Nestin (Nes), mRNA	yz97f09.r1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;	Rat statin-related protein (s1) gene, complete CDS	B. taurus mRNA for RF-36-DNA-binding protein	H. saplens DNA for endogenous retroviral like element	Gallus gallus Wpkci-8 gene, complete cds	B. taurus mRNA for RF-36-DNA-binding protein	Mus musculus ligand of numb-protein X (Lmx), mRNA	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)	Homo sapiens partial TUB gene for tubby (mouse) homoloo and LMO1 dene for LIM domain coly 1 profein	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element;
and I low air	Top Hit Database Source	EST_HUMAN	EST_HUMAN		NT.	$\overline{}$	Z Z		IN IN	N		- LN		١	N	IN	EST_HUMAN		_	N	L	NT TN	NT	IN		EST_HUMAN /	SWISSPROT	TN TN	LN LN	T_HUMAN
	Top Hit Acession No.	4.9E-02 AA400914.1	4.9E-02 AW167821.1	4.9E-02 AW167821.1	٠		4.9E-02 AF008303.1	8923880 NT	4.9E-02 M19364.1	4.8E-02 D16471.1		-			254280.1	4.8E-02 U91914.1	4.8E-02 AW388497.1	6981261 NT	_	4.7E-02 M62752.1	K15543.1	K89211.1	4.7E-02 AB026678.1	K15543.1	6754565 NT	4V648521.1	52951	4.7E-02 AJ277662.1		
	Most Similar (Top) Hit BLAST E Value	4.9E-02	4.9E-02	4.9E-02	4.9E-02 L00122.1	4.9E-02 L00122.1	4.9E-02	4.9E-02	4.9E-02	4.8E-02	4.8E-02	4.8E-02	4.8E-02 W51983.	4.8E-02 X17144.1	4.8E-02 Z54280.1	4.8E-02	. 4.8E-02	4.7E-02	4.7E-02 W01153.	4.7E-02	4.7E-02 X15543.1	4.7E-02 X89211.1	4.7E-02/	4.7E-02 X15543.1	4.7E-02	4.7E-02 AV64852	4.7E-02 P52951	4.7E-02	4.6E-02	4.6E-02
	Expression Signal	1.19	1.89	1.89	1.94	1.94	3.78	2.26	3.67	1.45	1.97	7.54	1.92	2.12	1.67	1.28	1.31	0.78	3.41	1.65	9.71	1.18	2.63	7.44	1.76	2.35	2.35	1.39	2.74	1.06
	ORF SEQ ID NO:		24404	24405	25023	25024	. 28805			20104	20104	20239	22014	22903		24722	26801	24586	26170	26117	26868	27245		27397	28270				20484	
	Exon SEQ ID NO:		14618	14618		15220		19107	19276	10287	10287	10424	12112	13097	14464		16611	14818	16030	15981	16679	17056	17066	17197	18024		19743	19365	10654	11177
	Probe SEQ ID NO:	3543	4733	4733	5239	5299	8705	9490	9751	327	328	480	2227	3172	4572	9209	6731	4940	2809	6134	0890	7179	7189	7321	8136	9305	9652	9881	722	1270

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Top Hit Descriptor	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5	xn24f03.x1 NCI_CGAP_Xid11 Homo saplens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1:	PM0-HT0339-251199-003-g05 HT0339 Homo sepiens cDNA	PMo-HT0339-251199-003-g05 HT0339 Homo sepiens cDNA
 | PM0-H10339-080400-009-G12 H10339 Home saniens cDNA | ol27h09.s1 Scares NFL T GBC S1 Homo sapiens cDNA clone IMAGE-1524737.3'

 | Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cols

 | Human germline immunoglobulin lambda light chain gene | RETINOIC ACID RECEPTOR BETA (RAR-BETA)

 | Marburg virus strain MS. Africal Johannesburg/1975/Ozolin VP35 gene, complete cds | Marburg virus strain MIS. Africal Johannesburg/1975/Ozolin VP35 gene. complete cds | HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
 | Xylella fastidiosa, section 110 of 229 of the complete genome | Homo sapiens chromosome 21 segment HS21C078 | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene | Arabidopsis thallana CCAAT-box binding factor HAP3 homolog gene complete ade | EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to nei m-DA matein | Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
 | 2443f11.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE 632403 51 | 601652154F1 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:3935388 5 | Drosophila melanogaster extradenticle (EXD) mRNA, complete cds | HYPOTHETICAL PROTEIN (ORF 2280) | QV2-PT0012-010300-070-902 PT0012 Homo saplens cDNA
 | Myxococcus yanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds | Homo sapiens S164 gene, partial cds, PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| Top Hit
Database
Source | EST_HUMAN | EST HUMAN | EST HUMAN | EST_HUMAN | EST HUMAN | TN | N | N | EST HUMAN
 | EST HUMAN | EST HUMAN

 | IN

 | LN L | SWISSPROT

 | IN | N | SWISSPROT
 | N. | Z. | L _N | LN. | EST HUMAN | Ι.
 | EST_HUMAN | EST HUMAN | V | SWISSPROT | EST_HUMAN
 | TN | TN |
| Top Hit Acesslan
No. | AV727059.1 | AW236023.1 | BE153583.1 | BE153583.1 | BE153583.1 | AF220365.1 | X61624.1 | X61624.1 | AI149574.1
 | | 8.1

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 | 1 | P22448

 | AF005730.1 | AF005730.1 | P32182
 | AE003964.1 | AL163278.2 | | | AA325216.1 | 11418013
 | AA191097.1 | BE972733.1 | L19295.1 | P31568 | AW875475.1
 | AF159160.1 | 4.4E-02 AF109907.1 |
| Most Similar
(Top) Hit
BLAST E
Value | 4.6E-02 | 4.6E-02 | 4.6E-02 | 4.6E-02 | 4.6E-02 | 4.6E-02 | 4.6E-02 | 4.6E-02 | 4.6E-02
 | 4.6E-02 | 4.6E-02

 | 4.6E-02

 | 4.6E-02 | 4.5E-02

 | 4.5E-02 | 4.6E-02 | 4.5E-02
 | 4.5E-02 | 4.5E-02 | 4.5E-02 | 4.5E-02 | 4.5E-02 | 4.5E-02
 | 4.5E-02 | 4.4E-02 | 4.4E-02 | 4.4E-02 | 4.4E-02
 | 4.4E-02 | 4.4E-02 |
| Expression
Signal | 2.74 | 2.51 | 1.51 | 0.98 | 96.0 | 1.22 | 3.64 | 3.64 | 1.31
 | 3.65 | 3.58

 | 1.34

 | 2.68 | 1.84

 | 0.85 | 0.85 | 3.55
 | 2.04 | 3.83 | 1.54 | 23 | 4.43 | 1.74
 | 3.41 | 4.79 | 1.29 | 6.15 | 1.29
 | 1.88 | 1.08 |
| ORF SEQ
ID NO: | 21100 | 22212 | 20052 | | | | 26792 | 25793 | 26200
 | 27097 |

 |

 | | 20207

 | 20955 | 20956 | 21535
 | 21850 | 23364 | 25794 | 26965 | 27793 | 25331
 | 25009 | | 20770 | | 22214
 | 23291 | 24203 |
| Exon
SEQ ID
NO: | 11242 | 12315 | 10235 | 12904 | 12904 | 13936 | 15684 | 15684 | 16053
 | 16906 |

 |

 | 19343 | 10383

 | 11110 | 11110 | 11662
 | 11953 | 13576 | 15685 | 16770 | 17568 | 19000
 | 19637 | 10184 | 10926 | 11940 | 12317
 | 13502 | 14420 |
| Probe
SEQ ID
NO: | 1336 | 2438 | 2777 | 2977 | 3451 | 4033 | 5777 | 5777 | 6070
 | 7029 | 8707

 | 9633

 | 9845 | 439

 | 120 | 1200 | 1763
 | 2063 | 3662 | 5778 | 6891 | 77.18 | 9301
 | 9691 | 213 | 1008 | 2049 | 2440
 | 3588 | 4527 |
| | Exon ORF SEQ Expression NO: Crop) Hit Signal Top Hit Acession No. Top Hit Acession No. Top Hit Acession No. Top Hit Acession No. | Exon ORF SEQ Expression ID NO: Top Hit Signal Top Hit Acession ID NO: Database Source ID NO: Source ID NO: Av727059 HTC Homo sapiens cDNA clone ID | Exon
SEQ ID
NO: ORF SEQ
Signal
NO: Expression
Signal
Signal
Signal
NO: (Top) Hit
Signal
Aulue Top Hit Acession
No. Top Hit Acession
No. Top Hit Acession
No. Top Hit Acession
Source 11242 21100 2.74 4.6E-02 AV727059.1 EST_HUMAN 12315 22212 2.51 4.6E-02 AW236023.1 EST_HUMAN | Exon
SEQ ID
NO: ORF SEQ
Signal
Signal
Signal Expression
(Top) Hit
BLASTE
Value Top Hit Acession
No. Top Hit Acession
No. Top Hit Acession
Source
AVAZZ7059.1 Top Hit Acession
Source
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Signal Expression
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Source 11242 21100 2.74 4.6E-02 AV727059.1 EST_HUMAN 12315 22212 2.51 4.6E-02 AV236023.1 EST_HUMAN 12304 22703 0.98 4.6E-02 BE153583.1 EST_HUMAN 12804 22703 0.96 4.6E-02 BE153583.1 EST_HUMAN 13836 1.22 4.6E-02 BE153583.1 EST_HUMAN 1584 25792 3.64 4.6E-02 AF220365.1 NT 1584 25792 3.64 4.6E-02 AF220365.1 NT 16063 26200 1.31 4.6E-02 AF20365.1 NT 16084 25793 3.64 4.6E-02 AF4024.1 NT 18524 28806 3.65 4.6E-02 AF4024.1 NT 18524 28806 3.66</td> <td>Exon
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Table 4
Single Exon Probes Expressed in

					5		Single Exon Propes Expressed in Heart
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Descriptor
4527	14420	24204	1.08		4.4E-02 AF109907.1	Ę	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,
4637			3.12	4.4E-02	4.4E-02 AJ222689.1	N.	Pour user State Olde stripe COAAT anhancer blade
7084	16961	27164	1.96	4.4E-02	4.4E-02 AA736969.1	EST HUMAN	Inv13h03.s1 NCI CGAP SS1 Home engine Apply
8423			4.11	4.4E-02	4.4E-02 AF060669.1	ļ ½	Hepatitis E virus strain HEV-US2 polyprotein (ORF3), (ORF3), and capsid protein (ORF2) genes, complete
8533		28670	2.39	4.4E-02	Γ	EST HUMAN	ag33f04 r1 Gassler Wilms trimar Dans and
9029			1.88	4.4E-02	Γ	u	Homo saniene mRNA for KIA 4402
9210	19753		1.44	4.4E-02		EST HIMAN	601878746F1 NIH MOO EE U
764		20532	5.74	4.3E-02/			Morone savatile mysel bean chair E1/24 / 71-1418 5
2521		22286	1.23	4.3E-02		EST HUMAN	AV704878 ADB Home seniors of DNA clean of the ADB ADB ADB ATB ATB ATB ATB ATB ATB ATB ATB ATB AT
3383		23101	7.04	4.3E-02		NT	Home sentings chromosome 24 section 1100 cm
3609	J		1.07	4.3E-02/	Ī	L.	Homo sapiane promisionalia in item:
6141		24779	0.92	4.3E-02 X51594.1		LN LN	Pea P4 crans specific securities and a miger protein (PLZF) gene, complete cds
5914		25944	4.93	4.3E-02 P30427		SWISSPROT	
5914	15820	25945	4.93	4.3E-02 P30427		SWISSPROT	PI ECTIN
8242		28372	2.48	4.3E-02 X17012.1		- L	Raf (QE) name for include files and at C. L. U
802	10734	20577	2.05	4.2E-02	7.1	HI IMANI	THE TOTAL TOTAL IN THE STORY I SECTION I SECTI
848	10775	-	1.88	4.2E-02			AU 123327 NITABNA 1
						7	w34401x1 NCI CGAP Pirt Homo seniens cDNA close in the contract of the contract
8/8	_	20654	0.83	4.2E-02	5.1	EST HUMAN	L1 RETROPOSON. ORF2 MRNA "conferes 1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
1690	11592		1.21	4.2E-02 AL445066.		Г	Thermoplasma acidophilum complete ganome, source 1/15
3117	13042	22838	60	4 2F-02 AI403472		Total In Total	9y95f10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to qb;M35718
5172	15038		1.07	4.2E-02 D63484 1	Ī	T	HIMMA MENN GROW IN FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN);
6444	16305	26470	4.45	4.2E-02 AF278752	-		rement in such up gene, partial cds
7114	16991	27183	3.88	4 2F-02 Posner	Ī	Toddool	At Directing of statistics percentage (ketA) gene, complete cds
7845	17895	27941	128	4.2E-02/016650		Т	ALT THANK IN IN IN WON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
8627	18492	28764	2.33	4.2E-02 BF815822	23.4	T	1-DINAIN-I FRO LEIN (1-BUX BRAIN PROTEIN 1) (TBR-1) (TES-56)
8627	18492	28765	2.33	4 2F-02 RE815825		Т	PINE TRICKET CONTROLLED BN01/4 Home capiens cDNA
8795	18609	28900	173	4 2E 02 AE476459		NAME OF THE PERSON OF THE PERS	rivis-più i 14-zausuu-009-d10 BN0174 Homo sapiens cDNA
9563	19681		2,80	4 2E 02 A1002404 4			PRRS Isolate PRRSV36 envelope glycoprotein gene, complete cds
2643	12510	22401	0 07	4 4E 02 AE003484.		ESI HUMAN	W49g10.X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
3824	13736	23526	98 0	4 4E 02 B	,		Chlamydla muridarum, section 60 of 85 of the complete genome
		1,77,77	200.0	4.1E-UZ BEZ9/Z36.		EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'

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Table 4
Single Exon Perhase Expresses

	<u> </u>			Most Similar		gle Exon Pro	Single Exon Probes Expressed in Heart
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acassion No.	Top Hit Database Source	Top Hit Descriptor
3824		23527	0.86		4.1E-02 BE297236.1	EST HUMAN	601177907F1 NIH MGC 17 Homo saniens CDNA clone IMA CE 3633353 E
4372	14268		7.37		4.1E-02 AW893484.1	EST HUMAN	QV1-NN0012-180400-164-f06 NN0012 Home capiene - PNA
6436	16297	26459	1.84		7662347 NT	N	Homo saplens KIAA0867 protein (KIAA0867), mRNA
6565	16423	26604	2.44		4 1F-02 AF02R108 4	F	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 fromolog (SMC1) gene,
9873			12.83		4.1E-02 AJ271909.1	LN LN	Brassia native dus de relevim channel alpha-1 subunity
3206	13130	22932	2.68		4.0E-02 AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5304	15225	25029	4.92		4.0E-02 AF280107.1	TN	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6528	16387	26567	5.69	4.0E-02	4.0E-02 L23838.1	TN	Strongylocentrolus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7059		27126	2.8		4.0E-02 P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
7572		.27638	2.42	4.0E-02	4.0E-02 AJ000941.1	N-	Methanobacterium thermoautotrophicum strain Marburg Thiol-furnarate coductors contacts to
8983	. 1		1.94	4.0E-02	4.0E-02 AJ001018.1	TX	Kluweromyces lactis gene for Ca++ ATPece
9198		25135	4.96	_		N	Ovis aries mRNA for acetyl-cod carbov/lase
1104	. 1	20863	2.77	3.9E-02	49.1	EST HUMAN	UI-H-BW1-anx-h-08-0-UI-sT NCI CGAP Sub Homo senions control state in the control of
1322	_ [21084	3.46			SWISSPROT	FAS ANTIGEN LIGAND
1918	11813	21691	3.04	3.9E-02	3.9E-02 AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2671	i		2.29	3.9E-02		N TN	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5105	- 1	24748	0.98	3.9E-02	8924019 NT	IN	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
5105		24749	0.98	3.9E-02	. 8924019	LN.	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
9284		26654	1.22	3.9E-02	1	HUMAN	601906848F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE:4434770 F
9028	19644	1	5.45	3.9E-02	3.9E-02 AB042553.1		Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
2696	19248		1.57	3.9E-02	3.9E-02 (U68061.1		Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV14S1, TCRBV14S1, TCRBV3S1 TCRBV3S1 TCRBV4S141 TPV4 TPV4 TPV8 TPV8 TPV8 TPV8 TPV8 TPV8 TPV8 TPV8
9811	19568		7.38	3 9E-02	5		Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc
1909		21683	46.0	3.8E-02	1	T HIMAN	Intiger protein 92, mmxq28ort 601510801F1 NIH MGC 21 Home Control International Control
]	7	COLORGO II TAILL MICCO I LOMO Sapiens CONA clone IMAGE:3912215 5

Page 107 of 413 Table 4 Single Exon Probes Expressed in Heart

					OIII	gie Exon Pio	Single Exon Probes Expressed in Heart
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ : ID NO:	· Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6331	16194	26355	1.74	3.8E-02	FN 0075008	Į.	Homo sapiens ATP-binding cassette, sub-family A (ARC1) member 8 (ARCA8) mDNA
7033			1.39	3.8E-02	M60675.1	F	Human von Willebrand factor gene, exons 23 through 34
8045			2.45		3.8E-02 AF143952.2	뉟	Homo sapiens PELOTA (PELOTA) gene, complete cds
976	10899	20746	4.59	3.7E-02 P19137	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1366	11272	21128	0.0	3.7E-02	3.7E-02 L14561.1	Ę	Homo saplens plasma membrane calcium ATPase Isoform 1 (ATP2B1) gene, alternative splice products, partial cas
2190	12077	21982	6.3	3.7E-02	3.7E-02 Al984806.1	EST HUMAN	WR85e08x1 NCI CGAP Kid11 Homo saniens cDNA clone IMAGE:24045022
2533	12407	22299	16.0	3.7E-02	3.7E-02 AB018261.1	N .	Homo sapiens mRNA for KIAA0718 profein narial cale
3012	12940	22733	8.0	3.7E-02 P79944		SWISSPROT	EOMESODERMIN
3013	12941	22734	3.45	3.7E-02	3.7E-02 BF312963.1	EST HUMAN	601898233F1 NIH MGC 19 Homo sapiens cDNA clone (MAGE: 4175584 F)
3408	13325		1.1	3.7E-02	30541	F	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Konma3), mRNA
9095	٠,	29119	3.4	3.7E-02		EST HUMAN	601762117F1 NIH MGC 20 Homo septiens cDNA close IMA GE 4024022 E
9755		25063	1.62	3.7E-02	1418392	Ί.	Homo sapiens solute carrier family 22 (grantic cation transporter) member 1 (St Cook 1) DNA
3604	13518	23306	0.85	3.6E-02	3.6E-02 X73221.1	NT L	H.vulgare Ss1 gene for sucrose synthase
3612	13526	23313	0.8	3.6E-02	3.6E-02 AL096806.1	l k	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5135	15002	24773	0.84	3.6E-02	-		Homo saplens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo saplens
6028	15932	26062	3	3.6E-02,	3.1	EST HUMAN	CM2-EN0013-110500-192-510 FN0013 Home servieus -DNA
6028	15932	26063	2	3.6E-02		EST HUMAN	CM2-EN0013-110500-192-b10 FN0013 Home seniens cDNA
6214	16080	26229	1.82	3.6E-02		N F	Chromatium vinosum sulfur globule protein CV2 precursor (sob2) gene complete ede
6324	16187	26349	2.63	3.6E-02	3.8E-02 AA714521.1	EST_HUMAN	nw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2_TUBULIN BETA-1 CHAIN (HUMAN);
7402	17269	27473	2.08	3.6E-02 U20608.1		NT	Dictyostelium discoldeum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
7402	17269	27474	2.08	3.6E-02 U20608.1		Į.	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
877	10803	20653	1.15	3.5E-02 U09506.1		N	Drosophila melanogaster tiggrin mRNA complete As
392	10913	20758	1.53	3.5E-02	+	Į.	Homo sapiens microsomal epoxide hydrolase (FPHX1) nene complete ode
1544	11449	21309	1.49	3.5E-02 E	_	EST HUMAN	602085136F1 NIH MGC 83 Homo saciens cDNA clone IMAGE-4246377 F
1544	11449	21310	1.49	3.5E-02	1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA done IMAGE-4249377 5
4120	14020	23798	2.01	3.5E-02/	3.5E-02 AE001773.1	FN	Thermotoga maritima section 85 of 136 of the complete genome

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Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | CYSTATHIONINE BETALYASE PRECURSOR (CRI.) (BETA-CYSTATHIONING BETALYASE PRECURSOR (CRI.) | EST370539 MAGE reseduences. MAGE Homo seniens china | HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION | Maize actin 1 gene (MAc1), complete cds | 601644701R2 NIH MGC 56 Hamo sapiens cDNA clone IMAGE:3929737 3' | L.lactis MG1363 grpE and dnalk genes | PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA | PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA | 601178765F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3543833 57 | Homo sapiens mRNA for FLJ00013 protein, partial cds
 | Homo sapiens mRNA for FLJ00013 protein, partial cols | Homo sapiens mRNA for FLJ00013 protein, partial cris | Homo saplens mRNA for FL 100013 protein, partial cds | W.26407.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE::2814253 3' similar to SW:C211 HUMAN P53801 PUTATIVE SURFACE GI VCOPROTEIN CALORE PER PER PER PER PER PER PER PER PER P | Homo sapiens twoothetical profein FI. 113220 (FI. 113220) PRIA | yc20e06.r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains
 | Homo saniens chromosome 21 segment HS21 Chro | RC3-FN0155-060700-011-d10 FN0155 Homo seniens cDNA | RC6-UM0015-210200-021-A10 UM0015 Homo sabiens cDNA | M.musculus S-antigen gene promoter region

 | LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG) | Caenorhabditis elegans mRNA for DYS-1 protein, partial
 | Human lysyl oxidase-like protein gene, exon 3 | wi99d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3' | zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to | TR:G1017425 G1017425 | IPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGRYEITAANSSGTTKAFINIVVLDRPG | PPT GPVVISDITEESVTLKWEPPKYDGGSQVTNYILLKRETSTAVWTEVSATVARTMMKVMKL | 275e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
 | Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds | Homo saplens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| Top Hit
Database
Source | SWISSPROT | EST HUMAN | SWISSPROT | NT | EST_HUMAN | Ę | EST HUMAN | EST_HUMAN | EST_HUMAN | F
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 | SWISSPROT | LΝ
 | NT | EST_HUMAN | | | | EST_HUMAN | EST HUMAN
 | Z | LN L |
| Top Hit Acession
No. | P53780 | AW958469.1 | P47144 | J01238.1 | 3E958970.1 | X76642.1 | AW861641.1 | 4W861641.1 | 3E276948.1 | ∿K024424.1
 | | | | 3W274020.1 | 11345459 |
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Value | 3.5E-02 | 3.5E-02/ | 3.5E-02 | 3.5E-02 | 3.5E-02 | 3.5E-02 | 3.5E-02 | 3.5E-02 | 3.5E-02 | 3.4E-02
 | 3.4E-02 / | 3.4E-02/ | 3.4E-02/ | 3.4E-02 | 3.4E-02 | 3.45-02
 | 3.4E-02 | 3.4E-02 | 3.4E-02 | 3.4E-02

 | 3.4E-02 | 3.4E-02
 | 3.4E-02 | 3.4E-02 A | | | - CO L | 3.4E-UZ A | 3.3E-02 A
 | 3.3E-02 A | 3.3E-02 A |
| Expression
Signal | 1.43 | 0.96 | 0.84 | 1.88 | 2.35 | 1.72 | 1.76 | 1.76 | 3.51 | 1.78
 | 1.78 | 3.31 | 3.31 | 3.77 | 10.22 | 2.06
 | 125 | 1.07 | 3.18 | 2.41

 | 3.43 | 1.28
 | 4.19 | 4.78 | | | 0 | 70.0 | 13.10
 | 13.17 | 1.08 |
| ORF SEQ
ID NO: | 23895 | | | | | | | | |
 | | | | 20795 | | 22120
 | 23102 | 23405 | 23550 | 24174

 | | 24650
 | 24868 | | | | | | 20000
 | 70807 | 21383 |
| Exon
SEQ ID
NO: | | 14429 | | | | | | | - 1 | 10504
 | 10504 | 10504 | 10504 | 10953 | 11098 | 12223
 | 13302 | 13622 | 13756 | 14388

 | 14867 | 14884
 | 15105 | 16687 | | | 17046 | 10224 | 11084
 | 101 | 11525 |
| Probe
SEQ ID
NO: | 4220 | 4536 | 5154 | 5773 | 7012 | 7755 | 8785 | 8785 | 9749 | 564
 | 564 | 565 | 565 | 1035 | 1188 | 2343
 | 3384 | 3709 | 3845 | 4494

 | 4992 | 59
 | 6095 | 8808 | | | 7460 | 200 | 1454
 | 200 | 1021 |
| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession OC Signal BLASTE No. Source | Exon SEQ ID NO: Signal Value No. 23895 1.43 3.5E-02 P53780 SWISSPROT | Exon ORF SEQ Expression Blanch Top Hit Acession No: Top Hit Acession Signal Top Hit Acession Source Database Source Source Source Source Source Ace Ace Ace Ace Ace Ace Ace Ace Ace Ace | Exon
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Page 109 of 413 Table 4 Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	<u> </u>	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value 3.3E-02	Aces:	Top Hit Database Source	Single Exon Probes Expressed in Heart Top Hit Descriptor Source Aquifex aedicus section 32 of 109 of the complete genome
2038		}	2.77	3.3E-02	3.3E-02 R09112.1	EST_HUMAN	y/25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888-5'
4086	- 1		224	3.3E-02	3.3E-02 AF110763.1	NT	Homo saplens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4366	- 1		1.88	3.3E-02	6755862 NT	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
5875	_		18.26	3.3E-02	3.3E-02 BF245995.1	EST HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5
5875	j	25902	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8464		28601	3.39	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
9290			1.78	3.3E-02 T96545.1	T96545.1	EST_HUMAN	7949F11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 1121101 gr
9441			1.59	3.3E-02	3.3E-02 M81890.1	N	Human Interleukin 11 (IL11) gene, complete mRNA
127			1.13	3.2E-02	3.2E-02 AJ002005.1	N.	Oryctolagus cuniculus gene encoding ileal sodium-denendent bile acid transporter
1110			12.7	3.2E-02	3.2E-02 AF096275.1	N	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 alleie, complete and
1110		20868	12.7	3.2E-02 AF09627	5.1	N	Drosophila melanodastar heat shock profession of the procession of the procession of the procession of the profession of the procession of
1734		21503	1.14	3.2E-02 AF12889	7.	N FN	Homo sapiens (elomerase reverse franscrintase (TERT) gane aware 7.18 and annulate das
2072	11962		0.91	3.2E-02 P28955		SWISSPROT	LARGE TEGUMENT PROTEIN
2809		19923	1.15	3.25-02	3.2E-02 AJ002005.1	ΝŢ	Oryctolagus cuniculus gene encoding ileal sodium, dependent bile exid transporter
3095			10.71	3.2E-02		EST HUMAN	601442431F1 NIH MGC 65 Homo sanians cDNA clone IMAGE 2848737 51
3653		23354	1.05	3.2E-02/	3.2E-02 AL163203.2		Homo saplens chromosome 21 segment HS21Cnn3
4124	14024		12.36	3.2E-02 X94768.1		M	H. sapiens RP3 gene (ALRP gene 3)
-	_						
4036	ᆚ	24333	2.88	3.2E-02,	2.1	N	Saxifraga nidifica maturase (matk) gene, chloroplast gene encoding chloroplast protein. partial cyts
2399	_L	25365	1.48	3.2E-02 X68709.1		NT	S.griseocameum whiG-Stv gene
230	_	25366	1.46	3.2E-02 X68709.1			S.griseocameum whiG-Stv gene
6931	15836	26959	2.26	3.2E-02		M	Rat/polyomavirus left junction in cell line W98.14
5932	15837		28.50	2 JE 02 Teocsey 4			yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
598		26013	2 67 6	20-02		NAMOL	Alu repentive element contains LTR1 repetitive element;
6830	18700	2000	4/5	325-02	1,3043.1		Sagunus oedibus tissue Kalilkrein gene, complete cds
3	60/01	70607	3.48	3.21-02	6680565 NT		Mus musculus kinesin family member 3c (Kif3c), mRNA
7786	17636		3.82	3.2F-02	3.2E-02 AA719795.1		2g54b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
9952	19487		138	3 2E-02 AB02468	: -	אלשיטיים וכון	Washer of Locarounic Condesse PolyPer III (HUMAN);
1239	11148		20.5	9 15 02	1500440		Malchanua poymorpha genes for 26S fRNA, 5S fRNA, 18S fRNA, 5.8S fRNA and 26S fRNA
1283	1,0	24042	20.7	9.15-02	4503410	1000	Homo sapiens dual specificity phosphatase 4 (DUSP4).mRNA
1050	14746	2017	1.20	3.1E-02 P18845		VISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
2007	04/1	17017	1.35	3.15-02	6671564		Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1831	11826	1	1.09	3.1E-02/Z50097.1		닏	Drosophila melanogaster mRNA for headcase protein

Page 110 of 413 Table 4

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	AU119006 HFMBA1 Home capiens CONA class LEMBA100000 E	OVAL TRAIA-25020 - 1200 - 20 FOOT TOOM COME TEMBRICAND STATEMENT TO ST	zs84a06 r1 NCI CGAP GCR4 Home emission and all contractions and all contractions are seen as a second and all contractions are seen as a second and all contractions are seen as a second and a second a	Enterococcus faecalis surface protein practirs of annual contractions.	Diff. Lifetime.	i iyonwanes minuws cylochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product	Sachermung condition that Homo sapiens cDNA clone IMAGE:727253 5	Poeudaminity es derevisite stem-toop mutation supressor SSL2 gene, complete cds	OV2-ST0286-150200-040-00-ST0208-U	EST74530 Pineal right II Home contact and 25 cm.	601472331F1 NIH MCC 67 Ucms collination and a series of the series of th	Homo sapiens nel roulin 2 /NRP3) rems complete de la complete de l	Homo saniens nel roniin 2 (NRP2) sans committee dus, auenauvely spliced	Home saplens mRNA for KIAA4572 motein and a special model of spliced	Conduits camin mRNA for Individual to the conduits camin mRNA for Individual to the conduits camin mRNA for Individual to the conduits camin mRNA for Individual to the conduits camin mRNA for Individual to the conduits camin management of the conduits camin manage	601512206F1 NIH MCC 71 Home control of the control	601512206F1 NIH MGC 71 Home saniens cDNA clone IMAGE:3913848 5	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete	Human dystrophin cere	Omithorhochus anafinus accompliance for the Contraction for the Co	Thermotoga marijima sertion 100 of 136 of the	Himan creamination feeter XIII (ES).	ne87f04 s1 NCI CGAP Kird Home contract A (F10) gene, exon 1	W63404 s1 Squas plexesta Nk2UD U.	QV4-NN0038-270400-187-h05 NNnn38 Homo sanlans CDNA	Rattus norvanicus I IDD-Calminocontant but	Homo sapiens mitochondral glutathione reductase and cytosolic glutathione reductase (GRD1) gene,	601338428F1 NIH_MGC_53 Hamo sapiens cDNA clone IMAGE:3680605 F
gle Exon Pro	Top Hit Database Source	EST HUMAN	EST HIMAN	EST HUMAN	TN	F	EST HIMANI	LA LA	LZ	EST HUMAN	EST HUMAN	EST HUMAN	LN	TN	LN	LN	EST HUMAN	EST HUMAN	L	5	L		N-I	LZ	Т	EST HUMAN	Т			T HUMAN
Sin	Top Hit Acesslon No.	3.1E-02 AU119006.1	3.1E-02 AW835313.1	3.1E-02 AA278478.1	3.1E-02 AF034779.1	3 0F-02 AF487125 4		Γ	4.1		3.1			-			×		3.0E-02 AF213884.1	3.0E-02 AF213884.1		1	1		7		3.0E-02 AW895565.1			2.9E-02 BE565644.1
	Most Similar (Top) Hit BLAST E Value	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.0F-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02 M86524.1	3.0E-02	3.0E-02/	3.0E-02 M81357.1	3.0E-02/	3.0E-02	3.0E-02/	3.0E-02 AF048687	2.9E-02	2.9E-02
	Expression Signal	0.82	0.99	2.33	2.62	2.82	1.07	1.07	2.61	0.96	1.18	0.89	6.02	6.02	2.88	2.71	3.58	3.58	1.79	1.79	1.54	2.11	1.71	3.09	7.7	1.66	4.67	2.09	1.	1.07
	ORF SEQ ID NO:		24440		27843		22305	23234	23305			24444	24624	24625	 • 	26196	26109	26110	26101	26102	26311		28069	28701	29039	24909			22157	22687
	Exon SEQ ID NO:	14052	14652	15211	17615	11511	12415		13517	13598	13777	_ !	14858	14858		16050	15974	15974	15967	15967	16158	16983	17828	18432	18745	19730	19273	19723	12720	12889
	Probe SEQ ID NO:	4152	4767	5290	7765	1606	2541	3518	3603	3685	3866	4773	4983	4983	5312	9909	6127	6127	6207	6207	6292	7106	7978	8562	8937	9386	9740	9780	2385	2962

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Table 4
Single Exon Probes Expressed in

Single Exon Probes Expressed in Heart	Similar Top Hit Acession Database Top Hit Source Source	2.9E-02 BE565644.1 EST HUMAN 60/338428F1 NIH MGC 53 Homo senions - DNA - Least MACHE CONTROL OF THE CONTROL	EST HUMAN		N	3.1 EST HUMAN	7.1 EST HUMAN	9.1 EST HUMAN	9.1 EST HUMAN	3.1 EST HUMAN	Τ	LN.	8393751 NT	T HUMAN	N	EST HUMAN	28E-02/X06322.1 NT Yeast CN31C chromosome III RAHS CNA Harm transmitted to the content of the	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCDBV6S2T TCRBV3S1, TCRB	2.7E-02 U66059.1	1.2 NT	EST HUMAN	Weeh12.rl Soares multiple sclerosis 2NbHMSP Home senions CDNA clara MAACE 20048/	EST HUMAN	EST_HUMAN	TN	EST_HUMAN	AA490021.1 EST_HUMAN	6754241 NT	6754241 NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t,	
Single Exon F	ression	4.1 EST	EST	Z		<u> </u>	7.	9.1	9.1	Γ			8393751							2	Γ						.1		6754241 NT		T
	Most Similar (Top) Hit BLAST E Value													L		L				2.7E-02 AL1									2.6E-02		
	Expression Signal	1.07	0.92	1.32	1.32	6.47	10.33	1.94		0.87	1.27	1.27	0.98	11.41	1.33	1.51	1.33		1.26	2	2.07	2.07	1.9	1.52	1.14	1.04	29	2.86	2.86	1,55	140
	ORF SEQ ID NO:	22688	23555	24593	24594	25817	26319	27635	27636		23046	23047		25140	26920				21242	23103	23783	23784	26099	25134	20305		22093	22095	22098		
	Exon SEQ ID NO:	12889	13762	14827	14827				[10494	13241	13241	14112	15293	16728	19574	19237		11378	13303	14007	14007	15965	19500	10499	11251	12196	12198	12198	12812	13704
	Probe SEQ ID NO:	2962	3851	4950	4950	5799	6298	7568	7568	553	3321	3321	4214	5373	6847	9674	9680		1473	3385	4107	4107	6205	9648	228	1345	2315	2317	2317	2885	2882

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Table 4
Single Exon Probes Expressed in

	Top Hit Descriptor	- C	Delinococus radioturans R1 section 153 of 200 of the	xa52b04.x1 NCI_CGAP_Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN_O15544 HYDOTLIETICAL BOTTELLI KANAGAGE	0027711X1 NCI CIAP Kirk Home samine Child Alexandres	601493473T1 NIH MGC 70 Home septems cDNA clears INVACE COSSESSIVE	recents colve fact (Note) mony	A4020) = BNA	ant HS21C103	2884c02.71 NCI CGAP GCR1 Homo saniens child Almo MACE 3044cm m	UI-HF-BN0-aki & 10-0-UI-r1 NIH MGC 50 Homo senions abby All-1-14 Act of a senions abby All-1-	602015501F1 NCI CGAP Bin64 Home series: ADMA CLESSOF (1756)	onzeros y S NCI Crap I He Home series and A size in A ST A FEET ST	on28f06.56 NCI CCAP Life Homo conjunt a DNA a long that CF 15575	601680305R2 NIH MiGC R3 Home septems cDNA close IMAGE CORRECTED	601680305R2 NIH MGC 83 Home septens colive clotte ilwa GE 33950665 3	apiers coine introc. 3830663 3	, complete cas	il oprilyil avc binding protein, Fcp1	John yn a'c binaing protein, Fcp1	28 Homes appears collect	h/36h08.x1 Soares NFL T GBC S1 Homo senions cDNA Appa MACE-2002 2015 21	7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.f1 L1		CONTRIBUTION OF A PRINCE SERVICE CON CIONE IMAGE:3928054 5	GOZDOSEZ I NOL COAP BITTO REPORT SAPIENS CLINA CIONE IMAGE:4213406 5'	HYPOTHETICAL 48 7 KN PROTEIN CAGGA AS IN CURA CIONE IMAGE: 4213406 5	CISCIONALIN CHROMOSOME I	17.10	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II hata chain (IEAalpha) and major histocompatibility protein class II hata chain (IEAapha)	's coulding the second of the	
Single Exon Probes Expressed in Heart	dit Se	Chicken dorsalin-1 mBNA complete ada	Deinococcus radiodurans R1 section		Т	Т	Т	Homo sepiens KIAA 1070 protein (KIAA 1070) meMA	Homo sapiens chromosome 21 segment HS21C103	Г	T	1	7	т	Т	Т	Т	H carterae mRNA for furnishing chlocativity of the	H Carterae mRNA for finovonthin chicata.	Т	Т	Т		Т	Т	Т	Т	_	_	Mus musculus major histocompatibil chain (IAalpha) and major histocomp	butyrophilin-like (NG9), butyrophilin-li>	Home concern and a second
igle Exon	Top Hit Database Source	Į	Z	EST HIMAN	EST HUMAN	EST HUMAN	E	N _T	N.	EST HUMAN	EST HUMAN	EST HUM	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Ľ	Į.	Z	EST HUMAN	EST HUMAN	EST HUMAN	arail Log	EST LINAN	EST HIMAN	EST HIMAN	SWISSPRO	SWISSPROT	LN L		닐	12
<u>เรีย</u>	Top Hit Acession No.	2.6E-02 L12032.1	2.6E-02 AE002014.1	2.6E-02 AW241154.1		2.6E-02 BE621748.1	6981271 NT	11432020 NT	2.6E-02 AL163303.2	2.6E-02 AA279351.1	2.6E-02 AW500547.1				2.5E-02 BE974314.1	2.5E-02 BE974314.1	2.5E-02 U12571.1	2.5E-02 X99897.1	2.5E-02 X99697.1	2.5E-02 BE701165.1	2.5E-02 BE701165.1	2.5E-02 AW592114.1	2 SE_02 BE670139 4	2.5F-02 RF746888 1	2.5E-02 BF526722 1	2.5E-02 BF526722 1			2.5E-02 AJ237936.1		2.5E-02 AF050157.1	
	Most Similar (Top) Hit BLAST E Value	2.6E-02	2.6E-02	2.6Ë-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.6E-02	2.5E-02	2.5E-02	2 FF-03	2.6F-02	2.5E-02	2.5E-02	2.5E-02 Q10335	2.5E-02	2.5E-02		2.5€-02	2.5F-021
	Expression Signal	3.69	1.67	2.06	6.95	2.08	6.09	1.19	4.87	21	1.89	1.55	1.45	1.45	12.83	4.77	2.59	4,4	4.4	1.09	1.09	5.07	4 48	3.86	1.57	1.57	245	2.45	3.38		3.33	1.74
	ORF SEQ ID NO:		24637	24667		25895	26113	27512	28038		28949	24906	20274	20275	20562	20628		22052	22653	23643	23644	23788			26555	26556	28320	28321	28370		1	_
	Exon SEQ ID NO:	14695	14873	14898	15678	15776	15977	17306	17798	18579	18660	19715	10463	10463	10721	10778	12597	12853	12853	15070	15070	14011	15667	15674	16378	16378	18071	18071	18118	1	18735	3/83
	Probe SEQ ID NO:	4811	4998	5025	5771	5870	6130	7388	7948	8692	8848	9320	521	251	792	821	2736	2926	2926	3929	3929	4111	5759	5767	6219	6219	8185	8185	8238	i c	07.00	0260

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		T		T		T		T	T	T	T			T	fitive	VG23,	√G23,		1			ete	T	T	Ī	T	T	\prod
Single Lybressed III near	Top Hit Descriptor	Homo saplens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'	to72c07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:20701563	w75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K/B))	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K/B))	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECLIRSOR (H-2K/B))	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECLIRSOR (H. 2K/B))	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gblK02909IRATSR7K Rat (rRNA):contains A3R b1 A3R repetitive element	AV692954 GKC Homo sapiens cDNA clone GKCDSC03 6	nh07b12.s1 NC]_CGAP_Thy1 Homo saplens cDNA clone IMAGE:943583 similar to contains Alu repetitive element;contains element PTR5 repetitive element :	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 denes, complete cfs; and unknown neares	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23	ividio fibridady, ollor, Nez4, Nez2, and Nez6 genes, complete cds; and unknown genes.	Mis misculis DinB hambar 4 (E. All) (Disk4) DNA	MRO-FT0175-310800-202-806 FT0175 Homo saniens cDNA	Homo sapiens SNCA isoform (SNCA) gene, complete cds. alternatively sniliced	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds	yy08a06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA cinne IMAGE:270840 5:	602153281F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE-4294173 F1	SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN)	za84g08.r1 Soares fetal lung NbHL19W Homo sepiens cDNA clone IMAGE-290294 5:	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exch 4	S.cerevisiae chromosome IV reading frame ORF YDL245c
DIA L'AOII PIO	Top Hit Database Source	IN	LN	EST_HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	LN	SWISSPROT	SWISSPROT	LN TN	EST HUMAN	EST HUMAN	EST HUMAN	Ę		- EN	L	EST HUMAN	Z.	IN	EST HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	NT	LN.
	Top Hit Acession No.	11420078 NT	11433220 NT	3E973327.1	1378582.1	165884.1	201901	201901	105110.1	201901	01901	NL161595.2	169442.1	2.4E-02 AV692954.1	2.4E-02 AA493894.1	2.4E-02(AF109905.1		AF TUSSUD, I	6753635 NT	2.4E-02 BE928869.1	F163864.1	2.4E-02 AB008569.1		F679477.1	,	V05340.1		
	_	2.5E-02	2.5E-02	2.5E-02 BE97332	2.4E-02/	2.4E-02 H65884.1	2.4E-02 P01901	2.4E-02 P01901	2.4E-02 J05110.1	2.4E-02 P01901	2.4E-02 P01901	2.4E-02 AL 16159	2.4E-02 N	2.4E-02	2.4E-02 A	2.4E-02.A	. L	2.4E-02.0	2.4F-02	2.4E-02 B	2.4E-02 AF16386	2.4E-02 A	2.4E-02 N42980.1	2.4E-02 BF67947	2.4E-02 P54643	2.3E-02 W05340.	2:3E-02 U94165.1	2.3E-02 Z74293.1
	Expression Signal	2.19	1.63	239	1.01	1.89	2.22	2.22	1.4	1.43	1.43	11.51	10.36	217	2.98	1.96	2	58.7	272	2.03	1.27	3.87	1.6	1.38	1.59	5.79	7.89	2.52
	ORF SEQ ID NO:			25271	19956		21784	21785	23948	24099	24100		27032	27714	27808	28956	2006	10003	25357	25326								22081
	Exan SEQ ID NO:	19657	19528	19167	10139	11484	12710	12710	14171	14314	14314	14987	16840	17493	17584	18669	19660	18856	18947	18984	19036	19120	19138	19141	19667	11726	11740	12183
	Probe SEQ ID NO:	9280	9463	9581	167	1580	1998	1998	4272	4420	4420	5119	6962	7643	7734	8857	7360	9080	9224	9282	9368	9202	9532	9538	2266	1829	1844	2302

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Table 4
Single Exon Probes Expressed in F

Single Exon Probes Expressed in Heart	Similar Top Hit Acession Database Surce Source		.3E-02 220377.1 (EST_HUMAN HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA	TN	N	2.3E-02 AW899107.1 EST_HUMAN CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA	EST_HUMAN	2.3E-02 BE935225.1 EST HUMAN CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	2.3E-02 BF026487.1 EST_HUMAN 601672279F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:395386 5'	EST HUMAN	EST_HUMAN	INT	5.2 NT	LN.	2.3E-02 AE000199.1 NT Escherichia coli K-12 MG1635 section 89 of 400 of the complete genome	2.3E-02 AE000199.1 NT Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCAN 1,4-ALPHA-D-GLUCAN GLUCAN 1,4-ALPHA-D-GLUCAN		ŢN		2.2E-02/AF018267.1 NT Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein,	4557448 NT	ŢN	3.1 NT	EST_HUMAN	TN	2.2E-02 AW601317.1 EST_HUMAN PM0-BT0340-170100-004-b03 BT0340 Homo saptens cDNA	
Single	Acession Vo.		.1			07.1			Γ								5.2						-		1426388		4557448 NT					17.1
	Most Similar (Tap) Hit To BLAST E		2.3E-02 Z20	2.3E-02 L24	2.3E-02 L24	2.3E-02 AW	2.3E-02 BEG	2.3E-02 BE	2.3E-02 AW	2.3E-02 AW	2.3E-02 BE	2.3E-02 BFC	2.3E-02 BFC	2.3E-02 A17	2.3E-02 AI7	2.3E-02 U86	2.3E-02 AL1	2.3E-02 U63	2.3E-02 AEC	2.3E-02 AE0	2.3E-02 P08	2.3E-02 BE2	23E-02 U39	23E-02 U11	23E-02	2E-02 AF0	2.2E-02	2E-02 Z82	2E-02 AF1	2E-02 AA5	2E-02 AF0	2E-02 AW
	Expression (To Signal BL/	1	4.79	1.19	1.19	1.26	0.81	0.81		0.94		2.39	2.39	,F	1	3.57	4	5.67	1.51	1.51	2.15	4.41	.1.94	2.27		3.09	1.53	1.78	1.4			1.05
	ORF SEQ ID NO:		23329	23735	23736	24002	24027	24028	24029	24030	24155	24171	24172	24591	24292	25027	26018	26665	27841	27842	28302		25219			20482		21752	22448			23477
	Exon SEQ ID NO:		13542	13959	13959	14220	14244	14244	15072	15072	14366	14384	14384	14825	14825	16223	15895	16478	17614	17614	18050	19512	19254	19756	19609	10652	11614	11861	12730	13306	13509	13691
	Probe SEQ ID NO:		3628	4057	4057	4323	4347	4347	4348	4348	4472	4480	4490	4948	4948	5302	2330	6598	7764	7764	8162	9201	9713	9767	9961	720	1713	1968	2695	3388	3595	3779

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	S.cerevisiae chromosome IV reading frame ORF YDL245c	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	ne47h07,srf NCI CGAP Co3 Homo saniens cDNA clone MAAGE onnE44.3' cimiliar to contains All.	element,	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'	Dictyostelium discoideum histidine kinase C (dhkC) mRNA, complete cds	Becillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds	Mus musculus macrophage migration inhibitory factor (MIF) gene. 5' flanking region and partial cde	Mus musculus macrophage migration inhibitory factor (MIF) nane 5' flanking region and nartial cde	Tegula aureotinota major acrosomal protein precursor (TMAP) mRNA, complete cds	yx43h07.r1 Soares melanocyte 2NbHM Homo sablens cDNA clone IMAGE 284541.5	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA	PM2-BT0546-120100-001-f11 BT0548 Homo sapiens cDNA	2x63b09.r1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 51	S.cerevisiae chromosome IV reading frame ORF YDI.245c	Borrella burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509.31	A.thaliana mitochondrial genome, part A	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384628 3'	Homo saplens partial 5-HT4 receptor gene, exons 2 to 5	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene commises ods	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3 MER1 repetitive element:	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
	Top Hit Database Source	NT S	EST_HUMAN A	NT	NT	H LN	Ŧ		_	EST_HUMAN A	_	MT NT				EST_HUMAN JX	EST HUMAN PI	EST_HUMAN PI	T_HUMAN			EST_HUMAN WE		EST HUMAN W	•	Ĭ	NT TN	NT	EST HUMAN MI	П
	Top Hit Acesslon No.	Z74293.1	2.2E-02 AV699721.1	2.2E-02 AL161515.2	2.2E-02 AL161515.2	2.2E-02 AB026898.1	2.2E-02 AB026898.1		2.2E-02 AA503553.1		2.1E-02 AF029726.1	2.1E-02 U72073,1	2.1E-02 AF204395.1	2.1E-02 AF204395.1	2.1E-02 AF190899.1	2.1E-02 N29266.1	2.1E-02 BE072546.1	2.1E-02 BE072546.1	2.1E-02 AA461271.1	2.1E-02 Z74293.1	2.1E-02 U44914.1	2.1E-02 AI768127.1	2.1E-02 Y08501.1	2.1E-02 AI823432.1	2.1E-02 AJ243213.1	AJ243213.1	2.1E-02 Y19213.1	2.1E-02 AF183913.1	2.0E-02 BF002932.1	2.0E-02 AW895565.1
10 40 14	(Top) Hit BLAST E Value	2.2E-02	2.2€-02	2.2€-02	2.2E-02	2.2E-02	2.2E-02		2.2E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.0E-02	2.0E-02
	Expression Signal	0.99	3.78	2.26	2.26	2.33	233		2.24	5.56	7.99	7.43	1.91	1.91	0.95	3.98	0.85	0.85	1.23	0.89	1.61	1.03	4.65	0.86	1.8	1.8	4.99	3.33	1.35	7.86
	ORF SEQ ID NO:			26952		27651	27652					20998	21125	21126	21694	20530	21776	. 21777	23247	23719	24022	24033	24288	24386	27618	27619		25184	19795	19796
	Exon SEQ ID NO:	13755			16755	17436	17436		19096	10359	10385	11149	11270	11270	11815	10693	11883	11883	13451	13941	14239	14247	14499	14600	17404	17404	15095	19348	10004	10005
	Probe SEQ ID NO:	3844	6297	6876	6876	7585	7585		9466	413	44	1242	1365	1365	1920	2785	3110	3110	3535	4038	4342	4351	4611	4714	7553	7553	9449	9857	17	18

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Single Exoll Plobes Expressed in hear	Top Hit Descriptor	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3 MER1 repetitive element:	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	(Sema6b), mRNA	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end	Homo sapiens chromosome 21 segment HS21C078	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'	Japanese encephalitis virus envelope protein mRNA, partial cds	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE.2298315 3'	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds	Homo saplens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA	Homo saptens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	601478819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA done IMAGE:24675 5'	nf19a07.s1 NCL_CGAP_Pr1 Homo saplens cDNA clone IMAGE:914196 similar to contains L1.f1 L1	repetitive element;	EMPTY SPIRACLES HOMEOTIC PROTEIN	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C103	Arabidopsis thallana DNA chromosome 4, contig fregment No. 50
le Exoli Piopes	Top Hit Database Source		EST_HUMAN as		Ho NT sa						T HUMAN			NT	'AL IN	NT TN	EST_HUMAN as	NT	EST_HUMAN wa	INT	NT			T_HUMAN	NT An	EST_HUMAN 60	EST_HUMAN yd	Г		ISSPROT			NT
Buile	Top Hit Acessian No.	6753635 NT	2.0E-02 AA456538.1	6753635 NT	2.0E-02 AL096805.1	TN 1622391	R922391 NT	8922453 NT	2.0E-02 8922453 NT	AL 161532.2	2.0E-02 BF002932.1		7305474 NT	2.0E-02 AF095588.1	2.0E-02 M18095.1	2.0E-02 AL163278.2	3.1	2.0E-02 U70408.1			D88184.1		10947055 NT	2.0E-02 AA456538.1	2		2.0E-02 T80037.1		1.9E-02 AA572764.1		.2	1.9E-02 AL163303.2	2
	Most Similar (Top) Hit BLAST E Value	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02		2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02 Z73966.1	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02		1.9E-02	1.9E-02 P18488	1.9E-02	1.9E-02	1.9E-02
	Expression Signal	2.63	2.62	1.75	0.97	1.61	1.61	2.31	2.31	1.75	1.96		1.16	3.33	1.5	0.99	0.99	1.8	1.59	2.01	2.55	3.09	3.09	1.41	1.56	1.72	4.08		1.68	0.84	2.52	2.52	0.87
}	ORF SEQ ID NO:	20040	20077	20550	20830	20938	20939	21600	21601		19795				23614	24725	24730	-	28019	28175	28849	29031	28032	24730					20432	21364	21779	21780	22230
	Exon SEQ ID NO:	10225	10256	10711	10987	11092	11092	11727	11727	12630	10004		13031	13114	13834	14949	14955	17529	17780	17929	18566	18739	18739	14955	12630	19536	19404		10611	11504	11887	11887	12335
	Probe SEQ ID NO:	259	292	781	1071	1181	1181	1830	1830	2768	3040		3105	3189	3925	5079	2082	7679	7930	8037	8678	8931	8931	9019	9481	8828	9935		678	1599	1993	1993	2458

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2875	i I	22596	7.08	1.9E-02	1.9E-02 AA713856.1	EST_HUMAN	rw04f05.s1 NCI_CGAP_SS1 Hamo sapiens cDNA done IMAGE:12383373'
2923	12850		1.53	1.9E-02	1.9E-02 AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3222	13146		0.82		AB033611.1	IN	Urotrichus talpoides mitochondrial gene for cytochrome b, complete cds
3560	13474		1.25		1.9E-02 N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sepiens cDNA clone IMAGE:284331.3'
3644	13558		5.75		1.9E-02 BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:3839564 5'
3654	13568	23355	0.98	1.9E-02	1.9E-02 Al301183.1	EST HUMAN	qn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element,
3961	13868	23646		1.9E-02	1.9E-02 AF141940.1	TN	Mycoplasma imitans VIhA1 precursor (vIhA1) and VIhA2 precursor (vIhA2) genes, partial cds
4099	13999	23777	1.47	1.9E-02 P09081	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4099	13999		1.47	1.9E-02 P09081	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4441	14335	24125	2.51	1.9E-02	1.9E-02 Al452999.1	EST HUMAN	146d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element:
4944	12335		1.9	1.9E-02	1.9E-02 AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5356	15276		1.29	1.9E-02	1.9E-02 L47572.1	IN	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
6985	16862		1.29	1.9E-02	1.9E-02 AL162754.2	TN	Neisserla meningitidis serograup A strain Z2491 complete genome; segment 3/7
7377	17246			1.9E-02	1.9E-02 BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5
11111			1.31	1.9E-02	1.9E-02 BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
9234	19516	25137	2.55	1.9E-02	1.9E-02 AF101065.1	NT	Hirudo medicinalis intermediate filament gilarin mRNA, complete cds
343	10302	20117	1.44	1.8E-02	1.8E-02 AW771104.1	EST HUMAN	hn52c06.x1 NG_CGAP_Co17 Homo saplens cDNA done IMAGE:3027274 3' similar to contains element MER29 repetitive element;
670	10604	20421	1.14	1.8E-02	1.8E-02 BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4139983 5'
1144			1.34	1.8E-02	1.8E-02 X17664.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1417			1.23	1.8E-02	1.8E-02 AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
2645	_	22403		1.8E-02	1.8E-02 AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3174				1.8E-02	1.8E-02 AIB05829.1	EST_HUMAN	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 31
3812	_ {	23513	1.09	1.8E-02	1.8E-02 AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3812	1		1.09	1.8E-02	1.8E-02 AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3896	- 1		1.15	1.8E-02	1.8E-02 AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:1406935 3'
4332	- 1			1.8E-02	1.8E-02 AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
4873	l		1.05	1.8E-02 O60810	060810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
4887	_		1.06	1.8E-02	1.8E-02 A 288701.1	EST_HUMAN	qm06b04.x1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1881007 3'
6075	16058	26207	3.96	1.8E-02 P14310	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW S'REGION
7560	17411		2.49	1.8E-02	1.8E-02 AA897543.1	EST HUMAN	aj62709.s1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN):

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Table 4
Single Exon Probes Expressed in Heart

					<u>, </u>		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
501	10443		1.58	1.6E-02	1.6E-02 AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1635	11539	21399	1.13	1.6E-02 Y18889.	Y18889.1	TN	Treponema maltophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2202	L	21990	1.13	1.6E-02 Q64176	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2202	12089	21991	1.13		Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2518	12392	22284	86.0				Homo sapiens KVLQT1 gene
2606	L	22368	1.47	1.6E-02		EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2662	12529		1.14		1.6E-02 AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3481	13397	23202	3.83		1.6E-02 AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxdoreductase, NG29,
4084	13086		2.46		1 6F_02 AF110520 1	F	KIFCT, Fas-binding protein, BINGT, tapasin, KalGUS-like, KEZ, BING4, beta 1,3-galactosyi transferase, and RPS18 cenes, complete cds: Sacm21 cene, partial>
4203	1	23885			1.6E-02 AW875407.1	EST HUMAN	QV2-PT0012-140100-030-f07 PT0012 Homo sepiens cDNA
5456	1_	1		1 6E-02	F671715 NT	.1	Mus musculus CD5 antigen (Cd5), mRNA
6003				1.6E-02	AB01528	NT	Candida albicans CaGCR3 gene, complete cds
6758	1			1.6E-02		IN	Human apoC-II gene for preproapolipoprotein C-II
212			271	1.6E-02	1.6E-02 AF079764.1	LN.	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
							nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
7954	17804	28044	1.47		1.6E-02 AA572818.1	EST_HUMAN	P29294 TELOKIN. [1];
							nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
7954	17804		1.47		1.8E-02 AA572818.1	EST_HUMAN	P29294 TELOKIN [1];
8280	19473	28401	2.17	1.6E-02	1.6E-02 Z94828.1	Ν	G gallus microsatellite DNA (LE10280 (=116iiE11))
8544	18416	28683	2.52		-	INT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8544	<u> </u>		2.52		1.6E-02 AL161508.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8801	18615	28905			1.6E-02/AI373558.1	EST_HUMAN	qz36e10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442.3'
9211	12089	21990	1.35		1.6E-02 Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9211	L		1.35		1.6E-02 Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9577	19165		2.3		1.6E-02 X92751.1	N.	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)
9973	19433		1.42	1.6E-02	-	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
734	10666		24.9	1.5E-02	8923734 NT	NT	Homo sapiens transcription factor (HSA130894), mRNA
2095	L	21879	3.81	ŀ	N39521.1	EST_HUMAN	yv27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2128	12016	21914	2.38		1.5E-02 AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3023	12951	22743	1.44		1.5E-02 AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3023	12951		1.44		1.5E-02 AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
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		T	T	T	T	T	7	Ţ	Ţ	Ţ	T	T	T	T	Ţ	T	٦	7	Т	Ţ	T	T	1	_	1	Т	Ţ	Т	T	T	Т	\top	Т
Single Exon Probes Expressed in Heart	Top Hit Descriptor	MR4-TN0115-080900-201-b12 TN0115 Home saniens cDNA	zq40g10.r1 Stratagene hNT neuron (#937233) Homo saniens cDNA Acres NAAGE: 622226 E1	Homo sapiens TESTIN 2 and TESTIN 3 nemes commissed alternatively exists.	HYPOTHETICAL CALCIUM-BINDING PROTEIN CARA 4 A A IN CHOOL COME	Ovanophora paradoxa cyanelle, complete genome	Homo sapiens KIAA1009 protein (KIAA1009) mRNA	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens valvi-RNA synthetises 27/VARS2 minute	602019135F1 NCI CGAP Bring? Homo saniens china clara IMACE: 4154564 51	Saccharomyces cerevisiae chromosome VI plasmid Gardon Carrolla Car	yh54b10.rf Soares placenta Nb2HP Homo sapiens cDNA clone MAACE パッススススス だ	yh54b10,r1 Soares placenta Nb2HP Homo saniens cDNA clone IMAGE-193531 5	Plasmodium falciparum (strain FCR3) variant enerdic eurfore anadain (var. 2 var. 2)	RC4-CN0049-140100-011-c11 CN0049 Home series anna A	AU134730 PLACE1 Homo saplens cDNA clone PI ACE1non374 ボ	Chlamydophila pneumoniae AR39 section 58 of 64 of the complete anneae	Homo sapiens NESH protein (LOC51225) mRNA	Haemobilius influenzae Rd section 115 of 163 of the complete concess	Xenopus laevis neurodenin related 1h (X-NGNR-4h) mDNA	Homo sapiens headpin gene, complete cds	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and albha-calactosidase (anli)	genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xylR) gene, partial cds	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE: 5575783 3'	Arabidopsis thaliana DNA chromosome 4, contin fragment No. 82	Arabidopsis thaliana DNA chromosome 4 confin framment No. 82	Homo sapiens coagulation factor XII (Hageman factor) (F12) mRNA	Mus musculus histocompatibility 2, complement component factor R (H2 BF) mBNA	EST374761 MAGE resequences, MAGG Homo saniens cDNA	EST374761 MAGE resequences, MAGG Homo seniens conta	601567403F1 NIH MGC 21 Homo sabiens cDNA clone IMAGE:3842280 F	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842780 5
JIE EXON Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	LN	SWISSPROT	N.	N F	N	Į.	EST HUMAN	L	EST HUMAN	EST HUMAN	LN.	EST HUMAN	EST HUMAN	L	 	N	5	M	EST_HUMAN		•	EST_HUMAN	NT	N-	ト	ヒラ	EST_HUMAN	Γ	Г	Г
SIIIC	Top Hit Acession No.	2.1	1.5E-02 AA160967.1			11467282	11418713 NT	1.5E-02 AL163303.2	739	1.5E-02 BF345554.1					34.1			5980			1.4			9.2	12.1	5.2	5.2	4503628 NT	6996918 NT				2.1
	Most Similar (Top) Hit BLAST E Value	1.5E-02 BF09294	1.5E-02	1.5E-02 AF26022	1.5E-02 Q09711	1.5E-02	1.5E-02	1.5E-02	1.5E-02	1.5E-02	1.5E-02 D44606.	1.5E-02 R32667.	1.5E-02 R32667.	1.5E-02 L40609.1	1.5E-02/	1.5E-02	1.4E-02/	1.4E-02	1.4E-02 U32800.	1.4E-02 U67779.1	1.4E-02/	1.4E-02		1.4E-02/	1.4E-02 AW0742	1.4E-02 AL16158	1.4E-02 AL16158	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02 BE73314	1.4E-02 BE73314;
	Expression Signal	0.9	1.23	0.91	1.91	1.66	1.36	1.53	3.44	1.23	2.07	1,25	1.25	2.5	1.32	1.47	1.45	3.58	1.35	2.82	0.94	0.96		1.9	0.99	5.21	5.21	0.98	6.16	7.29	7.29	6.7	6.7
	ORF SEQ ID NO:	23365	23727	24048	25819		26399	26664	26668	27195	27545	27717	27718	28647				20860						22905	23074	23161	23162	23197	23308	24062	24063	24445	24446
	Exen SEQ (D NO:	13577	13951	14263	15707	16195	16239	16476	16480	17003	17339		17498	18380	19559		10357	_	11143	11184	11280	11405		13101	13272	13356	13356	13392	13520	14283	14283	14659	14659
	Probe SEQ ID NO:	3663	4049	4367	5801	6332	6377	9629	0099	7126	7520	7646	7646	8508	9429	8980	411	1102	1236	1276	1374	1501	i	31/8	3352	3439	3439	3476	3606	4387	4387	4775	4775

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				_	-	_		-			_											_		_		_				
Single Latin France Explessed III nealt	Top Hit Descriptor	n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;	ni11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'	Human IFNAR gene for interferon alpha/beta receptor	Arabidopsis thaliana F21,92 mRNA, complete cds	Homo saplens sperm associated antigen 7 (SPAG7), mRNA	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'	Homo sapiens chromosome 21 segment HS21C001	602129475F1 NIH MGC 56 Homo saplens cDNA clone IMAGE 4286203 5	602129475F1 NIH_MGC 56 Hamo sapiens cDNA clone IMAGE:4286203 5	Mus musculus beta-sarcoglycan gene, complete cds	Homo sapiens chromosome 21 segment HS21C001	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxx28orf	Mus musculus chromosome X contide: X-linked lymphocyte requisited 5 name. Zinc finner moteln 275. Zinc	finger protein 92, mmxq28orf	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu reneillive element	Homo sapiens human endogenous refrovirus W dag 33 G dag (nag) nage complete ade	Mouse kidney androgen-regulated protein (KAP) gene complete cds	xx34e03.x1 Soares NFL T GBC S1 Home septems cDNA close IMAGE-2815038 3	1x/34e03.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE-0815036 3	Yeast ABP1 gene for actin binding protein	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870	Human herpesvirus 6B, complete genome	Homo saplens V1b vasopressin receptor (VPR3) gene, complete cds	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
שום באטוו רווט	Top Hit Database Source	EST_HUMAN	EST HUMAN	N	EST_HUMAN	LN LN	LN	TN	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	N L	N	Į.		본	Z	Z.	EST HIMAN	NT	Į.	EST HUMAN	EST HUMAN	TN	TN.	FN	Ę	LN	ŇT
OBO I	Top Hit Acession No.	1.4E-02 AA559030.1	1.4E-02 AA559030.1	1.4E-02 AL022073.1	1.4E-02 BE544561.1	X60459.1	1.4E-02 AF324985.1	11426968 NT	1.3E-02 BE739263.1	AL163201.2	1.3E-02 BF697081.1	1.3E-02 BF697081.1	1.3E-02 AF169288.1	1.3E-02 AL163201.2	1.3E-02 AL049866.2		1.3E-02 AL049866.2	1.3E-02 AL 161546.2	4L161546.2		Σ.		4W268563.1	4W268563.1	(51780.1	299117.1	TN 6905536	1.3E-02 AF152238.1	1.3E-02 AF009179.1	(87344.1
	Most Similar (Top) Hit BLAST E Value	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02 X60459.1	1.4E-02	1.4E-02	1.3E-02	1.3E-02 AL16320	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02		1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02 AF156961	1.3E-02 M63707.1	1.3E-02 AW26856	1.3E-02 AW26856	1.3E-02 X51780.1	1.3E-02 299117.1	1.3E-02	1.3E-02	1.3E-02	1.2E-02 X87344.1
	Expression Signal	4.62	4.62	1.82	2.07	4.79	1.55	1.89	0.86	2.41	1.99	1.99	1.41	1	1.36		1.36	1.35	1.35	4.77	1.74	1.87	4.39	4.39	2.92	1.6	1.8	28.64	1.32	0.94
. }	ORF SEQ ID NO:	25887	25888			28790				21684	22906			21684	24854			24856	24857	26499	27010	27956	28484	28485					24912	
	Exon SEQ ID NO:	15768	15768	16612	17275	18885	19102	19277	11718	11807	13102	13102	13799	11807	15135		15135	15114	15114	16332	16817	17712	18237	18237	19705	19694	19170	19486	19744	10177
	Probe SEQ ID NO:	5862	5862	6732	7408	9126	9476	9763	1821	1912	3177	3177	3888	5176	5212		5212	6156	6156	6473	6839	7862	. 8360	8360	9102	9482	9586	9758	9949	206

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		,					_	-	_		_	,														_		_	
Ingre Lyon From Lineau	Top Hit Descriptor	zf65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element ;	HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3'REGION	qd68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMACE:1734670 3' similar to contains L1.t1 L1 repetitive element	Homo sapiens chromosome 21 segment HS21C013	1x/37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 31	DF 3	601068406F1 NIH_MGC_10 Hamo sapiens cDNA clone IMAGE:3454608 5	xi37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432.3'	Zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis IHI A-H) nane RoRet nane and codium phosphoto transporter MiDTO	Onces by thousand Bury, and Contain properties desirable of the 19 years, cumplete cos	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'	Rana rugosa mRNA for caireticulin, complete cds	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5	AV732093 HTF Homo sapiens cDNA done HTFBJC09 5	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NACGS) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (S13GAIA,2)	Homo sapiens fringe protein mRNA, partial cds	Homo sapiens fringe protein mRNA, partial cds	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds	Homo sapiens Spast gene for spastin protein	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER)	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-557G06 5	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE: 530924 3'	H.sapiens LIPA gene, exon 4	H.sapiens LIPA gene, exon 4
gie Laui F 10	Top Hit Database Source	EST_HUMAN	SWISSPROT	EST HUMAN	Į.	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	L Z	L	EST HUMAN	LN LN	LN.	EST_HUMAN	SWISSPROT	Ę	۲	EST_HUMAN	L L	Ę	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	IN	LN
200	Top Hit Acesslan No.	1.2E-02 AA059299.1	P38898	1.2E-02 Al183522.1	AL163213.2	1.2E-02 AW172350.1	1.2E-02 BE538310.1	1.2E-02 BE538310.1	1.2E-02 AW172350.1	AA075418.1	R62805.1	J91328 1	1.2E-02 AB019786 1	1.2E-02 AV731704.1	D78589.1	1.2E-02 AF175412.1	1.2E-02 AV732093.1	211205	AF193612.1		T76987.1	4B031013.1	4,1246003.1	015534	917139	C18119.1	1.1E-02 AA070364.1	X75491.1	K75491.1
	Most Similar (Top) Hit BLAST E Value	1.2E-02	1.2E-02 P38898	1.2E-02	1.2E-02 AL16321	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02 AA07541	1.2E-02 R62805.1	1.2F-02 [191328	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02 Q11205	1.2E-02 AF19361	1.2E-02 AF19361	1.2E-02 T76987.1	1.2E-02 AB03101	1.2E-02 AJ24600;	1.2E-02 015534	1.2E-02 P17139	1.2E-02 C18119.1	1.1E-02	1.1E-02 X75491.1	1.1E-02 X75491.1
	Expression Signal	1.74	1.48	2.98	1.99	1.23	1.1	1.1	1.27	6.18	1.89	204	1.73	2.12	1.96	5.33	6.37	2.11	1.22	1.22	1.17	. 2.45	1.23	1.78	1.5	3.47	1.32	1.99	1.99
	ORF SEQ ID NO:	20128	20210	20483		22167	22223		22167		22971	24495		24659	25497	26216	26352	26742	26832	26833				25345			21004	21451	21452
	Exen SEQ ID NO:	10310	10389	10653		12271	12325				13173	14712	L.	14891	15434	16066	16190	16545	16644	16644	17029	17408	17426			19286	11155	11581	11581
	Probe SEQ ID NO:	352	445	721	2130	2393	2448	2448	2596	3063	3250	4830	4974	5017	5516	6180	6327	6665	6765	6765	7152	7557	7575	9177	9588	9766	1248	1679	1679

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Single Exon Probes Expressed in Heart

Probe E SEQ ID SE NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
	11886	21778	4.35	1.1E-02	1.1E-02 BF345263.1	EST HUMAN	602018037F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2848	12776		3.53	1.1E-02	1.1E-02 N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5
	12860	22660	10.39	1.1E-02	1.1E-02 AF055068.1	NT	Homo sapiens MHC class 1 region
3478	13394	23200	2.46	1.1E-02	1.1E-02 AI653508.1	EST_HUMAN	tq95b10.x1 NCI_CGAP_Ov23 Homo saplens cDNA clone IMAGE:2216539 3' similar to SW.XPF_HUMAN Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
3937	13846		0.87	1.1E-02	1.1E-02 BE144637.1	EST_HUMAN	PM3-HT0175-300989-001-h06 HT0175 Homo sapiens cDNA
4016	13921		76.0	1.1E-02	1.1E-02 AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4723	14609	24395	1.81	1.1E-02	7	EST_HUMAN	DKFZp586E0924_s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
	14704		0.92	1.1E-02	1.1E-02 AW820281.1	EST_HUMAN	QV2-ST0296-150200-028-c11 ST0296 Homo sapiens cDNA
	16339	26506	2.26	1.1E-02	1.1E-02 BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
7160	17037	27230		1.1E-02 Q61982	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
77.10	17560	27785	2.25		1.1E-02 AA082578.1	EST HUMAN	2024a01.1 Stratagene neuroepithelium NT2RAMI 937234 Homo saniens cDNA clone IMAGE-E48338 51
ı	17660	27900	4.1		1.1E-02 AA314665.1	EST HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 6' end
	18224	28476	3.38	1.1E-02	11435505 NT	IN	Homo saplens T-box 5 (TBX5), mRNA
-							ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
9064	18845		2.23	1.1E-02	1.1E-02 AA668239.1	EST HUMAN	Alu repetitive element;
9	9992	19785	3.35	1.0E-02	1.0E-02 AW846120.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Hamo sapiens cDNA
1506	11411	21270	0.91	1.0E-02	1.0E-02 AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
	12399		1.2	1.0E-02		EST_HUMAN	oc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
	12978	22771	2.37	1.0E-02	1.0E-02 BE835556.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
]	13150	22950	1.18	1.0E-02	1.0E-02 BE968999.1	EST_HUMAN	601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
l	13380		0.89	1.0E-02	1.0E-02 AW845621.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo saplens cDNA
	13717	23505	0.79	1.0E-02	1.0E-02 Al065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
	14553	24345	4.26	1.0E-02	6753521 NT	NT	Mus musculus corticotropin releasing hormane receptor 2 (Crhr2), mRNA
	14621	24407	2.38		1.0E-02 R96567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5
4995	14870	24633	0.85		1.0E-02 AF218910.1	NT	Homo saplens attractin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced
5149	15016		0.82	1.0E-02	1.0E-02 BE876539.1	EST_HUMAN	601486286F1 NIH_MGC_69 Hamo sapiens cDNA clane IMAGE:3888908 5'
	15659	25766	2.74		1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
	15659	25767	2.74	1.0E-02	1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Hamo sapiens cDNA
	16037	26178	2.06			INT	Z.mays U3snRNA pseudogene
_1	17270	27475	4.65		1.0E-02 BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
7403	17270	27476	4.65	1.0E-02	1.0E-02 BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'

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ssion (Ton) Hil	Most Similar Expression (Top) Hit	_
	(10p) Hit 10p Hit Acession BLAST E No.	Signal BLASTE No.
0.86 8.0E-03 U47048.1 NT	8.0E-03 U47048.1	8.0E-03 U47048.1
25.1	8.0E-03 BE171225.1	0.97 8.0E-03 BE171225.1
	8.0E-03 AJ131016.1	8.0E-03 AJ131016.1
1.07 8.0E-03 AF058764.1 NT	8.0E-03 AF058764.1	1.07 8.0E-03 AF058764.1
5.12 8.0E-03 BF363327.1 EST_HUMAN	8.0E-03 BF363327.1	8.0E-03 BF363327.1
2.7 8.0E-03 AF110520.1 NT	8.0E-03 AF110520.1	8.0E-03 AF110520.1
22.1	8.0E-03 AP000002.1	8.0E-03 AP000002.1
	8.0E-03 P55577	8.0E-03 P55577
2.19 8.0E-03 M17197.1 NT	8.0E-03 M17197.1	8.0E-03 M17197.1
67.1	8.0E-03 AB038267.1	8.0E-03 AB038267.1
92.1	8.0E-03 AW808692.1	8.0E-03 AW808692.1
Γ	8.0E-03 BE086509.1	4.72 8.0E-03 BE086509.1
1.1	8.0E-03 BE788441.1	8.0E-03 BE788441.1
	8.0E-03 Z49652.1	2.78 8.0E-03 249652.1
1.75 8.0E-03 AA828817.1 EST HUMAN	8.0E-03 AA828817.1	1.75 8.0E-03 AA828817.1
8.0E-03 AA828817.1	8.0E-03 AA828817.1	8.0E-03 AA828817.1
	8.0E-03 AF064589.1	4.83 8.0E-03 AF064589.1
1.34 8.0E-03 M69035.1 NT	8.0E-03 M69035.1	8.0E-03 M69035.1
3.36 8.0E-03 AB038161.1 NT	8.0E-03 AB038161.1	3.36 8.0E-03 AB038161.1
		11.58 7.0E-03 AF097183.1
	7.0E-03 AF097183.1	11.58 7.0E-03 AF097183.1
2.01 7.0E-03 AF243376.1 NT	7.0E-03 AF243376.1	2.01 7.0E-03 AF243376.1
2.6 7.0E-03 AV731712.1 EST HUMAN	7.0E-03 AV731712.1	7.0E-03 AV731712.1
	7 0E 03 OE40E0	7 0E 03 OE40E0
7 05 05 4 60 505	7 00 00 4 80 000 7	7 05 05 4 60 505
7.0E-03 AA668298.1	7.0E-03 AA668298.1 EST	13.73 7.0E-03 AA668298.1 EST
7:0E-03 AW303599.1 EST	7:0E-03 AW303599.1 EST	7:0E-03 AW303599.1 EST
7.0E-03 P04929	7.0E-03 P04929	2.24 7.0E-03 P04929
1.27 7.0E-03 AW444463.1 EST_HUMAN	7.0E-03 AW44463.1	7.0E-03 AW44463.1

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Single Exon Probes Expressed in Heart

			Most Similar			
SEQ ID ORF SEQ E NO:	Ш	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	l op Hit Database Source	Top Hit Descriptor
13653 23436		1.01	7.0E-03	7.0E-03 AF196344.1	N	Rattus norvegicus neuronal nicctinic acetylcholine recentor schimit / Alchadol
14329		1.23	7.0E-03	7.0E-03 AW117711.1	EST HUMAN	xe34f09.X1 NCLCGAP_Uff Homo saplens cDNA clone IMAGE: 2609033 3' similar to TR: 012987 Q12987 ACIDIC 82 KDA PROTEIN
14389		1.01	7.0E-03		EST HUMAN	Ph89a05 of NCI CGAP G1/1 Homo contons a DNA stand 144 CF concessor at
14795		1.76		7.0E-03 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
14910 24683		1.1	7.0E-03	7.0E-03 BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:3039807.3' similar to TR:O93434 093434 RETICULOCALBIN.
14910 24684		1.1	7.0E-03	7.0E-03 BE044191.1	EST HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:093434 O93434 RETICUI OCAI RIN .
19452		5.07	7.0E-03	1.6	Т	RC1-CT0286-050400-018-018 CT0288 Home conjunctions
	1	1.49	7.0E-03		Т	243310.rl Soares fetal heart NhHH10M Home coming and all the property of the state
15844 25967	N	3.46	7.0E-03	5	HUMAN	EST30874 Colon Homo seciens cDNA 5' end
15859 25980	Q	1.3	7.0E-03	7.0E-03 BE857385.1		7g34b10.x1 NCI_CGAP_Bm23 Homo septens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOTHETICAL PROTEIN 384D8 3 constituting to the constitution of the con
	7	2.39	7.0E-03			CM2-CT0478-230800-347-b11 CT0478 Home series - NAA
	Я	4.98	7.0E-03	7.0E-03 Z35838.1	П	S.cerevisiae chromosome II reading frame ORE VRI 077
	25	4.98	7.0E-03 Z35838.1			S.cerevisiae chromosome reading frame ORE VRI 077
	ន	2.29	7.0E-03	7.0E-03 BE175667.1	EST HUMAN	RC5-HT0582-160300-011-D02 HT0582 Home series about
	ō	2.53	7.0E-03 P48982		Г	BETA-GALACTOSIDASE PRECLIBION / ACTARE)
17456 27671	-	2.53	7.0E-03 P48982		Ī.	BETA-GALACTOSIDASE PRECYIRSOR (I ACTARE)
	┪	1.27	7.0E-03	7.0E-03 AV687379.1	EST HUMAN	AV687379 GKC Homo sapiens cDNA clone GKCAFCD7 F
18086 28337	덝	3.36	7.0E-03	7.0E-03 AB008852.1	Γ	Bos faurus mRNA for NDP52, complete cds
19750		1.55	7.0E-03 H94065.1		EST HIMAN	W16h01.s1 Soures fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:242833 3' similar to contains.
19194	┢	1.88	7.0E-03	1	Т	601145154F9 NIH MGC 10 Homo conform -PNIA
19425	\dashv	1.83	7.0E-03	-	Т	RC0-SN0052-110400-021-a04 SN0052 Home saniars ANA
11129 20979	<u>0</u>	9.29	6.0E-03	6.0E-03 AW511148.1	EST HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo solphens cDN4 clone IMAGE:2910224.3' similar to SW:PXR_HUMAN 075469 ORPHAN NI ICI FAR PERCETTOR DATA
11129 20980	Ö	9.29	6.0E-03/	6.0E-03 AW511148.1	EST HIMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens control clone IMAGE.2910224.3' similar to
	6	1.09	6.0E-03	Γ	Т	Danio rerio chorant recentor gene allustra
	ᆕ	3.11	6.0E-03/	_	T HUMAN	ah78e11st Spares testis NHT Hama contons and a contons at
12790 22682	ليح	3.11	6.0E-03	-	Т	ah/8e11s1 Spares besite NHT Home capiens could specified to the contraction of the country of th
	ł					The course of the section of the sec

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Table 4
Single Exon Probes Expressed in Heart

		T	Τ.	: [T	Т	Ţ	T	Т	T	Т	Т	Т	Т	T	Т	_	Т	Т	Т	Τ_	Т	Т	Т	7_	1_	7	-
	Top Hit Descriptor	yr77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'	Notoncus sp. cytochrome c oxidase subunit II gene, partial cats: mitrochondrial gene for mitrochondrial produces	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin denes, complete cris	Zc13a11.r1 Soares pareflying tumor NbHPA Home senions cDNA close (MACE 2223472) 21	UI-H-BI4-apm-c-08-0-UI:S1 NCI CGAP Sub8 Homo seniens cDNA clone IMA GE-3087784 31	Mus musculus glucosamine-6-phosphate deaminase (Gnol.) mRNA	RC0-CT0204-240999-021-b10 CT0204 Hamo sapiens cDNA	600942904F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE 2959513 51	1962h10.s1 Soares, multiple, sclerosis, 2NbHIMSP Homo septens cDNA cone IMAGE: 778170 21	ov33c11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE-16xq124.3	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Ahr reneat	Homo sapiens chromosome 21 segment HS21C081	gle5g09.s1 Soares parathyroid furnor NbHPA Homo saplens cDNA clone IMAGE:1404758 2	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds	ow13a04.x1 Scares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10 b1 MFR10 renetitive element:	RC0-UM0051-210300-032-002 UM0051 Homo saniens cDNA	601454915F1 NIH MGC 66 Home sapiens cDNA cinne IMAGE 3858678 8	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein	122c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN	Mitempformicients complete plasmid vEV4 DNA	EST374237 MAGE recognished MAGE Lame conjune DNA	Homo sapiens hypothetical zinc finger protein FI J14011 (FI J14011) mRNA	te91c12.X1 NCI_CGAP_Pr28 Homo septiens cDNA done IMAGE:2094070 3' similar to TR:O00519 O00519	tegrin Acid Awilde Hithrolasse.; tegrin Acid (GGAP) P/28 Homo sapiens cDNA done IMAGE;2094070 3' similar to TR:O00519 O00519	Mis misculing airs financiarism and in a second of the control of	was mascular and the protein mixing, complete cas
201	Top Hit Database Source	EST_HUMAN	ΙΝ	N	L	EST HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	TN	EST HUMAN	1	EST HUMAN	Т	Π	Π	EST HIMAN	T	Т	1545814 NT	П	T	Т	1444
	Top Hit Acession No.	H75690.1	6.0E-03 AF190338.1	6.0E-03 U90880.1	_	-	_	34029	84.1	6.0E-03 BE250108.1		İ	6.0E-03 AA324242.1			6.0E-03 AF128894.1	<u> </u>	37.1	Γ				6.0E-03 AW962164 1	11545814	6 0F. na A 1420786 4			
	Most Similar (Top) Hit BLAST E Value	6.0E-03 H75690.	6.0E-03	6.0E-03	6.0E-03 U90880.	6.0E-03	6.0E-03	6.0E-03	6.0E-03 AW8472	6.0E-03	· 6.0E-03 N58946.	6.0E-03	6.0E-03	6.0E-03	6.0E-03 AA88997	6.0E-03	6.0E-03 A1033980	6.0E-03 /	6.0E-03	6.0E-03 D10548.1	6 0F-03 A1432661	6.0E-03 X68366.1	6.0E-03	6.0E-03	8 OF 73 A	SOTOCALA SOT TO A	6.0E-03 U14556 1	A OF AS DETASAS
	Expression Signal	2.06	0.82	1.24	1.24	1.05	3.62	1.28	0.93	1.18	0.87	1.37	6.82	1.83	0.89	1.97	7.04	2.44	1.41	8.21	194	1.5	2.23	2.21	189	8	3.91	3 54
	ORF SEQ ID NO:			23062	23063				23551				24271	24758	24767	26542	26657	26724		27506		28039	28263		28356	78357		28479
	Exon SEQ ID NO:	13132	13187	13256	13256	13416	13524			13784	14129	14166	14485	14983	14996	16365	16466	16530	16569	17297	17626	17789	18015	18072	18102	18102	18227	18228
	Probe SEQ ID NO:	3208	3264	3336	3336	3489	3610	3711	3846	3873	4231	4267	4597	5115	5129	9209	9299	6850	6899	7509	7776	7949	8127	8186	8220	8220	8350	8351

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
9185	18922		1.59	6.0E-03	6.0E-03 AF010496.1	TN	Rhodobacter capsulatus strain SB1003, partial genome
9310	19519		3.6	6.0E-03	6.0E-03 AE000833.1	LΝ	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete denome
9372	19038		1.34	6.0E-03	6.0E-03 AB025356.1	NT	Anguilla japonica mRNA for activin B. complete cds
9392	19583		2.21	6.0E-03	6.0E-03 U30790 1	IN	Prelimonsells carinit for cott arresting analysis to it.
9722	19262		1.57	6.0E-03	=	EST HUMAN	601482621F1 NIH MGC 68 Homo saniens cloud buttone INA CE 3005200 5.
9741	19274		1.34	6.0E-03		N TN	Brassica napus sig gene for S-locus alvocarotein cultivar T2
653	10589	20406	1.9	5.0E-03	L25105.1	TN	Chiamydia trachomatis partial ORFB; aminoscyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
653	10589	20407	1.9	5.0E-03 L25105.	1.25105.1	NT	Chlamydia trachomatis partial ORFB, aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
654	10589	20406	2.92	5.0E-03 L25105.	125105.1	NT	Chlamydia trachomatis partial ORFB; aminoacy-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
654	10589	20407	2.92	5.0E-03 L25105.	1	LN	Chiamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1096	11012	20854	1.38	5.0E-03	57.1	N	Arabidopsis thaliana mRNA for DEAD how RNA helicase RH3
1552	11457		0.91	5.0E-03 AI13897		EST HUMAN	dd/9d05 x/ Soares fastis NHT Homo senions of NA clara IAA CE 472 Eco. 01
2648	12515	22405	3.44	5.0E-03		Г	Homo sapiens mRNA for KIAA1180 protein partial cds
2905	12832	22629	96.0	5.0E-03	5.0E-03 BE266057.1	EST HUMAN	601194796F1 NIH MGC 7 Homo sapiens CDNA clone IMAGE-3538709 57
3097	13024	22820	4.08	5.0E-03 T87623.		EST_HUMAN	yc81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE-27305 2
3116	13041		1.75	5.0E-03	1.2		Arabidopsis thaliana DNA chromosome 4, conting fragment No. 3
3,128	13054	22853	1.04	5.0E-03 R71794.		EST_HUMAN	y/86g02.s1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE-155668 3
3240	13163		1.08	5.0E-03 /			Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3641	13555	23341	4.16	5.0E-03	19.2	N	Pseudomonas aeruginosa strain PAO1 penicillin-binding profein 18 (mon8) gene
3698	13612	23396	0.83	5.0E-03 U38914.		LN L	Oftrus sinensis seed storage protein citrin mRNA complete case
3830	13801		1.38	5.0E-03 AA29967	6.1	EST HUMAN	EST122/8 Uterus fumor I Homo sapiens CIDNA 5' ead
4207	14106	23886	0.93	5.0E-03 H78355.	-	Т	VI79q10,r1 Soares fetal liver shipen 1NH S Homo senione - DNA -dras IVA CE 2 senione -
4209	13612	23396	0.91	5.0E-03 U38914.	_	Т	Oltrus sinensis seed storage protein citrin mRNA complete adv
4503	14396	24181	0.94	5.0E-03 AJ13101	6.1	NT	Homo sapiens SCL gene locus
4619	14507	24296	2.49	5.0E-03 A1752367		EST HIMAN	21455-02 V Normal Himan Trakemins Done Call 11
5541	15458	25528	5.34	5.0E-03 P35500		1	SOUILM CHANNEL PROTEIN DADA (DADA) VIIIS DEGETINALE
						7	COSC CONTROLL NO ICIN FANA (PANAL TIC PROTEIN)

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Single Exon Probes Expressed in Heart	Tap Hit Descriptor	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITIN-SPECIFIC BROYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980871 3'	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds	Homo sapiens MASL1 mRNA, complete cds	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	Mouse complement receptor (CR2) mRNA, 3' end	694F Heart Homo sapiens cDNA clone 694	xn59g05.x1 Soares_NHCeC_cervical_tumor Hamo sepiens cDNA clone IMAGE:2698040 3' similar to contains L1.t2 L1 repetitive element :	xn69g05.x1 Soares_NHCeC_cervical_tumor Homo sepiens cDNA clone IMAGE:2698040 3' similar to	violego 4.1 Stratagene placenta (#037275) Homo saniens cDNA clone INA CE: 70696 FI	Mus musculus hynothetical protein MNCh-4780 (1 OC8942) why a	746604.VINCI CGAP Brn52 Home saniens citiva clone MAACE-2204222 F	Gallus gallus glyceraldehyde-3-phosphate dehydrodenase mRNA commists cde	Brugia malayi Y chromosome marker	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds	2x75a03.s1 Soares ovary fumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' stmilar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENDI_OXIDASE A2 COMPONENT.	602077774F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE:4252002 5	UI-H-Bi3-akf-f-08-0-UI.s1 NCI CGAP Sub5 Homo seniens cDNA clone IMAGE-27342318 2	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (I.C.COLLAGEN)	2574905.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE-309368 3	UI-HF-BN0-akc-h-04-0-UI.r1 NIH MGC 50 Homo sapiens cDNA clone IMAGE-3076831 5'	yg51e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE-35088 3	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PITDINS 3-KINASE) (PINA)	on 75g12.s1 Scares NFL T GBC S1 Homo sapiens cDNA clone IMAGE-15R9-588 9	yg51e04.s1 Soares infant brain 1NIB Homo saniens cDNA clone IMAGE-35988 3	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA	zl81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
Jie Exon Probe	Top Hit Database Source	PH FF Y SWISSPROT	EST_HUMAN 60		II.	SWISSPROT BE	NT	EST_HUMAN 66	EST HUMAN CO				T HUMAN	Т			EST HUMAN SI	Г	Г	Г	EST_HUMAN 2	EST_HUMAN UI	Т	SWISSPROT PH	EST HUMAN ON	Π	Г		EST_HUMAN RO
	Top Hit Acession No.	000507	5.0E-03 BE300091.1	5.0E-03 AB025024.1	5.0E-03 AB016816.1	5.0E-03 P48982	5.0E-03 M61132.1	5.0E-03 T19586.1	5.0E-03 AW170334.1	5 NE-03 AW370334 1	5.0E-03 T49153.1	10946753 NT	BE04805	5.0E-03 AF047874.1	5.0E-03 AF067253.1	5.0E-03 L10347.1	5.0E-03 AA456597.1	5.0E-03 BF572332.1	5.0E-03 AW 449109.1	Q02388	5.0E-03 AI668709.1	4.0E-03 AW500196.1	4.0E-03 R46482.1	P54675	4.0E-03 AA939339.1	4.0E-03 R46482.1	4.0E-03 AW749101.1	7.1	4.0E-03 AW 794740.1
	Most Similar (Top) Hit BLAST E Value	5.0E-03 O00507	6.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.05-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03 Q02388	5.0E-03	4.0E-03	4.0E-03	4.0E-03 P54675	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03
	Expression Signal	2.43	6.17	6.02	6.26	1.97	6.92	7.44	3.17	3.17	1.95	1.77	3.73	5.04	8.65	1.55	1.28	4.16	1.94	1.4	1.41	2.97	2.18	0.94	3	1.81	3.43	32.55	1.58
	ORF SEQ ID NO:	25695		24877	26605	26865			28435	28436	28527	28563							25197			20015	20097	20203	20333	20637		20889	20910
	Exon SEQ ID NO:	15594	15881	15101	16424	16673	16883	17993	18187	18187	18275	18307	18508	19709	18091	19153	19174	19529	19301	19601	19400	10201	10280	10380	10526	10785	10819	11047	11066
	Probe SEQ ID NO:	5685	5977	6091	6566	6794	7006	8103	8310	8310	8399	8433	8644	9327	9460	9555	9592	9616	9791	8086	9929	232	318	436	588	820	88	1133	1153

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Table 4
Single Exon Probes Expressed in Heart

	~~~			_	_	_		_		_	_	_			_			_		_				_						
Top Hit Descriptor	Homo sapiens KIAA0345 gene product (KIAA0345). mRNA	te49b11.x1 Soares_NFL_T_GBC_S1 Homo saptens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element	Homo sapiens chromosome 21 seament HS21C009	Homo sabiens chromosome 21 seament HS21 Ch78	Homo saplens chromosome 21 segment HS21Chne	PM4-BN0138-180600-002-b08 BN0138 Homo saniens CONA	601118164F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE 3028ng6 5'	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repelitive element,contains element MER31 repelitive element	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853932.3' similar to contains element TR5 repetitive element	RC3-ST0284.240400.045.873 ST0284 Library 2001/2001	Home englane Carlo associated bit at a 1011 at 1010 A	Homo Sablens profein kinese CK2 and the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the California of the Californ	Homo sabiens protein kinase CK2 actables about it appra gene, exon 1	no 7305.st NCI_CGAP_Pr2 Homo septens cDNA clone IMAGE:782984 similar to contains Alu repetitive	Homo sopione MID class 4 selections	Scereals (or Halo) mRNA for trioncal house, increases	Mus musculus intestinal trefail factor gene partial color	Mus musculus intestinal frefoil factor nene partial cde	Arabidopsis thaliana rpoMt gene	601237982F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE 3600033 57	IL2-UM0076-240300-058-D03 UM0076 Hamo saniens cDNA	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene expn 1 and 2	C.elegans samdo gene	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'	AV762392 MDS Homo sapiens cDNA clone MDSRSG01 5	ah04t09.y5 Gessler Wilms tumor Homo saniens CDNA clore IMACE:14 Escop e	S.cereale (ov. Hato) mRNA for triosephosphate isomerase	Raffus norvegicus gdnf gene	xu8.P10.H3 conorm Homo sapiens cDNA 3'	DKFZp761B0712_11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5
Top Hit Database Source	N	EST HUMAN	NT L	Z	N	EST HUMAN	EST_HUMAN	EST HUMAN	EST HIMAN	EST HIMAN	TN.	TN	Ł	FST HIMAN	MT	L	N	IN	LN	EST_HUMAN	EST_HUMAN	LN	N	EST HUMAN	EST HUMAN	EST HUMAN	L	IN	1	EST_HUMAN
Top Hit Acession No.	7662067 NT	4.0E-03 Al553983.1	4.0E-03 AL163209.2	AL163278.2	4.0E-03 AL163206.2	3E815173.1	4.0E-03 BE298290.1	4.0E-03 BF224125.1	4.0E-03 AW614598.1	4.0E-03 AW819141.1	11436955 NT	3.0E-03 AF011920.1	3.0E-03 AF011920.1			1				E379296.1	W802687.1			2.1	2.1	Г		1.1	.1	:
Most Similar (Top) Hit BLAST E Value	4.0E-03	4.0E-03	4.0E-03	4.0E-03 AL16327	4.0E-03	4.0E-03 BE81517	4.0E-03	4.0E-03	4.0E-03	4.0E-03/	4.0E-03	3.0E-03	3.0E-03/	3.0E-03.0A46811	3.0F-03/	3.0E-03 Z32521.1	3.0E-03 U46858.1	3.0E-03 U46858.1	3.0E-03 Y09006.1	3.0E-03 BE37929	3.0E-03 AW8026	3.0E-03 U34606.1	3.0E-03 Y12500.1	3.0E-03 AV76239;	3.0E-03 AV76239;	3.0E-03 A	3.0E-03 Z32521.1	3.0E-03 A	3.0E-03 AI536141	3.0E-03 AL119067
Expression Signal	2.02	7.4	4.41	3.38	5.64	3.95	2.25		1.57	1.57	1.52	1.62	7.66	184	0.87	3.9	1.12	1.12	0.84	4.53	2.62	1.95	6.75	7.43	7.43	1.58	1.34	11.91	4.37	0.88
ORF SEQ ID NO:	26841	27123									25168	20146	20638	21401			22023	22030		22765	22833	23089		23591	23592	23632		23978	24096	24309
Exon SEQ ID NO:	16653	16933	17028	17036	18345	19725	19009	19202	19640	19236	19416	10323	10787	11542	12097	12132	12133	12133	12890	12971	13037	13290	13297	13805	13805	13858	13360	14194	14311	14518
Probe SEQ ID NO:	6774	7056	7151	7159	8472	9295	9317	9628	9096	6296	9950	367	861	1638	221	2248	2249	2249	2963	8 4	3112	3371	33/0	388	3862	3920	4058	4236	4417	4630

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Single Exon Probes Expressed in Heart

Single Exolitiones Explicated III near	Most Similar (Top Hit Acession BLASTE No. Source Value	3.0E-03 A1732754.1 EST HUMAN repetitive element;	3.0E-03 BE787945.1 EST_HUMAN 601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'	Π	4506414 NT	8922499 NT	3.0E-03 AJ249981.1 NT Mus musculus mRNA for hypothetical protein (ORF2 ortholog)	3.0E-03 AA456701.1   EST_HUMAN   aa13f10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'	3.0E-03 AJ011419.1 NT Kluyveromyces marxianus popi3 gene for purine-cytosine permease	3.0E-03 AB021736.1 NT Oryza sativa gene for bZIP protein, complete cds	3.0E-03 N92580.1 EST_HUMAN 2b27b04.s1 Scares_parethyroid_tumor_NbHPA Homo sepiens cDNA clone IMAGE:304783 3*	3.0E-03 P51989 SWISSPROT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP AZ(A))	LN L	3.0E-03 Q9QM81 SWISSPROT NONSTRUCTURAL PROTEIN V	TO TO	SUE-COLAWO STITE EST TOWAN TEpeduve etailetti,	2	3.0E-03 Al016731.1 EST_HUMAN HISTONE H2B.2 (HUMAN):	SWISSPROT	SWISSPROT	SWISSPROT	AL163303.2 NT	33028 NT		NT	3.0E-03 AF094481.1 NT Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	Ā		SWISSPROT	3.0E-03 Al525056.1 EST_HUMAN promina-5.E07.r bytumor Homo sapiens dDNA 5'	3.0E-03 AA993154.1 EST_HUMAN contains L1.t3 MER26 repetitive element;
T alfillo	Acession lo.	14		4506414 NT	4506414 NT	8922499 NT					_		Γ		7		Ī	<u>-</u>				3.2	5803028 NT							-	
		3.0E-03 A	3.0E-03 B	3.0E-03	3.0E-03	3.0E-03	3.0E-03 A	3.0E-03 A	3.0E-03 A	3.0E-03 A	3.0E-03 N	3.0E-03 P	3.0E-03 A	3.0E-03 Q	2 20 20 8	3.05-03 A	3.0E-02					3.0E-03 A	3.0E-03	3.0E-03 A	3.0E-03 A	3.0E-03 A	3.0E-03/A	1	3.0E-03 P	3.0E-03 A	3.0E-03 A
	Expression Signal	1.54	60.7	1.11	1.11	3.17	1.41	6.6	1.54	11.8		1.29	1.57	1.38	0 50	0.02	-	8.9	3.48		1.46	4.05	2.69	2.11	2.01	3.06	3.06	,	1.93	2.02	1.54
	ORF SEQ ID NO:	24399	24416	24733		24837	25380		26297			27001	27011			27207		27317				27931		28856		28877	28878		28942		28780
	Exon SEQ ID NO:	14613	14630	14959		15143	15330	15851			16620		16818	16868	47076			17121	17449							18590	18590		_	19542	18870
	Probe SEQ ID NO:	4727	4745	5089	5089	5220	5410	5946	6277	6442	6741	6928	6940	6991	7100	7230	203/	7244	7598	7694	7742	7836	8222	8685	8744	8773	8773	77.00	8841	8908	9103

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Single Exon Probes Expressed in Heart	Top Hit Detablese Top Hit Descriptor	Į.		SIMISCODOT	7.	SWISSPRO!	NAT TOWAR	EST LIMAN	LN LN				/Iccoport	CAT LEATING	NA HOMAN	12	FST HI MAN	EST LIMAN	EST HIMAN	H	Į.	SWISSBOT	Т				NT	EST_HUMAN	N	N	<u>N</u>
S	Top Hit Acessic No.	3.0E-03 AB009688 4	3.0F-03 A 120R2R2 4	2.0E-03 004652	2 0F-03 O04652	2.0E-03 T70874 1	2.0E-03 M20783 1	2.0E-03 AA661605 1	2.0E-03 AF28446.1	P48509	455783	455792	1	2.0F-03 AA450198 4	2.0E-03 AF302691 4	2.0E-03 AL163302 2	AW 137782 1	2.0E-03 AA450138 1	2.0E-03 BF568955.1	87344 1	B040802 1		68491 1	42512.1	42512 1		F223391.1	87773.1	JZ45167.1	Y005150.1	2.0E-03]AY005150.1
	Most Similar (Top) Hit BLAST E Value		3.0F-03	2.0E-03	2 OF-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03 P48509	2.0E-03	2.0E-03	2.0E-03 P29400	2.0F-03	2.0E-03/	2.0E-03/	2.0E-03 AW 1377	2.0E-03/	2.0E-03	2.0E-03 X87344 1	2.0E-03 AB04080	2.0E-03 P03374	2.0E-03 U68491 1	2.0E-03 L42512.1	2.0E-03   42512 1		2.0E-03 AF223391	2.0E-03 R87773.1	Z.UE-03 AJZ45167.1	2.0E-03 A	2.0E-03 A
	Expression Signal	1.35	233	0.89	0.89	7.01	1.93	1.59	126	1.11	1.91	1.91	4.94	1.38	2.17	40:	4.62	4.03	1.02	4.87	0.92	2.15	9.77	1.93	1.93		0.94	7.7	70.0	1.04	1.04
	ORF SEQ ID NO:		25296		20259		21104		21115	21243	21263	21264		21502	21731	21992		23088	23093	23315	23572	23703		24130	24131	24.00	C9747	+	24820	24624	17047
	Exan SEQ ID NO:	19668	19019		10446				11259	11379	11404	11404	11477	11634	11845	12090	12409	13289	13294	13520	13780	13927	14027	14340	14340	14408	14500	14947	15057	15057	
	Probe SEQ ID NO:	9159	9339	504	504	768	1340	1343	1353	1474	1500	1500	1573	1733	1950	2203	2535	3370	3376	3615	3869	4024	4127	4446	4446	4608	4612	5077	5194	5194	

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Single Exon Probes Expressed in User

Single Exon Probes Expressed in Heart	Top Hit Descriptor  Top Hit Descriptor		H. saptens M1 gene for muscarinic acetylcholine receptor	Human DNA for CD38, exon 1		Homo sapiens MSH55 gene, partial cds, and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, Get DATE, CEL	1	T		7	7	Т		T	T	Homo conface and N. C. Kens			T	T	Human MUCz gene, promoter region	Human MUC2 gene, promoter region	Indino sepiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15		T	$\top$	Control and (SLS) genes spiced leader RNA (SL3 alpha), (SL4), and (SL5) genes
ngle Exo		Ŀ	2 1	Z	EST HIMAN	_ <u></u>	EST CHANK	EST HIMAN	FST HIMAN	100	FST HIMAN	EST LIMAN	NOW CONTRACT		OWISSING NT	Į	TOBESIMS		TACCOUNT	SWISSPRO			EN EN	EST HUMAN	10	NT HOMAN	
is	Top Hit Acession	2 0F_03 V00508 4	2 0E-03 100300.1	20E-03 AL 163203 2	2.0E-03 Al375037.1	2.0E-03 AF129756 4	2.0E-03 AV697966 1	1.0E-03 H96471.1	1.0E-03 AI720263.1	1 0F-03 A1720263 4	1.0E-03 Al865788.1	1.0E-03 A1954572 1		T	6.1					1.0F-03 (168064 4				1.7	1.0E-03 BF246K36 1		
	Most SImilar (Top) Hit BLAST E Value	205	200	20E-0	2.0E-0.	2.0E-0	2.0E-0	1.0E-0	1.0E-03	1.01	1.0E-03	1.0E-03	1.0E-03	1 0F-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0F-03	1 OF O3	1.0F.03	1.0E-03	1.05-03	1.0E-03	1.0E-03	1.0E-03	
	Expression Signal	1.59	0.62	2.92	1.57	127	1.66	1.38	2.38	2.38	2.14	1.44	1.45	3.61	8.02	1.15	2.26	2.26	1.16	0.79	0.79	1.24	1.02	3.54	3.77	0.87	
	ORF SEQ ID NO:	25278						20198	20587	20588	20836	20857	20906	21768	21896	22676	22879	22880	22984	23218	23219		23559	24013	24054	24244	
	Exen SEQ ID NO:	19066	19087	19134	19569	19247	19521	10377	10740	10740	10995	11015	11063	11875	11997	12878	13079	13079	13185	13413	13413	13528	13766	14231	14273	14456	
	Probe SEQ ID NO:	9414	9455	9525	9582	 9696	9820	432	812	812	1079	1090	1150	1982	2108	2951	3154	3154	3262	3496	3496	3614	3855	4334	1	4564	

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Table 4
Single Exon Probes Expressed in Heart

		T			abla				T	T	Ţ	T	1				T		ã		Ī	T	T	T	T	T	T	T		7	T	195		ſ
Liver Topics Lypressed III real	Top Hit Descriptor	ov45c04.x1 Sogres testis NHT Homo saniens clina clina MACE: 48403623	045604.x1 Soares testis NHT Home seniers that And And And And And And And And And And	PM0-HT0339-200400-010-D02 HT0339 Homo saniens c DNA	APOLIPOPROTEIN A-IV PRECIPEOR (APO. ANA)	AV685870 GKC Homo septiens of DNA close CKCONAE44 ET	284401.rf NCI CGAP GCB1 Homo sepiens cDNA clane IMAGE: 700345 F.	Homo saplens KVLOT1 gene	Ebstein-Barr virus (AG876 isolate) 1/2-182 domain encoding mucles and the EDNAS	Epstein-Barr virus (AG876 Isolate) 112-182 domain encoding muclear analysis EDNAC	COLLAGEN ALPHA 1(VII) CHAIN PRECIESOR /I ONG-CHAIN COLLAGEN / COCH A CENT	Mouse nucleolin gene	Homo saplens T.cell Ivmphoma invasion and motochasic 4 (TIAMA) DAIA	vd93a11.r1 Soares fetal liver spleen 1NFI S Homo capiens ANA Alone 144 Activities and an analysis and a special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special specia	0V3-NN1024-260400-171-015 NN1024 Home parisms of NNA	Human dene for faurth somafostatin recentor subtance	Homo sapiens 959 kb conflo between AMI 1 and CBR1 on chromosome 214.22	Year :	rruno sapiens XZS region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR)	CDM protein (CDM), adrenoleukodystrophy protein >	Human 1RPM-2 protein gene, exons 1,2 and 3	Homo sapiens partial steerin-1 gene	Homo saplens exostoses-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds	V.carteri gene encoding volvoxopsin	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA. complete cds	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds	Thermotoga neapolitana alpha-1.6-galactosidase (aqlA) gene complete ede	Thermotoga neapolitana alpha-1, 6-dalactosidasa (adiA) gana, complete ede	RC1-CT0279-181099-011-a09 CT0279 Homo seniens cDNA	RC1-CT0279-181099-011-a09 CT0279 Homo sanions clinia	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA	#73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:22464463' similar to TR:Q26195 Q26195	PVATGENE.; AV750040 MDS Ummannim DNA. 1 MAGGET	TO PRESENT A CARDINA CARDINA CARDINA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA CARDA
יופור באסון ו וסאם סופוי	Top Hit Detabase Source	EST HUMAN	Г	Т	Τ	L	Т		E		SWISSPROT	Г		T HUMAN	Т	L	Т											IN IN	EST HUMAN R	EST HUMAN R	Т		EST HIMAN A	
	Top Hit Acession No.	1.0E-03 AI073485.1	1.0E-03 AI073485.1		046409	1.0E-03 AV685870.1	=	1.0E-03 AJ006345.1	1.0E-03 K03332.1			-	11526176 NT	1.0E-03 T87761.1	1.0E-03 AW902585.1		1.0E-03 AJ229042.1					-	2.1				-		1.0E-03 AW362393.1	1.0E-03 AW362393.1	1.0E-03 BE170859.1	4 DE 03 AIE02047 4		
	Most Similar (Top) Hit BLAST E Value	1.0E-03	1.0E-03	1.0E-03	1.0E-03   O46409	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03 Q02388	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03		i i	1.0E-03	1.05-03	1.0E-03	1.0E-03	1.0E-03 Y11204.1	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03 /	1.0E-03 /	1.0E-03	4 05 02	1 0F-03/	
	Expression Signal	1.78	1.78	6.23	16.98	0.93	2.03	3.06	2.01	2.01	1.69	4.08	8.56	1.32	1.4	24	1.37			3.53	3.13	5.35	239	1.4	4.27	4.27	1.85	1.85	22.37	22.37	2.44	2 60	3.4	;
	ORF SEQ ID NO:	24388	24389		24649	24747	24946	25042	25096	25097	25397			25842		26259				70037	2027	26707	/9997		27345	27346	27602	27603	28196	28197	28268			•
	Exon SEQ ID NO:	14603	14603	_	14883	· 14971	15173		15269			15577	15668	15730	15763	16108	16281		6000	10502	3	9100	/202	17052	17150	17150	17392	17392	17947	17947	18021	18083	18370	
	Probe SEQ ID NO:	4717	4717	4718	6009	5103	5250	5317	5349	5349	5423	9999	27.28	5824	5857	6242	6419		000	0300		200	8/6	7175	12/3	7273	<u>¥</u>	754	8056	8056	8133	8198	8497	

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Single Exon Probes Expressed in Heart	Top Hit Descriptor		Refus norvegicus transformation related protein 63 (Trp63), mRNA	repetitive element: CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Ak-	601468878F1 MILI MCC 671	Himen patingking.	APOLIPOPROTEIN A.IV PRECLIPSOS (150 Complete cds	Glycyrthiza glabra Gobast mBNA 6	Xlaevis mRNA for C4SR protein	y/1/2h/10,r1 Soares fetal liver spleen 1/1FT S Home	LINE-1 REVERSE TRANSCRIPTASE HOMOLOGICAL CONTROL (MAGE: 126691 5)	Homo saplens prion protein (PrP) gene, complete cols	#24c10.s1 Soares_fetal_heart_NbHH19W Home carplane_ching_1	th85s08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:3778743'	Homo saplens CYP17 gene, 5 end	Homo sapiens prion protein (PrP) gene, complete cds	Homo sapiens chromosome 21 segment HS21C010	Homo saplens chromosome X open reading frame R (OXODER)	wg36f09.x1 Soares NSF F8 9W OT PA P S1 Homo sepiens cDNA clone IMAGE:2367209 3' Homo sepiens Bruton's tyrosine kinase (PTK) I L L L L L L L L L L L L L L L L L L	(L44L) and FTP3 (FTP3) genes, complete cds	HSC28A072 normalized infant brain cDNA Homo saplens cONA	CM1-BT0614-110300-142-b12 BT0614 Home saniens CDNA	1913c06.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE 2220.g.	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1) mRNA	W10a11x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3/	num sapiens epsilon-1 pseudogene (IGHEP1) gene, 6' flanking regime.	riomo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking molen	nomo sapiens CCR8 chemokine receptor (CMKBR8) gene Complete Ad-	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRITATORE TO THE	UKFZp586M2024_r1 586 (synanym: hute1) Homo sapiens cinna clara clara pizzz.	RCZ-BN0120-250400-012-h11 BN0120 Homo sablens CDNA	Homo sapiens 959 kb contig between AMI 1 and CBR1 on chromosome 34, 25	U-H-Bi0-aab-e-09-0-Ui.s1 NCI_CGAP_Sub1 Homo sapiens cDNA chare INA CE 22222	NOCLEUSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
igle Exon Pro	Top Hit Database Source		2	EST HUMAN	EST HUMAN	Į.	SWISSPROT	N	LN L	EST_HUMAN	SWISSPROT	LN	EST_HUMAN	EST HOMAN		IN.			HUMAN	ヿ	$\neg$	T	HOMAN	T CHANNE	NAME IN	7		100000	Т	7	LO TOWAN	- 1	SWISSDOT N	7
Sin	Top Hit Acession No.		9507208 N	Al347355.1	1.0E-03 BE780572.1	.11910.1	208727	03.1						- - -		٤	1005470	210001			T	T	600588R						6	1 -		-		
	Most Similar (Top) Hit BLAST E Value	4 05 00	20-10:1	1.0E-03 AI3473	1.0E-03	9.0E-04 L.11910.1	9.0E-04 P06727	9.0E-04	8.0E-04 X96469	9.0C-04 K0/008.1	8 OF 04 130487	8 0F-04 A	8 0E-04 A1574000 4	7.0E-04   41825	7 0F-04   12048F	7 0F.04 At 18924	7.0E-04	7 0F-04 A178039	7 OF 04 HT005	7.0E-04 0780Z7.1	7.0F-04 RE077044 4	7 0F-04 D47226 4	7.0E-04	6.0E-04 AI862525	6.0E-04 K01315.1	6.0E-04 K01315.1	6.0E-04 U45983.1	6.0E-04 P4640R	6.0E-04 At 048507	6.0E-04 BE005850	6.0E-04 A.1229042	6.0E-04 AW01384	6.0E-04 Q01768	
	Expression Signal	1 95		2.15	4.2	0.81	1.56	1.42	1.39	4.2	230	2.08	2.16	1.61	1.13	3.28	1.03	2.24	3.2	2.61	3.29	2.72	3.28	1.34	0.85	0.85	3.28	4.35	3.13	2.24	2.07	6.32	2.45	
	ORF SEQ ID NO:	25287			1	24/03		1	23548		24332			21562	22127	22437	22965	-		28973				23576	23680	23681	23769			27887	28881	28950		
	SEQ ID NO:	1 19108	40003	上		L		L	L	13989		. }	- 1					15828	18663	18683	19155	19300	19321	13788	13905	CD82	13992	16470	17583	17650	18593	18664	18714	
	Probe SEQ ID NO:	9491	0517	9626	5131	5485	7564	1472	3843	4089	4656	8485	8616	1786	2350	2682	3243	2823	8851	8871	9558	9790	9813	) kg	3000	2000	4092	2000	7733	000 000 000 000 000 000 000 000 000 00	8//8	8852	8306	

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Table 4

<u> </u>	NOT HYPOTHETICAL 29.3 KD PROTEIN (ORF92)  IAN QV6-CT0225-021099-030-a07 CT0225 Homo saplens cDNA  IAZ7e11.s1 NCI_CGAP_Cor1 Homo saplens cDNA  IPPDEÜÜve element:					
rgle Exon Pr Top Hit Database Source Source EST_HUMAN	SWISSPROT EST_HUMAN EST_HUMAN	NT EST_HUMAN NT	EST HUMAN EST HUMAN EST HUMAN	NT HUMAN EST HUMAN EST HUMAN EST HUMAN NT	EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN SWISSPROT	NT EST_HUMAN EST_HUMAN
l ä IImi	5.0E-04 AA548931.1	5.0E-04 AF248054.1 5.0E-04 AA156080.1 5.0E-04 M23604.1		5.0E-04 AF248054.1 NT 5.0E-04 AA568513.1 ES 5.0E-04 AW241666.1 ES 4.0E-04 U327482.1 ES		4.0E-04 AF281074.1 NT 4.0E-04 AV696624.1 ES 4.0E-04 AA576331.1 ES
Expression Signal 2.26 1.49	1.42	2.19 5.72 13.6	5.67 1.45 4.69	17.6 2.27 1.46 1.13	1.57 3.92 1.68 1.19 2.73	2.75
ORF SEQ ID NO: 26170 20385	23085	25113 26026 26387	26710 27412 27606	25113	20606 20607 21218 21823 22348	23900
Exan SEQ ID NO: 19598 19421 10672	L 1 1	15281 15901 16227	16519 17213 17394 18220	15281 19530 19413 10333 10592	10756 10756 11354 11928 11976 12457	
Probe SEQ ID NO: 9225 9958 635	3367	596 5996 6364	6639 7345 7543 8343	8950 9164 9944 386 657		3316 1

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Single Exon Probes Expressed in Heart

	<del></del>	_	_				_	_		-	_	٠,			_,		_,											_	
Top Hit Descriptor	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECI IDSOR / JULIANANI	2061c08.s1 Stratagene muscle 937209 Home sexions of NA Jane 1846 Chicagos of	601345895F1 NIH MGC 8 Homo septiens cDNA clane IMA CE-26280A F1	yy78b10.s1 Soares_multiple_sclerosis_2NbHMSP Homo septens oDNA clone IMAGE:279643 3' similar to	W39e12r1 Spares melancade 2NhHM Home contract CDNA -1 1/14 Springs -	ov87h03.s1 Soares testis. NHT Homo septems CDNA clare IVA CE.264142 5	Mus musculus neuropiiin-2/a17) mRNA alternativaly colliced complete car.	Homo sapiens SMARCA4 isoform (SMARCA4) gene complete cuts alternative.	FORMIN (LIMB DEFORMITY PROTEIN)	DKF2p761J221 11 761 (synonym: ham/2) Horne cantans cDMA close DKEZ-zes toos m	180 KD SECRETORY PHOSPHOLIPASE 42 RECEPTOR DRECLIDSON ON AS BY	Human short chain acid CoA dehivdirreness areas exercised and a	th 23a02 x1 NCI CGAP Pr28 Home saniens chive clone INACE 2446062 2	INTERNALIN B PRECURSOR	GLUTAMATE DEHYDROGENASE 3 PRECLIBSOB (GRU)	Homo sabiens Xa oseudosurbscome regions sciences 419	PM0-HT0339-190200-007-012 HT0339 Home continue continue continue	QV3-DT0045-221299-046-409 DT0046-Home continue DNA	V. carteri gene encoding volunoscein	Homo sapiens chromosome 21 segment HS21 Cha1	Homo saplens chromosome 21 segment HS21Cn78	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FIGER A)	2x48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471.5' similar to gb:M82762 VACUOLAR ATP SYNTHASE 16 KD PROTECI IDID SURI INIT (HI IMAAN).	el 24905.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN TA (HUMAN)	nc38e04.r1 NCL_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains 1 1 21 1	repetitive element;	Homo sapiens mRNA for KIAA0749 protein partial cds	DKFZp547L185 r1 547 (synonym: hfbrt) Home saniers cDNA clara DKE7-5471 4 mm m	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Т	Т	Г	TN	SWISSPROT	EST HUMAN	Т	Γ	EST HUMAN	Т	SWISSPROT	Т	T HUMAN	Т	Т		IN	SWISSPROT	EST HUMAN	EST HUMAN		THUMAN	F	EST HUMAN	
Top Hit Acession No.	4.0E-04 AA576331.1	4.0E-04 AA086324.1	4.0E-04 BE560660.1	4.0E-04 N48313.1	4.0E-04 N25507.1	4.0E-04 Al025699.1	4.0E-04 AF022855.1	4.0E-04 AF254822.1	Q05860	3.0E-04 AL119426.1	P49259	3.0E-04 U83991.1	3.0E-04 Al399674.1	P25147		35.1	Γ			2	3.0E-04 AL163278.2	•	3.0E-04 AA454055.1	3.0E-04 AA781201.1		1	.1	3.0E-04 AL134483.1	-
Most Similar (Top) Hit BLAST E Value	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04 Q05860	3.0E-04	3.0E-04 P49259	3.0E-04	3.0E-04	3.0E-04 P25147	3.0E-04 P49448	3.0E-04	3.0E-04	3.0E-04	3.0E-04 Y11204.1	3.0E-04	3.0E-04	3.0E-04 P22607	3.0E-04	3.0E-04		3.0E-04/	3.0E-04/	3.0E-04/	2.0E-04
Expression Signal	2.75	1.28	3.72	0.0	1.62	2.79	1.44	1.52	1.84	3.04	2.22	1.27	1.16	3.37	3.63	1.18	4.5	0.85	1.34	4.82	6.88	3.49	1.42	3.66		2.33	4.32	2.01	1.18
ORF SEQ ID NO:	23901	24121	24661	24770		27655						20639			23581			24456			26166	28875	27780	28068		24908	25068		19957
Exan SEQ ID NO:	14128	14332	14893	14999	16849	17439	17512	19505	19479	10124	10160	10788	11707	13190	13793	13876	14597	14669	14924	15843	16026	16685	17555	17827	7070	19/20	19576	19361	10141
Probe SEQ ID NO:	4228	4437	5020	5132	6972	7588	7662	9526	2296	<u>8</u>	188	862	1810	3268	3882	3900	4711	4784	5052	5735	98	9899	7705	7977	2	8118	9483	9874	169

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Single Exon Probes Expressed in Heart

ייין ובמון	Top Hit Descriptor Source	UMAN AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'	Π	Human dystrophin gene		Т	Mus musculus 5' fanking region of Pib3 gene		Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1,	HIMAN APPERONS of Johnston front Control In 1874, IRY6, TRY7, TRY8, TCRB01, TCRB0181, TCRB0182,	JMAN OV2-BT0638-070500-194-kg7 RT0838 Home services ADNA	Т	Τ		T	HUMAN M01e11.11 Soares, pineal gland N3HPG Homo sapiens cDNA clome IMAGE-232558 B	Π	Danio rerio hagoromo gene, exons 1 to 6, partial cds	Г			Г		Τ	Solanum lycopersicum phytochrome F (PHYF) gene, partial cris	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete crts)
26		EST HUMAN	ΙΝ	Z	FST HIMAN		¥	EST HUMAN	<u></u>	EST HI	EST HUMAN	Z	EST HUMAN	Ι	EST_HUMAN	EST_HU	¥	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPI	SWISSPROT	N L	<u>L</u>	본	L N
,   	Top Hit Acession No.	2.0E-04 AU146707.1	2.0E-04 M86524.1	2.0E-04 M86524.1	2.0E-04/AI286021.1	2.0E-04 AL163203.2	2.0E-04 AF224268.1	2.0E-04 AA478980.1	r raceal in a dic	2.0E-04 000001.1	2.0E-04 BE082317.1	2.0E-04 U34374.1	2.0E-04 AW978441.1	2.0E-04 U01029.1	2.0E-04 H96265.1	H96265.1	2.0E-04 U09226.1	2.0E-04 AB037997.1	2.0E-04 AV654352.1	2.0E-04 AI690862.1	2.0E-04 AU121712.1	P08548	P54296	2.0E-04 U32444.2	2.0E-04 U32444.2	2.0E-04 AB026898.1	2.0E-04 AB026898.1
	Most Similar (Top) Hit BLAST E Value	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	TO C	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04 P08548	2.0E-04 P54296	2.0E-04	2.0E-04	2.0E-04	2.0E-04
	Expression Signal	2.15	4.49	4.49	4	1.99	1.44	1.29	7.7	-	2.53	86.0	0.78	4.61	1.27	1.27	1.31	1.7	1.8	1.68	2.5	11.07	1.6	1.33	1.33	1.19	1.19
	ORF SEQ ID NO:	20232		20664	•						23105	23138	23541		24249	24250		24630	25371	25381			26527	26708	26709	26890	26891
	Exon SEQ ID NO:			10815	11075	11081	11689	12024	12402	12885	13307	13334	13748	13953	14461	14461	14575	14866	16322	15331	16155	16352	16356	16518	16518	16698	16698
	Probe SEQ ID NO:	470	889	880	1162	1169	1791	. 2136	2528	2958	3389	3417	3837	4051	4569	4569	4689	4991	2403	24.1	6291	6493	6497	6638	6638	6819	6819

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Single Exon Probes Expressed in Heart	Top Hit Descriptor		7	7	7	Т		7			$\neg$	П		Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete con	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, (LAMP) renae, complete antigen, ORF K14, v-GPCR, putative phosphoribosyfformydlycinamidine synthaes, and 1 And	Kaposi's sarcoma-associated herpesvirus ORF 88 gene narifal Adv. and ODF GO.	latent nuclear antigen; ORF K14, v-GPCR, putative phosphoribosyformydrychemidine starkens.	New york of the Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee	Hours capailus UNA, chromosome 24q14, microsatellite TKY36	Homo serviens members out a minopeptidase P (XNPEP2) gene, complete cds	hwasha salvens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	hwafions of No. 100 Per Homo sapiens cDNA clone IMAGE:3176366 3'	SPLICEOSOME ASSOCIATED PROSPERS CONA clone IMAGE:3176368 3	#01f11.x1 NCI_CGAP_Gas4 Homo seriens chiva chest in a control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t	element,	Mouse alpha 1 type-IV collagen mRNA	AV647727 GLC Homo saplens cDNA clone GI CRBDDA 2/	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	From Saptens NAA0237 gene product (KJAA0237), mRNA
ngle Exon P	Top Hit Database Source		NI	ES - HOMAN	ES! HUMAN	EST HUMAN	Z	EST HUMAN	EST HUMAN	NAMUL I CE	SWISSPROT	EST HUMAN	EST_HUMAN	Z	N.		Ł	LZ	L	L'N	EST HUMAN	EST HUMAN	SWISSPROT		EST_HUMAN	NI	EST_HUMAN	SWISSPROT	
S	Top Hit Aces:	2 OE OA A Escapeas	2.0E-04 RE440909.1	2 0E-04 A A A SET TA		2.0F-04 A 1243213.1			£0.1	244000	10	4 OF 04 AMOGRA	5		1.0E-04 AF148805.1			Γ			Γ					Ţ		7662015	
	Most Similar (Top) Hit BLAST E Value	2 OE 04	20F-04	2 0E 04	205-04	20F-04	2 OE-04	2010	1.0E-04	4 OF 04 D44000	1 0F-04	100	1.0E-04 AW01384		1.0E-04		1.0E-04	1.0E-04 A	1.0E-04 A	1.0E-04 A	1.0E-04 B	1.0E-04 BE218833.	1.0E-04 Q62203	105.04	4 0E 04 N4 40 40 4	1 0F-04 M 14042-1	1 0E-04 AV0477	1.0E-04	
	· Expression Signal	2.29	1.46	171	6.14	1.88	5.57	294	0.98	243	3.87	3.87	2.97		3.24		3.24	1.67	1.29	129	1.15	1.15	1.04	-	1 78	108	0.85	1.56	
	ORF SEQ ID NO:	27054	27801	27828	28360		28762	28866	20516	20819	20855	20856		-	21374		21375	21594	22363	22364	22411	22412	22969	23376	23654	23675	24043	24671	
	Exan SEQ ID NO:	16859		17604		18387	18490	18582	10680	10976	11014	11014	11216	-	11515		11515	41/11	2469	12409	7707	7707	131/0	13589	13878	13898	14258	14901	
	Probe SEQ ID NO:	6982	7729	7764	8225	8515	8625	8726	750	1059	1098	1098	1310		1610		1510	200	DOO S	2855	2855	300	3541	3675	3971	3991		5028	

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	1	1				Т	-	_	$\neg$			_	_	_	_		_	_		_	_	_	_	_	_	_	_		_	_	_
Single Exon Probes Expressed in Heart	. Top Hit Descriptor	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu	Received and including the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the sec	RC3-CT020B-220595-011-E04-CT020B Homo sapiens cDNA	HUM072014F Himan foves child Home control of the Child in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont	HUM072014F Human foves cDNA Homo seniens CDNA Alma EST LIFERATION	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR	Hamo sapiens chromosome 21 sourcest U.S.4.Co.7	Dichostellim discolderm gene for TDEA completed	Hamp sapiens chromosome 21 serment HS21Cn04	Caenorhabdilis elegans Skoth homology m BNA Camples 3.	Rat cytomegalovirus Maastricht complete cons	EST78713 Placenta I Homo earliene CNN	EST04984 Fetal brain. Stratagene (rattions of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of	Homo sapiens sarcoglycan, epsilon (SGCE) mRNA	Homo sapiens chromosome X enem reading frame & (CVODER) DMA	Homo sapiens chromosome X open reading frame 6 (CXORES) mBNA	wb54h06x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA	Lisaniens flowented chromosoms & Hisalli &	H. Saplens flow-sorted chromosome 6 Hindlii frament 806 April 1	Homo sapiens monocytelneutronbil elastics inhibitor constitution	CONTACTIN PRECIJESOR (2) VOODBOTEIN OBJACT	CONTACTIN PRECIJESOR (GLYCOPPOTEIN CP. 133)	W50a11 of Spares fetal lives an local AVID ST	PM4-NNORGA 310300 001 410 NNIASE 11	C48-BINDING PROTEIN PRECLIPSON (ARB)	CAB-BINDING PROTEIN PRECIDEND (CABP)	ye28c12.r1 Stratagene Lung (#837210) Homo samians cONA class (MA CELLACORCE)	y59d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu	rependive element, contains L. I.Y. repetitive element;	MR0-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA clone (MAGE:487035 5'
Jie Exon Pro	Top Hit Database Source	EST HIMAN	EST HIMAN	EST HIMAN	EST HUMAN	EST HUMAN	SWISSPROT	LN	LZ	N	N P	Į.	EST HUMAN	EST HUMAN		N N	トフ	EST HIMAN	N	N-	N.	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT			Т	
	Top Hit Acession No.	AA279333.1	AW847445 1	AW847445.1	-			78.2	Γ			9845300 NT	7.0E-05 AA387612.1		10835046 NT	4885170 NT	4885170 NT	6.0E-05 A 655241.1	-		6.0E-05 AF053830.1				8			-		5	10.1
	Most Similar (Top) Hit BLAST E Value	8.0E-05 AA2793	7.0E-05 AW847	7.0E-05 AW847	7.0E-05	7.0E-05 L49075	7.0E-05 Q22949	7.0E-05	7.0E-05	7.0E-05	7.0E-05 U60980	7.0E-05	7.0E-05/	7.0E-05 T07095	7.0E-05	6.0E-05	6.0E-05	6.0E-05/	6.0E-05 Z84506.	6.0E-05 Z84506.	6.0E-05	6.0E-05 Q12860	6.0E-05 Q12860	6.0E-05 N72829	6.0E-05	6.0E-05 P08607	6.0E-05 P08607	6.0E-05 T94149.	6 0F-05 R75630	6.0E-05 AA04401	6.0E-05 AW8901
	Expression Signal	3.45	2.9	2.9	1.05	1.05	2.32	5.24	5.78	1.27	0.82	0.84	1.12	3.04	2.89	1.57	1.57	1.42	0.89	0.89	2.45	3.33	3.33	1.49	2.61	1.37	1.37	1.28	3.68	3.59	8.44
	ORF SEQ ID NO:		20118	20119		20303	20800			23953	24023	24506		27505		21766	21767	22309	22409	22410	20415	25599	25600	25879	26989	27437	27438	27558	28267	28911	25073
	Exan SEQ ID NO:	19589	10303	10303	10496	10496			13046	14175	14241	14723	- [	1	18374	118/4	11874	12418	12519	12519	10598	15519	15519	15761	16796	17234	17234	17354	18019	18621	19587
	Probe SEQ ID NO:	9911	344	344	555	555	1039	2686	3121	4276	4344	4842	2202	200	839	<u> </u>	138	2544	2652	2652	238	2002	5605	6855	89 18	2330	2330	\$	8131	8807	9534

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Most Similar   Top Hit Acession   Top Hit Signal   Top Hit Acession   Top Hit Acession   Detabase   Source   Value   Detabase   Source   Value   Detabase   Source   Value   Detabase   Source   Value   Detabase   Source   Value   Detabase   Source   Value   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detabase   Detab			_	_					_			_							_		_	_,	_				_	_	
Most Similar   Top Hit Acession   Detabase	hi94e08.x1 NCI_CGAP_Lu24 Homo saplens cDNA done INAGE:3009638 3' Homo saplens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA EST84475 Colon adenocarcinoma IV Homo saplens cDNA 5' end	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:7018413'	501567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2nl), mRNA	AV726630 HTC Homo saplens cDNA clone HTCCFAM 5	qh84c10.xf Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848458 3' similar to	Homo sapiens NOD1 protein (NOD1) gene, excris 1, 2, and 3	EST 79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein	EST79996 Placenta I Homo sapiens cDNA similar to similar to n53-associated amtein	PM1-HT0521-120200-001-e10 HT0521 Homo saplens cDNA	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA	SKELEMIN	601461463F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5;	601461463F1 NIH MGC 66 Home saplens cDNA clone IMAGE-3865443 57	contains Afu repetitive element contains element KER repetitive element;	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2605192.3'	hl38c07xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element;	Homo sapiens PP1200 mRNA, complete cds	Human renin (REN) gene, 5' flanking region	RETINAL-BINDING PROTEIN (RALBP)	RETINAL-BINDING PROTEIN (RALBP)	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3	Human MLC1emb gene for embronic myosin alkaline light obain 31 mb	Homo saplens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT) axxxx 4	Homo sapiens MEP1A gene, promoter region and exon 1	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA	7g28a08.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:33n7766 3	·
Expression Signal         Most Similar Top Hit Aces Signal         Top Hit Aces No.           Signal         Value         No.           1.54         6.0E-05 AW392086.1           1.63         5.0E-05 AW392086.1           1.63         5.0E-05 AW392086.1           1.63         5.0E-05 AW392086.1           2.99         5.0E-05 AV392086.1           2.99         5.0E-05 AV392086.1           2.96         5.0E-05 AV392086.1           2.96         5.0E-05 AV392086.1           3.47         5.0E-05 AV39208.1           4.58         4.0E-05 AW417580.1           4.6         4.0E-05 AW477580.1           4.6         4.0E-05 AW477898.1           5.0E-05 AW477898.1         3.0E-05 BF037898.1           1.28         3.0E-05 BF037898.1           1.28         3.0E-05 BF037898.1           6.89         3.0E-05 BF037898.1           1.19         3.0E-05 BF037898.1           0.91         3.0E-05 BF149773.1           0.84         3.0E-05 AA368679.1           0.97         3.0E-05 AA284041.1           1.54         3.0E-05 BA284049.1           1.54         3.0E-05 BA284049.1           1.62         3.0E-05 AA284049.1           1.62	T_HUMAN		Т	Т	Т		П	Т	1	Т	П	Γ	Г	Г	П	П		L	Z	SWISSPROT	SWISSPROT	EST_HUMAN	TN	LN	ĮN	i	EST_HUMAN	EST HUMAN	Top Hit Database Source
Expression (T Signal Blue)   1.54   1.54   1.54   1.54   1.63   1.63   1.63   1.28   1.28   1.28   1.28   1.19   1.19   1.19   1.19   1.154   1.154   1.154   1.154   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155   1.155	2.1 3912431 2.1	2.1	3E733157.1	11072102	1.0726630.1	N248061.1			9.1	1.1	7:			Γ	A1248061.1	1		5.1		P49193	P49193	AV653544.1	X58855.1	AJ251884.1	AJ251058.1	8923891	AW392086.1	BE858403.1	Aces lo.
Expression Signal Signal 1.54 1.637 1.637 1.637 1.637 1.637 1.637 1.28 1.299 1.094 1.28 1.19 1.19 1.19 1.162 1.65 1.65 1.65 1.65 1.65 1.65 1.65 1.65	3.0E-05 AW77098 3.0E-05 AA372562	3.0E-05/	3.0E-05	3.0E-05	3.0E-05/	3.0E-05	3.0E-05	3.0E-05/	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05/	4.0E-05	4.0E-05	4.0E-05	4.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	6.0E-05	Most Similar (Top) Hit BLAST E Value
G: 4 8888	1.65	1.62	2.23	1.54	76.0	0.84	0.85	1.19	1.19	6.89	6.89	0.91	1.28	1.28	0.84	2.17	4.6	7.17	4.58	3.47	2.96	3.46	9.01	2.99	0.88	1.63	14.37	1.54	
통 <u> </u>	27225 27228 27447	26935	26677	25382	24786	20417	24197	24046	24045	23965	23964	22442	20871	20870	20417		28286		·			25652	25165	23593	22550		21141		ORF SEQ ID NO:
<u> </u>	17031 17035 17242	16742	16491	15332	15018	10599	14412	14261	14261	14184	14184	12553	11030	11030	10599	18989	18038	17356	10193	19173	19173	15559	15311	13807	12760				Exon SEQ ID NO:
Probe SEQ ID NO: 1382 1382 1382 1382 2831 2831 2831 2831	7154 7158 7373	7154	9811	5412	5151	4731	4519	4365	4365	4285	4285	2688	1115	1115	665	9287	8150	7486	2776	9590	9326	5646	5392	3897	2831	1819	1382	9965	Probe SEQ ID NO:

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Single Exon Probes Expressed in Heart	Top Hit Descriptor		Wg36f09-x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3' qh98e11-x1 Soares_NFL_T_GBC_S1 Homo sapiens_DNA_H_HABC_S1	MER3.b2 MER3 repetitive element;	Human adenosine deaminase (ADA) gene, complete cds	contains Alu repetitive element; ontains element 1 repositive classes.	RC3-BT0319-120200-014-H08 BT0319 Homo sabiens cDNA	Homo sapiens p47-phox (NCF1) gene, complete cds	H.sapiens DNA for endogenous retroviral like element	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV	UK-Zp566l084_r1 566 (synonym: hrkd2) Homo sapiens cDNA clone DKFZp566l064 5' qq13a08.x1 Soares_NhHMPu_S1 Homo saniens cDNA clone MAACE and a clone MAACE and a clone was a constant and a clone was a constant and a clone was a constant and a clone was a constant and a clone was a constant and a clone was a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and 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a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a cons	MER18.b3 MER18 repetitive element;	601236455F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE 3608682 E	Homo sapiens SCL gene locus	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	nw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE-1228E46 91	P. falciparum mRNA for AARP1 protein, partial	พน35ัท07-x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'	Heterodonfus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA8) HoxA5	(HoxA1) genes, complete cds	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7) HoxA6 (HoxA8) United the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5	Man Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme Land Comme 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State State State State State State State State State State State State State State State State State State State State State State State State State State State State State	RCS-HT0582 Jonaton 245 Feb. 18 Colon NHCD Homo sapiens cDNA clone IMAGE:2522077 3'	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:012832	TOUR OF TOURIN HEFY
le Exon Prot	Top Hit Database Source		ES I HOMAN	EST HUMAN	Z	EST_HUMAN	П			N. Cort	T	コ	HUMAN		Т	HOMAN	П	ESI_HUMAN				T HIJMAN		ESI HUMAN W	EST HUMAN	Т	EST HUMAN R	_	
Sinc	Top Hit Acession No.	3 0F 05 Alzenso4 4		2.0E-05/AI286021.1			2.0E-05 BE066036.1		]	,			4/1.1	T	2.0E-03 AJU11/12.1		T		F224262.1 NT		=224262.1 NT								1
	Most Similar (Top) Hit BLAST E Value	3 0E DE	100	2.0E.05		2.0E-05/	2.05-03	2 OF OF Venny	2 0E-05 X05465 4	2.0E-05/4	20 20 0	205.05	2.0E-05 BE378	20000	2.0E-03 A	2 0E-05 V08028 4	2 0E-05 A 100402E 4	7	2.0E-05 AF224262.1		20E-05 AF224262 1	2.0E-05 AI381040.1	2 OF OF NA47EA	20	2.0E-05 N41751	2.0E-05 AK	2.0E-05 BE175801.1	2.0E-05 BE348229.1	
	Expression Signal	3 15	F	302		7.21	760	1.14	-	0.85	8	1 00	0.84	140	2.19	2.19	8 04		2.21		2.21	2.3	2.45		2.45	2.42	2.93	2.98	
	ORF SEQ ID NO:		2205B	22302		22824	23027	23050			24191	-	24453	25502	26022	26108			26260		26261	28671	28116		28117		28141	_	
	Exan SEQ ID NO:	17421	12160	j .		12546	L	13243	13366	13649	14403	14480	14666	15438	15898	15972	15983	-	16109		16109	16483	17874	4702,	4/8/1	15983	17897	19514	
ŀ	Probe SEQ ID NO:	7570	2276	2538	2004	3098	3304	3323	3449	3737	4510	4592	4782	5520	5993	6125	6136		6243		6243	6603	8024	7000	1700	803	8/48	9335	
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Table 4
Single Exon Probes Expressed in Heart

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יישנים דייטון נספסס דייטון נספסס דייטון נספסס דייטון נספסס דייטון נספסס דייטון נספסס דייטון נספסס דייטון נספסס דייטון	Top Hit Descriptor	xa89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element:	Homo sapiens ABCA1 (ABCA1) gene, complete cds	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5	Homo saplens chromosome 21 segment HS210082	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene partial cite	MOSAIC PROTEIN LGN	Homo sapiens chromosome 21 segment HS21C003	zw69g04.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:781494 5'	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens Spast gene for spastIn protein	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.tf L1	L1 repairuve element;	noting september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the	52 KU KU PKOTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	Homo sapiens chromosome 21 segment HS21C027	2x35h12.s1 Soares, total fetus Nb2HFB_9w Homo saplens cDNA clone IMAGE:788519 3' similar to gb.102932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HI MAAN).	2805e11.r1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMACE:684332 5' similar to contains Alu	In H. Blanks 08.01 II st NOI COAD Site 1	UI-H-BI2-gark-a-08-0-UI ST NOT CGAP Suh4 Homo sanians of NA Alma IMA CE:2724306 3	ha07c10.x1 NCI_CGAP_Kid12 Homo saplens cDNA done IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element;	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and socilar phosphate fransporter (NDT3) rans.	tf73a06.x1 NCI_CGAP_HSC3 Hamo saplens cDNA clone IMAGE-2246386.3	
an How ord	Top Hit Database Source	EST HUMAN	Τ	T HUMAN		TN	ISSPROT	N.	Г	T_HUMAN		TN.		HOMAN		ISSPROI	Z	EST HUMAN		EST HIMAN	T	T	TN )	ŢN	T_HUMAN	Τ
	Top Hit Acession No.	2.0E-05 AW074604.1			2.2			1.0E-05 AL163203.2		34.1		1.0E-05 AJ246003.1	;	1.0E-05 AA04 1040.1 1.0E-05 AA04 1040.1	100000	,	1.0E-05/AL103227.2	1.0E-05 AA452578.1	. 5		1				-	
	Most Similar (Top) Hit BLAST E Value	2.0E-05	2.0E-05	2.0E-05	1.0E-05	1.0E-05	1.0E-05 P81274	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	10 10	1.05-03/	20 10	4 OF OF A1 4000	1.0E-09.1	1.0E-05	1 011 0 1	1 OF-05	1.0E-05/	1.0E-05/	1.0E-05 U91328.1	1.0E-05 U91328.1	9.0E-06 AI583811	
	Expression Signal	3.73	2.25	1.81	1.61	1.67	9.24	1.09	2.01	2.15	4.46	1.42	7 10 0	9.34	2	0.0	4.10	2.48	4,	12	1.2	1.78	2.2	22	6.59	
	ORF SEQ ID NO:			25257							,	26082	264.70					27312	27420		27779		28414	28415	22398	
	Exon SEQ ID NO:	19677	19503							$\perp$	- 1	15952	15003	1	ı		2	17117	17220		,	17701	18170	18170	12504	
	Probe SEQ ID NO:	9442	9486	9637	2663	3599	3886	4082	4180	4742	4882	6049	6244	6213	6577	7469	3	7240	7352	7704	7704	7851	8291	8291	2637	

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Single Exon Probes Expressed in Heart

	·			::16569123' similar to		DOWN-REGULATED	DOWN-REGULATED						similar to contains		contains Alu repetitive							:1655738 3' similar to				A		l) gene, complete cds
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Human elanine-dlynoxidate aminotransference (ACVT)	Homo sapiens differentiation antinen CD20 mans aways 6.8	©20g01.x1 Soares_fetal_fiver_spleen_1NFLS_S1 Homo saplens cDNA done IMAGE:1656912.3' similar to contains the remailing a company.	Homo sapiens chromosome 21 segment HS31Ch00	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)	Human anolinonrotein E (APOE) sems honotte soutes :	PUTATIVE SERINFTHREONINE DROTTEIN KINASE CONT.	RC3-C10282-201400-014-614 CT0389 LOSS - CASE 12,14C	ANKYRIN 1 (FRYTHROCYTE ANKYBIN)	JANKYRIN 1 (ERYTHROCYTE ANKYRIN)	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains	Homo sabians KIAA0555 dana product (KIA VOESE) DNIA	qw16g09x1 NCI_CGAP_U3 Homo sepiens CDNA clone IMAGE:1991296 3' similar to contains Alu repetitive	EST90205 Thirold Home conjune aDNA Florid - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	OV2-OTORS2250A00-473-604 OTORS 11	601881527F1 NIH MGC 57 Home seminar about 1 1110 C	QV3-BT0379-010300-105-d11 BT0379 Home series child	QV3-BT0379-010300-105-d11 BT0379 Home seriens of NA	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to	Mis miscillis E-calketh hinding action 67 miscillis	III.5-UM0070-110400-063-002 I IM0070 Home contract - Chila	Homo sanians calcium channel unitario describility at	Homo sapiens chromosome 21 segment HS21 Chara	Himan ARI representational lateral at	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 67 and
gle Exon Pro	Top Hit Database Source	N L	Ā	EST HIMAN	N L	SWISSPROT	SWISSPROT	LN	SWISSPROT	EST HIMAN	SWISSPROT	SWISSPROT	EST HUMAN	L	EST LIMAN	EST HIMAN	FST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	EST HIMAN	TN	EST HUMAN	N-	NT	L L	EST_HUMAN
Sin	Top Hit Acession No.	9.0E-06 M61755.1	123416.1	A1034370.1	9.0E-06 AL163209.2	Q63769	263769	9.0E-06 U35114.1	210364	8.0E-06 AW362539.1	202357	202357	AA669729.1	7662177 NT	7.0E-06 Al368252.1	7.0E-06 AA385542 1		72.1		6.0E-06 BE069189.1		6.0E-06 A1040099 1			8157	5.0E-06 AL163246.2		1.1
	Most Similar (Top) Hit BLAST E Value	9.0E-06	9.0E-06 [23416.	9.0E-06 Al03437	9.0E-06	9.0E-06 Q63769	9.0E-06 Q63769	9.0E-06	9.0E-06 Q10364	8.0E-06/	8.0E-06 Q02357	8.0E-06 Q02357	7.0E-06 AA6697	7.0E-06	7.0E-06	7.0E-06/	7.0E-06 AW883	7.0E-06	6.0E-06	6.0E-06	6.0E-06 Q01456	6.0E-06.A	6.0E-06	6.0E-06	6.0E-06	5.0E-06	5.0E-06	5.0E-06 AA313620
	Expression Signal	2.94	2.58	10.24	1.16	2.81	2.81	4.58	3.35	1.55	2.24	2.24	1.7	3.19	99.9	0.85	5.73	5.39	1.09	1.02	1.77	2.01	1.46	1.88	1.8	3.58	1.98	6.9
	ORF SEQ ID NO:		25591	26611	27004	27257	27258	27394	28434	22251	29087	29088		21191				24900	22607	23336	22637	24328	24979		26195	25706	25843	27907
	Exon SEQ ID NO:	13473	15513	16428	16809	17069	17089	17193	18186	12722	18796	18796	10886	11326	12772	13432	15412	19698	12814	13549	12838	14539	15203	17520	19377	15604	15731	17667
	Probe SEQ ID NO:	3559	5599	6570	6931	7192	7192	7317	8309	2483	8992	8992	8	1420	2844	3516	5493	9072	2887	3835	4647	4663	5281	7670	9900	5695	5825	7817

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Top Hit Descriptor  HA0977 Human fetal liver cDNA library Homo sapiens cDNA ya48c371 NG CGAP_STATE than the first and the form sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element, contains L1 repetitive element; xc69g12.x1 NGI_CGAP_Exc2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element, contains element MER21 repetitive element; trisca63x1 NGI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' trisca63x1 NGI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' trisca63x1 NGI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' trisca63x1 NGI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' trisca63x1 NGI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2710425 3' Gallus gallus bank2 protein (Dach2) mRNA, complete cds tl-3-C10214-150200-074-Br03 CT0214 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element tl-3-C10214-150200-074-Br03 CT0214 Homo sapiens cDNA clone IMAGE:2432663 3' similar to contains to sapiens mRNA, chromosome 21 segment HS21C079 Homo sapiens nRNA, chromosome 1 specific transcript KIA40486 zi34008.s1 Soares_fetal_ilver_spleen_1NFIS_S1 Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains L1.11 L1 repetitive element; Homo sapiens process tetal_ilver_spleen_1NFIS_S1 Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains L1.11 L1 repetitive element; Homo sapiens process tests investment; trip trapetitive element; homo sapiens process tests investment; trip trapetitive element; trapetitive element; trapetitive element; trapetitive element; trapetitive element; trapetitive element; trapetitive element; trapetitive element; trapetitive elemen	Top Hit Database Source Source EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST H	Acession 40. 40. 40. 40. 41. 41. 41. 41. 41. 41. 41. 41. 41. 41	Most Similar (Top) Hit BLAST E Vatue 5.0E-06 Al06504 4.0E-06 R16267. 4.0E-06 Al033492 4.0E-06 Al033492 4.0E-06 Al033492 4.0E-06 Al033492 4.0E-06 Al033492 4.0E-06 Al033492 4.0E-06 Al033492 4.0E-06 Al03379 4.0E-06 Al03279 4.0E-06 Al03279 4.0E-06 Al03279 4.0E-06 Al03279 3.0E-06 Al032779 3.0E-06 Al0329 BE04709 3.0E-06 BE04709 3.0E-06 BE04709 3.0E-06 BE04709 3.0E-06 BE04709 3.0E-06 BE04709 3.0E-06 SX54816.1 3.0E-06 X54816.1 3.0E-06 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 BE04709 X54816.1 3.0E-06 B008549	Signal Signal Signal A.74 A.41 A.41 A.41 A.41 A.41 A.41 A.41 A.4	26204 20380 20380 20805 21074 21075 21075 21075 21075 21076 24504 24504 21805 21805 21805 21805 21805 23413 23412 23413 234146	<del></del>	SEQ ID NO: NO: NO: 1312 1448 2218 3025 3819 3716 3716 4461 4461 6290
RC0-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA	EST HUMAN	62.1	3.0E-06 AW3852	4.17		19110	26.00
CO-LT0001-261199-011-A03 LT0001 Homo sapiens CDNA	Г	62.1	3.0E-06)	4.17		19110	휲
INEST REVERSE I RANSCRIPTASE HOMOLOG	7		20.7		$\dagger$	10440	ţ
18.10	100000		1 20 E	4 85		16154	290
lomo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N- eminis )		-	3.0E-06	4.31	24146	14355	194
spetitive element	1	1 50,200.1	9.VE-7VC	2.0	-		†
b78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1		TEASER	10 c	0	24053	14272	78
q64d12.x1 NCI_CGAP_HN13 Hamo sapiens cDNA clone IMAGE:3124151 3'	$\neg$	ł	3.0E-06	1.20	23413	9000	╛
q64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'	•	-	3.05-06	7.20	234.12	13020	<u> </u>
INE-1 LIKE PROTEIN ;contains L1.t2 L1 repetitive element;	7		3.0E-06	2.14		73151	at:
422a05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734							
TR1 repetitive element;		8.1	3.0E-06	0.95	-	12818	티
k48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains I TR1 ra							
Iomo sapiens PP1200 mRNA, complete cds		5.1	3.0E-06	1.37		12105	8
contains L1.11 L1 repetitive element;	HUMAN	2.1	3.05-06	1.27	21802	ולחמס	Ξţ
334b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to					2000	0000	1
contains L1.11 L1 repetitive element;		AA700562.1	3.0E-06	1.27	21904	12006	딜
134508.s1 Soares fetal liver spleen 1NFLS S1 Homo saniens cDNA clare IMAGE: 423662 21-11-14						7	
fomo sapiens mRNA, chromosome 1 specific transcript KIAA0486			4.0E-06	3.74	28139	_i	₹ 1
Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region			4.0E-06	3.1		1	2
dano sapiens chromosome 21 segment HS21C079			4.0E-08	1.02			3
AER22 repetitive element;	T HUMAN	9.1	4.0E-06	1.58			Į
vl94c10.x1 NCI_CGAP_Brn25 Homo saplens cDNA clone IMAGE:2432562 3' similar to contains element							- {
L3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA	П	AW848295.1	4.0E-06	1.78	23520	_ i_	魺
3allus gallus Dach2 protein (Dach2) mRNA, complete cds			4.0E-06	1.39		_1	g
JI-H-BI0-eat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo saplens cDNA clone IMAGE:2710425-3'		AW015401.1	4.0E-06	1.22			2
2V2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA		BF365612.1	4.0E-06	2.23			8
b33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'		Al334928.1	4.0E-06	5.18		$\perp$	312
b33e09.x1 NCI_CGAP_HSC2 Homo saplens cDNA clone IMAGE:2056168 3'		Al334928.1	4.0E-06	5.18			312
epetitive element; contains element MER21 repetitive element;		AW 103354.1	4.0E-06				828
c69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu							
epetitive element; contains L1 repetitive element;		R16267.1	4.0E-06			10568	8
PA48c03:r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5 similar to contains Alu			1			į	
-1A0877 Human fetal liver cDNA library Homo sapiens cDNA	7	AI065045.1	5.05-06				8
	7		Vælue				Ì
Top Hit Descriptor	Top Hit Database Source		Most Similar (Top) Hit BLAST E Vatue	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	8 ℃ ∴

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1550	11455		6.27	2.0E-06 P21414	P21414	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)
000		00,00		100			wa04s03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA done IMAGE:2297068 3' similar to contains MER30.b1
2326			2.95	2.0E-06	2.0E-06 AI672138.1	EST_HUMAN	WER30 repetitive element;
2418			2.14	2.0E-06 P04929	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2519			2.69	2.0E-06 P06719	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3475		23196	1.11	2.0E-06	2.0E-06 AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3700		23398	1.5	2.0E-06	2.0E-06 AA173518.1	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5
3710	13623	23406	1.5	2.0E-06	7.	N-	Mus musculus gene for odorant receptor A16, complete cds
5878	15784	25904	5.08	2.0E-06,	2.0E-06 AI819424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7136	17013	27206	1.65	2.0E-08	H62051.1	FST HIMAN	w37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN TYPE II CYTOSKEI ETAL 8 (HI MAN)
9403	19699	24901	1 25	SOF DR	2 AE-AR D23240	CMISSEDAT	PROTEIN MOWAD
		Ĭ		200	CT-202	DATE OF THE O	
9548	19148		2.46	2.0E-06	2.0E-06 BE328232.1	EST_HUMAN	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE.3144699 3' similar to contains L1.t2 L1 repetitive element;
3	10018	19813	1.9	1.0E-06 O76082	076082	TORGESIWS	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH- AFFINITY SODII M-DEPENDENT CARNITINE COTRANSPORTED)
641	L	L	161	1.0E-06	54.1	LN	Mis misculus DRMMSE richain (DRMm5a) mBNA complete cle
1435	١		222	1.0E-06 P09125		SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1507	11412	21271	1.09	1.0E-06,	78.2	NT.	Homo sapiens chromosome 21 segment HS21C078
							zi06a12.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to
1554	11459	21317	0.93	1.0E-06	1.0E-06 AA034141.1	EST_HUMAN	contains Alu repetitive element;
1554	11459	21318	0.93	1.0E-06/	1.0E-06 AA034141.1	EST HUMAN	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982.3' similar to contains Alu repetitive element:
1565	11470		1.2	1.0E-06 P27625	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1949		21729	4.74	1.0E-06	1.0E-06 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1949	11844	21730	4.74	1.0E-06	1.0E-06 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4273	14172	23949	11.11	1.0E-06	1.0E-06 U07561.1	LΝ	Human ABL gene. expn 1b and infron 1b and entative MRR04 Met protein. (MRR04 Met) and commetee.
5043	14915	24688	1.38	1.0E-06/	25	NT	Homo sapiens chromosome 21 segment HS21C085
5043	14915	24689	1.38	1.0E-06/	1.0E-06 AL163285.2	TN	Homo sapiens chromosome 21 segment HS21C085
5233	15157	24925	4.69	1.0E-06	1.0E-06 BF333015.1	EST HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
6107	16001	26139	6.11	1.0E-06 P02671		SWISSPROT	FIBRINOGEN ALPHAALPHA-E CHAIN PRECURSOR
6813	16692	26881	1.16	1.0E-06	1.0E-06 Al347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAPCos Homo sapiens cDNA clone IMAGE:1926842.3'

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Table 4
Single Exon Probes Expressed in Heart

			_		_				_	_		_		_	_		_														_
	Top Hit Descriptor	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MR repetitive element	Homo saciens show gene alternatively enlined products complete and	Homo sapiens show gene, alternatively colliced products, complete cos	2017e08.r1 Stratagene colon (#937204) Homo septiens CDNA claracting in AGE 682437 21	2004d11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA fone IMAGE:785493 3' similar to	Homo satisfies chromosome 21 segment DS24200	RC4NT0054-120500-012-h03 NT0054 Home seniors DNA	Homo sapiens ADP/ATP carrier profein (ANT.2) nene complete ade	Homo sapiens p47-phox (NCF1) gene, complete cds	Homo satiens 647-rhox (NCE-1) riene complete cdr	Homo sapiens alvairen 3 (GPC3) nene, pertial cute cute.	Homo sapiens alvoicen 3 (GPC3) gene wortigl Adv and Banking repeat regions	Homo sapiens chromosome 21 segment HS210A4	q/82g07.x1 Soares NhHMPu S1 Homo saniens c/DNA clane MACE-4878878 21	482407.x1 Spares NHHMPI S1 Home centers CDNA clothe INFACE: 1878876.3	POL POLYPROTEIN (CONTAINS: PROTEINS: DEVERSE TRANSCOCKET CONTAINS)	Homo saniens IIDP-dirigingsouthen-forms (1975)	EST05660 Fetal brain. Stratagene (rattorsons) Home conjunction (1978)	Homo sapiens chromosome 21 segment HS21Chan	Homo caniens mambrane introduction 4 conseq.	CM3-CT0277-221099-024-e11 CT0277 Homo sentiens CNA	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP218), complement component C4 (C48) G11, helicase (SKI2M), RD, complement component C4 (C48) G11, helicase (SKI2M), RD, complement component C4 (C48) G11, helicase (SKI2M), RD, complement component C4 (C48), G11, helicase (SKI2M), RD, complement component C4 (C48), G11, helicase (SKI2M), RD, complement component C4 (C48), G11, helicase (SKI2M), RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4, RD, complement C4,	(Bf), and complement component C2 (C2) genes.>	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION	7g94f07x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075920 075020	4F5L.;	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA	wh64f10.x1 NCI CGAP Kid11 Home sapiens cDNA circae IMAGE: 2385547 2	EST93615 Supt cells Homo sapiens CDNA 5' end	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3
21 11127 216	Top Hit Database Source	EST HUMAN	N.	N	EST HUMAN	EST HUMAN	L	EST HUMAN	N	NT	LN LN	NT	IN	TN	EST HUMAN	EST HUMAN	SWISSPROT	LN	EST HUMAN	IN	L	EST HUMAN		LZ	SWISSPROT		EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	11
}	Top Hit Acession No.	AI287878.1	U82668.1	J82668.1	AA132811.1	1.0E-06 AA449257.1	1.0E-06 AL163203.2	1.0E-06 AW890941.1	.78810.1	1.0E-06 AF184614.1	AF184614.1	9.0E-07 AF003529.1	9.0E-07 AF003529.1	9.0E-07 AL163281.2	1/288596.1	8.0E-07 AI288596.1	21414	VF135416.1		22	]	38.1		13.1				2.1	-	1.1	-
	Most Similar (Top) Hit BLAST E Value	1.0E-06 AI28787	1.0E-06 U82668.	1.0E-06 U82668.	1.0E-06 AA13281	1.0E-06	1.0E-06	1.0E-06	1.0E-06 L.78810.1	1.0E-06	1.0E-06 AF18461	9.0E-07	9.0E-07	9.0E-07	8.0E-07 AI288596	8.0E-07	8.0E-07 P21414	8.0E-07 AF13541	8.0E-07 T07770.1	8.0E-07 AL 16328	7.0E-07 AF16734	6.0E-07 AW8555		6.0E-07	6.0E-07 P41479		6.0E-07 BF001867	6.0E-07	5.0E-07 AI831893.	5.0E-07 AA38063(	5.0E-07 AI831893
	Expression Signal	1.53	3.72	3.72	4.86	3.73	1.52	4.81	2.99	1.84	1.84	1.49	1.49	2.38	4.49	4.49	7.45	7.89	7.2	4.15	0.94	2.36		241	1.65	1	1.35	1.81	3.55	2.9	0.87
	ORF SEQ ID NO:	27013	27647	27648	27676				25280	21729	21730	20134	20135	28708	24336	24337					21599	21641		22247	1	100	7/351		1		
	Exon SEQ ID NO:	16822	17433	17433	17460	17488	17839	18720	19077	11844	11844	10314	10314	18440	14547	14547	15504	16547	18703	18838	11719	11766	ç	12319	13802	474 ED	81.7	2005	10284	10959	12923
	Probe SEQ ID NO:	6944	7582	7682	7609	7637	7989	8912	9440	9536	9536	357	357	8572	4661	4661	5589	6667	8893	9055	1822	1870	5	2442	3891	7070	6171	2202	228	1041	2995

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Probe         Exm           SEQ ID         SEQ ID           NO:         NO:           A547         14440           6203         15963           6348         16211           7932         17782           8805         18618           8805         18618           8806         18618           8803         18675           9712         19556           3918         13827           7235         17712           8308         18185           8308         18185           8308         18185           8308         18185           8308         18185           8308         18185           8308         18185           8308         18185           8308         18185           8424         10379           2420         12297           2420         12297           2420         12297           4654         14540           4654         14871	10 ORF SEQ 10 ID NO: 10 ID NO: 11 26373 2 26095 2 26097 2 28021 2 28021 2 28021 2 28021 2 28031 2 28031 2 28032 2 28032 2 28032 2 28032 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Expression Signel Signel Signel 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.7	Most Similar (Top) Hit ABLASTE S.OE-07 AF149774 5.0E-07 A7393981. 5.0E-07 A7393981. 5.0E-07 A7393981. 5.0E-07 A7393981. 5.0E-07 A74933987. 5.0E-07 A74933887. 5.0E-07 A749338. 5.0E-07 A74938. 5.0E-07 A74938. 5.0E-07 A74938. 5.0E-07 A74938. 4.0E-07 A765528. 4.0E-07 A765528. 4.0E-07 A765528. 4.0E-07 A765528. 4.0E-07 A765528. 4.0E-07 A765528. 4.0E-07 A765528. 4.0E-07 A765520. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201. 3.0E-07 A7650201.	Hit Acess No. No. No. 1774.1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HIT POP HI	Top Hit Descriptor  Top Hit Descriptor  Top Hit Descriptor  Top Hit Descriptor  Source  Top Hit Descriptor  FEST_HUMAN  GOEDOSAT NOT. CGAP_CLI.1 Homo septens cDNA clare MAGE-270783 3' similar to contains Atu additions and the propertive element.  EST_HUMAN  FEST_HUMAN
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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5476		25462	10.28	3.0E-07   088807	088807	SWISSPROT	PROTEIN ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE AI PHA)
6026			5.32	3.0E-07	3.0E-07 AA815175.1	EST HUMAN	004c10.s1 NCI CGAP GCB1 Homo saplens cDNA clone IMACE:1330800.2
6433	16294	26456	က	3.0E-07	3.0E-07 AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
8918	18726		ಣ	3.0E-07	3.0E-07 AF029308.1	LN	Homo saplens chromosome O dunitication of the Tracil
666	19408		2.76	3.0E-07	3.0E-07 AJ132352.1	<u>L</u>	Rattus norveolous mRNA for 45 kDa secretory matein neatical
26	10013	19807	2.62	2.0E-07	2.0E-07 AF262988.1	IN.	Homo sapiens TRF2-interacting felomenic RAP1 profesion (RAP1) mBNA
148		19940	4.75	2.0E-07	2.0E-07 L77569.1	Į.	Homo sapiens DiGeorge syndrome critical realon teloment and
148		19941	4.75	2.0E-07	2.0E-07 L77569.1	TN	Homo sapiens DiGeorge syndrome critical region relation and
176		19962	116.1	2.0E-07	2.0E-07 U38849.1	N	Fugu rubripes beta-cytoplasmic (vascular) actin gene complete cris
731	10663	20495	1.71	20E-07	20E-07 AF003530.1	IN	Homo sapiens homeobox protein CDX4 (CDX4) neme commission and standard control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
731	10663	20496	1.71	2.0E-07	2.0E-07 AF003530.1	LN	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	10853	20701	3.11	2.0E-07	2.0E-07/AA223260.1	EST HUMAN	z08b07.s1 Stratagene NT2 neuronal precursor 637230 Homo sapiens cDNA clone IMAGE:650869 3' similar to ab:1.31860 GI YCOPHORIN A PRECURSOR (HI IMAN) combine All positions of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content o
929	10854	20702	3.38	2.0E-07 T63042 1	T63042.1	EST HIMAN	yc (5g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1
1147	11060	20903	1.28	2.0E-07 Q26768	026768	SWISSPROT	I/6 AUTOANTIGEN
1582	11486	21347	1.84	2.0E-07 Q09701	209701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7 10 IN CHROMOSOME I
3633	13547	2334	14.74	2.0E-07	2.0E-07 AF125348.1	Z.	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
6078	14948	24723	0.97	2.0E-07	2.0E-07 AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS:
5078	14948	24724	0.97	2.0E-07	20E-07 AW070995.1	EST HUMAN	xa05h07.x1 Source_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBARI F RARGAP DOMANING
5198		24826	0.95	2.0E-07	2.0E-07 AL163301.2	N.T.	Homo sapiens chromosome 21 serment HS2C1014
5277		24975	1.73	2.0E-07	-	EST HUMAN	RC3-NN0066-260400-021-011 NN0066 Home servieus - DNA
6009		26041	1.69	2.0E-07,		EST HUMAN	9958405.x1 Soares testis NHT Homo sapiens chNA chore 1/4 AGE-1826/77 21
6934	16812		3.91	2.0E-07	2.0E-07 AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
7627	17478		1.61	2.0E-07	2.0E-07 AL163303.2	NT L	Homo saplens chromosome 21 seament HS21C103
7897	17741	27984	6.48	2.0E-07	2.0E-07 AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-e08 NN0003 Homo sepiens cDNA
9094	19557		1.48	2.0E-07	2.0E-07 A1732462.1	EST HUMAN	zn85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element:
1086	11002		121	1.0E-07 /	2	Т	Homo sapiens chromosome 21 segment HS21C082

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2331	12212	22110	0.94	1.0E-07	1.0E-07 P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	12280	22177	0.94	1.05-07	7549818 NT	N FA	Homo sapiens RAB, member of RAS oncodene family-like 2A (RABI 2A) transcrint variant 2 mRNA
2797	11410	21269	1.75	1.0E-07 P09256		SWISSPROT	GLYCOPROTEIN GPV
3684			1.33	1.0E-07	1.0E-07 AL163282.2	NT	Hamo sapiens chromosome 21 segment HS21C082
4195			2.37	1.0E-07	1.0E-07 AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4195			2.37	1.0E-07		EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6103			5.2	1.0E-07		EST_HUMAN	1243d08.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 51
6103			5.2	1.0E-07	1.0E-07 BE047871.1	EST HUMAN	1243d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
6424	16285		9.04	1.0E-07	1.0E-07 N55081.1	EST HUMAN	yv43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484.3'
6782		26850	2.81	1.0E-07 P97435	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
6782		26851	2.81	1.0E-07 P97435	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
7180		27246	3.24	1.0E-07	1.0E-07 AA693576.1	EST HUMAN	য51e10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cONA clone IMAGE ধর ধরন র'
7714	17564	. 1	2.37	1.0E-07		EST HUMAN	602137714F1 NIH MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5
7716	17566	277792	1.28	1.0E-07	1.0E-07 AA386311.1	EST_HUMAN	EST 185054 Brain IV Homo sapiens cDNA
7980	17830		1.56	1.0E-07	1.0E-07 AL163282.2	NT	Homo sapiens chromosome 21 segment HS21 C082
9364	19533	. 25060	66	1 0F-07	1 0F-07 BE048770 1	NAMIN TRA	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212.3' similar to TR:095722 095722
0407			1 27	4 05 07		- LA	Hospitan Ald All and Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the
966			4 64	4 OF-07		F	Lespirens ALAD gene for porpriorimogen synthase
7680	L	277765	1 67	O OF OR	,	T CHIMANI	Average removed institution of the constant region conjugate (gettilling)
	L		2	20.0		$\Box$	WISDBOT XI NCI CRAP Gas4 Home contains a DNA along MACE 2446002 21
8520	18392		2.91	9.0E-08	9.0E-08 AI891052.1	EST HUMAN	OFR repetitive element;
8922	18730	29025	3.91	9.0E-08	9.0E-08 AL163301.2	L	Homo sapiens chromosome 21 segment HS21C101
9316			3.09	9.0E-08	9.0E-08 AJ251973.1	LN.	Homo sapiens partial steerin-1 gene
591	12671		2.65	8.0E-08		EST HUMAN	wd16b05.x1 Scares NFL T GBC S1 Homo septens cDNA clone IMAGE-2328273 31
1034			0.88	8.0E-08	8.0E-08 BE795469.1	EST_HUMAN	601590133F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3943976 51
3498	13415		1.43	8.0E-08	8.0E-08 BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
7074	16051	27144	38	00	9 OF AN AIZESSES 4	1444	
		177	0000	0.00	_	ES L DOMAIN	GILIDOUZ.XI Normal Human Trabecular bone Cells Homo sapiens CDNA clone NHTBC_cn15c02 random
7074	1		3.38	8.0E-08		EST_HUMAN	cn15c02x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC cn15c02 random
7551		27616	2.89	8.0E-08	8.0E-08 AW970693.1	T_HUMAN	EST382776 MAGE resequences, MAGK Homo sepiens cDNA
8570	18438		2.39	8.0E-08		F	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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		_	_	_	_	_		_				-	_		_								_											
Single Exort Flobes Expressed III near	Top Hit Descriptor	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)	Rat mRNA for ribosomal protein L31	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	cong3,P11.A5 conorm Homo sapiens cDNA 3'	Rattus norvegicus Munc13-1 mRNA, complete cds	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	Homo saplens SCL gene locus	Homo sapiens chromosome 21 seament HS21C048	Homo sapiens chromosome 21 segment HS21C048	MR0-HT0166-191199-004-009 HT0166 Home saniene c.DNA	Homo sapiens chromosome 21 segment HS21C048	RETROVIRUS-RELATED POL POLYPROTEIN ICONTAINS: REVERSE TRANSCRIPTASE	ENDONUCLEASE]	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C103	nh03b09.s1 NCL_CGAP_Thy1 Homo saplens cDNA done IMAGE:943193 similar to contains Alturementations	element,	ALDEHYDE OXIDĀSE	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)	QV0-CT0225-131099-034-a12 CT0225 Homo saplens cDNA	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR	Oricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds	an 22d10.x1 Gessler Wilms fumor Homo sapiens cDNA done IMAGE:1699411 3' similar to contains Alu	repetitive element contains element MER22 repetitive element ;	672748724E4 NIH MCC 63 U	602248024F1 NIH MGC 62 Home capiene CDNA clane INACE: 4233300 5	zd65g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar in contains	L1.t1 L1 repetitive element;	tb95a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element :	
JIE CXOII FIO	Top Hit Database Source	SWISSPROT	NT	SWISSPROT	SWISSPROT	EST HUMAN	N-	SWISSPROT	SWISSPROT	μN	N	N	EST HUMAN	Z		SWISSPROT	N	Z		EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	NT.		ESI HUMAN	FOT HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	
	Top Hit Acession No.	7.0E-08 Q02357	7.0E-08 X04809.1	7.0E-08 P15305	7.0E-08 P15305	7.0E-08 AI535743.1	7.0E-08 U24070.1	7.0E-08 P15305	7.0E-08 P15305		6.0E-08 AL163248.2	6.0E-08 AL163248.2	BE144398.1	6.0E-08 AL163248.2			6.0E-08 AL163209.2	5.0E-08 AL163303.2		5.0E-08 AA493851.1	5.0E-08 Q06278		978.1			4.0E-08 L42571.1	7 2000301	4.0E-08 AIU30027.1	-			4.0E-08 W76159.1	4.0E-08 Al343353.1	
	Most Similar (Top) Hit BLAST E Value	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	6.0E-08	6.0E-08	6.0E-08	6.0E-08		6.0E-08	6.0E-08	5.0E-08		5.0E-08	5.0E-08	5.0E-08 P06681	5.0E-08	4.0E-08 P25723	4.0E-08 P25723	4.0E-08	00	4.0E-08	4 0F-08	4.0E-08		4.0E-08	4.0E-08	
	Expression Signal	3.27	12.71	1.09	1.09	4.63	5.6	4.54	4.54	1.89	2.84	2.84	1.73	0.99		2.26	1.74	3.06		1.97	1.12	4.36	1.94	7.	1.7	1.41	1 1 1	102	3.66	3.66		1.54	1.46	
	ORF SEQ ID NO:	19874	21102		23241		<b>12067</b>	23240	23241		20569	20570	22092	23829		28818		19880		21981	24809		1		21494	27350	28030	2003	28570	28571				1
	Exon SEQ ID NO:	10057	11244	13444	13444	18075	18734	13444	13444	19334	10729	10729	12193	14055		18534	18632	10063		12076	15042	18839	18958	11625	11625	17155	17788	18154	18313	18313		19680	19252	
	Probe SEQ ID NO:	73	1338	3528	3528	8189	8926	9770	9770	9834	800	800	2312	4165		8717	8819	£		7188	5178	3027	9245	1724	1724	7278	7938	8274	8439	8439	7000	Long	9703	
																					-													

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Single Exon Probes Expressed in Heart	Top Hit Database Source Top Hit Descriptor	П	T			EST_HUMAN   qs76f11.y5 NC _CGAP_Pr28 Homo saniens cPNA class 1111.5	Hano sapiens chromasame 21 segment HS21C046				П		7	7	П	Т				П		7	T	П			Homo saplens shox gene, alternatively spliced products						Tourio sapiens cDNA clone IMAGE:3257969 31
ngle Ey	P as 8		I SI	T	EST H	EST H	ž		EST_H(	EST HUMAN	EST HUMAN	FOR	NA HOMAN	100	ES HUMAN	EST HUMAN	ESI HUMAN		EST_HUMAN	EST HUMAN	1	EST HUMAN		SWISSPROT	SWISSPROT	ST_HUN	Ę	FOT LIMES		EST_HUMAN	EST HUMAN	EST_HUMAN	I
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Table 4
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Table 4
Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8787	4E7EA	25004	100	10		1	
3	50.52	10007	1.82	9.UE-UB	5.UE-U9 AA358454.1	EST HUMAN	ES 168746 Fetal lung II Homo sapiens cDNA 5' end
7811	17661	27901	2.69	5.0E-09	5.0E-09 AW 799567.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
210	10452		1.68	4.0E-09	4.0E-09 AL163282.2	N.	Homo sapiens chromosome 21 segment HS21C082
949	10873		2.31	4.0E-09	4.0E-09 AL163285.2	IN.	Homo expiens chromosome 21 segment HS21C085
1453	11358		0.95	4.0E-09	9558718 NT	NT	Homo sapiens hypothetical protein (AF038469), mRNA
2379	12259	22151	. 6.36	4.0E-09	4.0E-09 AA350878.1	EST_HUMAN	EST 58385 Infant brain Homo saplens cDNA 5' end similar to similar to heat shock protein on inc.
2303	12184	22082	3.82	3.0E-09	3.0E-09 BE222239.1	EST HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.t3 MER18 recetitive element:
2506	12380	22270	1.25	3.0E-09	3.0E-09 BE222239.1	EST HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.t3 MER18 renefitiue element
2614	12482	22371	1.1	3.0E-09 P23249		SWISSPROT	PROTEIN MOV-10
7000	0000						hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MFR18 t3
256/	13208	23008	1.1	3.0E-09	-	EST_HUMAN	MER18 repetitive element;
4329	14226	24008	3.22	3.0E-09	5.1	N	Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene. partial cds
4-1-1	14305	24088	1.54	3.0E-09		SWISSPROT	258.1 KDA PROTEIN C210RF5 (KIAA0833)
7884	17734	27978	1.73	3.0E-09	2	N	Homo sapiens chromosome 21 segment HS21C047
8384	18261	28510	3.8	3.0E-09	3.0E-09 BF109943.1	EST HUMAN	7172c08.x1 Scares NSF F8 9W OT PA P St Homo senients CDNA close IMACE 2522000 of
8384	18261	28511	3.8	3.0E-09	3.0E-09 BF109943.1	EST HUMAN	7172c08.xt Sogres NSF F8 9W OT PA P S1 Homo senioris APNA class NACE: 2522223.
795	10724		0.93	2.0E-09	2.0E-09 X16674.1	N	H.sepiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
123/	41.4	20995	5.23	2.0E-09	.2	TN	Homo sapiens chromosome 21 segment HS21C084
1637	11541		10.52	2.0E-09	2.0E-09 AL118573.1	EST_HUMAN	DKFZp76181710 r1 761 (synotym: hamy2) Homo saniens cDNA clone DKEZp.784181740 F
2278	12162	22059	2.25	2.0E-09 Q9Y3R5		SWISSPROT	258.1 KDA PROTEIN C210RF5 (KIAA0833)
3858	13769	23561	3.65	2.0E-09 O60241		SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6405	16268	00/30	0	L			2x63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains
7055	1000	22420	60	Z.UE-09.	_	ESI_HUMAN	Alu repetitive element
0007	10802	27.122	1.37	2.0E-09	-	N N	Homo sapiens Xq pseudoautosomal region; segment 1/2
800	icho!	28/26	2.11	2.0E-09,	2	NT	Homo sapiens chromosome 21 segment HS21C048
9/08	10/24		11.53	2.0E-09	2.0E-09 X16674.1	NT	H.sepiens PADPRP-I gene for NAD(+) ADP-ribosytransferase
0840	407.40			l			nc11c02.rl NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repelitive
100	4004	02000	7.67	Z.UE-09,	Z.UE-09 AA226070.1	EST HUMAN	elament,
200	300	70830	248	1.0E-09	5031624INT	LN.	Homo sepiens CCAAT-box-binding transcription factor (CBF2) mRNA
200	8001	20851	2.48	1.0E-09	031624		Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
10101	11520		0.95	1.0E-09/	1.0E-09 AJ229041.1		Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

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Single Exoll Plobes Expressed in Hear	Top Hit Descriptor	qy64e11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812.3' similar to contains MER12.t2 MER12.t2	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nato) and surdival motor neuron protein (nato) and surdival motor neuron protein (nato)	Homo sabiens nucleolar phosphorydein R23 (NPM4) mBN/	Hamo saplens nucleolar phosphopotein B23 (NPM1) mBNA campiers ods	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK)	601058602F1 NIH MiGC 10 Homo saniens cDNA clans MA CE 2445477 51	2h35b03.s1 Soares pineal gland N3HPG Homo septemb cDNA clone IMAGE:414029 3' similar to contains. Au repetitive element contains element and properties of the contains and the contains are contains.	Himan headmoint cliester rection (BOD) was	CIRCUMSPOROZOITE PROTEIN PRECLIBEOD (70)	Hamo saniens chromosome 21 segment US217003	Homo saniens GTP hinding profess 1 (GTPDDA) BNA	MRO-SNOON ON A SNOON DELICE STATE	The character control of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of 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DOLLARS COLOR SHIP
אופ באסוו בוסמ	Top Hit Database Source	EST_HUMAN	Į Į	LN		ISSPROT	Т		Т	Т	N-		T HI IMAN	Т	EST HUMAN		Т	T HUMAN	T	1				/ISSPROT	Τ	T	Т	T HUMAN	Т
Jillo	Top Hit Acession No.	1.0E-09 AI356086.1	1.0E-09 U80017.1				40.1				1.0E-09 AL163283.2	418127	9.0E-10 AW867740 1		-			5			2	7706225 NT	7706225 NT					_	
	Most Similar (Top) Hit BLAST E Value	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09 P11799	1.0E-09	1.0E-09)	1.0E-09	1.0E-09 P26694	1.0E-09	1.0E-09	9.0E-10/		9.0E-10 AI870071	9.0E-10 AI452982	8.0E-10 U63630.2	8.0E-10	8.0E-10	8.0E-10 U36308.2	8.0E-10 AL 163280.	7.0E-10	7.0E-10	7.0E-10 Q13342	7.0E-10 P08548	7.0E-10 P08547	7.0E-10 X00856.1	7.0E-10 AA345220	7 OF 40 D35084
	Expression Signal	0.94	1.51	3.25	3.25	1.23	0.78	4.26	1.37	3.21	3.1	2.14	1.8		6.03	4.63	9.43	0.87	2.82	2:32	2.31	12.45	12.45	1.87	1.01	16.88	2.65	3.98	130
	ORF SEQ ID NO:		22580	22814	22615		22722		25549			24996	21048		22532	26172	19935	23022	23782		29100	20444	20445	21371			22768	25769	
	Exon SEQ ID NO:	12330	12788	12822	12822	12876	12930	14578	15476	15644	17761	19689	11195		12733	16032	10115	13222	14006	17575	18808	10619	10619	11510	11867	12386	12976	15662	16373
	Probe SEQ ID NO:	2453	2860	2895	2895	2949	.3002	4692	5560	5736	7911	9478	1287		2803	6087	141	3300	4106	7725	9006	989	989	1605	1974	2512	3049	5754	6514

Page 159 of 413 Table 4 Single Exon Probes Expressed in Heart

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miles even i todas expressed il treali	Top Hit Descriptor	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene	(102d07.x1 NCT CGAP Pr28 Homo seniens cONA class MAGE:2005021.2	RC3-CT0254-031099-012-012-CT0254 Home sanisms - CNIA	EST384012 MAGE resentiones MACI Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone and Mage Homo contone	RC3-NN0070-110800-014-h07 NN0070 Homo saniams ADNA	DKFZp434N219 r1 434 (synonym: hises) Home sarians contractory along DKEY-424trages:	HYPOTHETICAL GENE 48 PROTFIN	601822184F1 NIH MGC 75 Homo saniens cDNA clara MACE 202242 F1	HYPOTHETICAL 67.9 KD PROTEIN ZKERR BIN CHEONACEONE III	HYPOTHETICAL 67.9 KD PROTEIN ZK688 8 IN CHROMOROME III	9909f09.x1 Soares_placenta_8to9weeks_ZNbHP8to9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8 b2 LTR8 repetitive element	hg58g03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete eds.	Homo sapiens X-linked anhidrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.	W32706.s1 Soares melancoyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains	Homo sanions extracellular discountein location access	Homo sabiens chromosome 21 segment HS2/Cnn2	Homo sapiens chromosome 21 segment HS21Cnn3	RHOMBOID PROTEIN (VEIN) ET PROTEIN)	ba76d08.y1 NIH MGC 20 Homo sapiens cDNA clone IMAGE-2008319 F	AV743302 CB Homo sapiens cDNA clone CBFRGD08 5	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA done IMAGE:2205113' similar to contains MER29	repeative element;	II.3-C.10219-100200-004-D00 C.10219 Homo sapiens cDNA	vol1e12.11 Strategene lung (#937210) Homo saniens cDNA
מוס דייסוו ו וסי	Top Hit Database Source	LZ	EST. HUMAN	EST HUMAN		EST HUMAN	EST HUMAN	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	FST HIMAN	NT		IN	EST HIMAN	TN	Z.	LN	SWISSPROT	EST_HUMAN	EST HUMAN	EST_HUMAN		Т	EST HIMAN	Т
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	Most Similar (Top) Hit BLAST E Value	6.0E-10	6.0E-10	6.0E-10	6.0E-10	6.0E-10	5.0E-10	5.0E-10	5.0E-10	5.0E-10 P34678	5.0E-10 P34678	4.0E-10	4.0E-10	4.0E-10	4.0E-10	4.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10 P20350	3.0E-10	3.0E-10	3.0E-10	A DE	3.05-10	3.0E-10	3.0E-10 T65891.1
	Expression Signal	2.81	1.47	2.51	1.79	3.54	4.5	1.48	1.82	1.79	1.79	0.99	4.	60.9	19.23	7.7	1.72	6.63	1.1	1.1	2.83	3.27	1.31	1.31	4.	147	1.47	2.56
	ORF SEQ ID NO:	20666	22402					23152		27570	27571		21732	22292	26278		20668		24117	24118	25779	25851	26599	26600	27136	27302	27303	
	Exan . SEQ ID NO:		12511	14522	18865	19597		13347	16197		17366	10087	11846	12401	16125	18310	10822	11236	14330	14330	15672	15739	16420	16420	16944	17110	17110	17829
	Probe SEQ ID NO:	895	2644	4634	9092	9947	744	3430	6334	7496	7496	106	1951	2527	6229	8436	897	1329	4435	4435	5765	5833	6562	6562	7067	7233	7233	7979

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Single Exon Probes Expressed in U. . .

Single Exon Probes Expressed in Heart	Top Hit Descriptor		nz36g03.s1 NCI_CGAP_GCB1 Homo sabiens cDN4 clars NACE	IL3-HT0618-110500-136-E07 HT0618 Hamo saplens cDNA	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN BY CENTRO	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) Homo sapiens basic transcription factor 2 and these actions.	protein (naip) and survival motor neuron protein (smn) genes completed.	(nPRG)  Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds: cytochrome P450	polypeptide 5 (CYP3A5) news matter 1 (CYP3A7) genes, complete cds; and cytochrome PA50	601586708E1 NILL MOC ZILL	MRO-SN0038-290300-001-00-00-00-00-00-00-00-00-00-00-00-	AV652123 GI C Homo Series Change Capters CDNA	OVO-CT0225-194400 Age An OTTO-CT04113'	QV2-TT0003-161199-019-210 TT0003-161199-019-210 TT0003-161199-019-210-2-210-2-210-2-210-2-210-2-210-2-210-2-210-2-210-2-2-2-2	DKFZp434N1317 11 424 (magain 11 10 10 10 10 10 10 10 10 10 10 10 10	Homo sapiens nuclear factor of kappa light polymentide general.	cds	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent mother in the containing of the containing of the containing of the containing of the containing of the containing of the containing of the containing of the containing of the containing of the containing of the containing of the 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pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon	n.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes		27.23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens CDNA Jone MA OF	H. sapiens DMA, DMB, H.A71 ippo 1 MBo 1 And 1	mes Caraca (1971), LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	zt86b10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729211 61
gle Exon Pro	Top Hit Database Source		EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	NT	OKING	Z	EST HUMAN	1	Г	Т	Т	Т		2		Ž							EST HIMAN S			EST HUMAN Z
Sin	Most Similar (Top) Hit Top Hit Acession BLAST E No.	3.0E 40 A A PERSON 4	3.0E-10 AA/09/294.1	2.0E-10 DE1/331/.1			-								1.0E-10 AL041685.1	1.0E-10 AF213884 1		1.0F-40   152444 2		1.0F-40   159444.9		1.0E-10 M30829 1		1.0E-10 X87344.1 NT	1.0E-10 AA081989 4				
-	Expression (To Signal BL/	1.54													0.91	5.44	l	4.51		4.51		206 1.0		0.93 1.0	4.59		1 43	$\perp$	
	ORF SEQ ID NO:		25227	19814	19815			70000	26380		21353		22470	01139	<del> </del>			23716		23717	23724			1		28408			
	Exon SEQ ID NO:	17876	19271		10019	11751	15463	15803	16230	11307	11493	12411	13372	13411	1	13842		13939		13939	13945	13981	0,040	13012	17709	18165	15012	18859	
	Probe SEQ ID NO:	8026	9737	32	32	1855	6547	5787	6367	1492	1589	2537	3456	3770		3933		4036		4036	4042	4079	74.45	0140	7859	8286		9084	

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Table 4
Single Exon Probes Expressed in Heart

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oligica Lyones Expressed in Heart	Top Hit Descriptor	IL 2-HT0203-291099-016-c08 HT0203 Home seniens - DNA	DKFZp547D225 r1 647 (swnonym: bfhr1) Homa sariens cDNN aless Birers stresses at	DKFZn547D225 11 547 (sunnym: hftx1) Home capiens CDNA 11 1577 7 1577 1577	DKF20547D225 1 547 (swowm: http://linearcomm.com/com/com/com/com/com/com/com/com/com/	DKF205471225 rt 547 (smonth: http://doi.org/10.1000/1000/1000/1000/1000/1000/1000/	8e78f01 s1 Strategien schizo brain S11 Home conjune ability and all the conjune ability and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a service and a servic	RC6-BT0627-140200-011-En6 BT08-27 Home capients cutta cione invace: 9/0297 3	C16535 Clontech human aorta polyA+ mRNA (#6572) Homo saniens CNNA clone CEN Exercise 2:	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains	ms4609 x1 NOI OGAP Kida Homo conice. Data 1	MAGARIS & Weizmann Official Entire III	EST34392 Embryo, 6 week I Homo sanions - PNA & St. Co. NA Clone IMAGE: 255298 31	Homo sapiens SNCA isoform (SNCA) gene complete of the first in the	RETROVIRUS-RELATED POL POLYPROTEIN ICONTAINS: REVERSE TRANSCRIPTASE; ENDONI ICI FASE:	AV701656 ADB Home earliers only aless APPAPARES	Human matrix Gla protein (MGP) gene complete of	Hunan matrix Gla protein (MGP) dene complete cus	LINE-1 REVERSE TRANSCRIPTAGE UNIVIOLE	AV727859 HTC Home senions cONA clare HTCASOAR FI	Homo sapiens chromosome 21 segment HS217082	Homo sablens chromosome 21 segment HS21Ch83	ALDEHYDE OXIDASE	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens protocedherin beta 3 (PC)HR31 mRNA	Homo saplens KIAA0851 gene (partial), XT3 gene and I ZTEI 1 gene	ZUO1612.r1 Soares testis NHT Homo sapiens CDNA clone IMAGE: 720550 R	601507531F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE 30n0305 F1	HUMSUPY089 Human brain cDNA Homo saniens cDNA close neo	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2	Homo saplens mannosidase; beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBF2)13) genes, complete and	RC1-HT0258-21010n-013-fns HT0258-H
אום ראחון גווחר	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HIMAN	EST HIMAN	Т	Τ	N.	SWISSPROT	Т	Т		ISSPROT	П	Т		SWISSPROT	TN		TN	EST_HUMAN		EST HUMAN	SWISSPROT	IN	H IMAN
	Top Hit Acession No.	9.0E-11 BE145600.1		5.1			Γ		1		1.7		12.1	7.0E-11 AF183864.1		56.1	_	1		59.1		33.2		3.2	11416799 NT			0.1			4.0E-11 AF224669.1	T
	Most Similar (Top) Hit BLAST E Value	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11 C16635.	8.0E-11 H19974	8.0E-11 AI47861	8.0E-11 N23712	7.0E-11	7.0E-11	7.0E-11 P11369	7.0E-11	6.0E-11 M55270.	6.0E-11 M55270.	6.0E-11 P08547	6.0E-11	5.0E-11 AL16328	5.0E-11 AL16328	5.0E-11 P48034	5.0E-11 AL16321	5.0E-11	5.0E-11	4.0E-11	4.0E-11	4.0E-11 D44666.1	4.0E-11 P20095	4.0E-11	4.0E-11 BE14942
	Expression Signal	1.2	5.43	5.43	2.25	2.25	1.09	4	2.69	9.97	0.83	4.03	2.11	2.55	122	1.31	5.16	5.16	3.58	6.49	0.92	1.48	1.49	1.69	14.59	1.79	1.4	8.45	1.37	2.94	3.66	1.59
	ORF SEQ ID NO:	20042	21843	21844	23064	23065	24079		25312		23580	23641	24202	27020	•		20180	20181	26568	26945	19788	19788	23811	25954	26472	29072		22514	24196	25927		
	Exon SEQ ID NO:	10226	11947	11947	13257	13257	14295	15342	19062	13005	13792	13865	11336	16827	17723	19145	10352	10352	16388	16750	2666	2666	14035	15831	16307	18780	11285	12622	14411	15803	16225	17272
	Probe SEQ ID NO:	261	2057	2057	3337	3337	4400	5421	9410	3078	3881	3957	1431	6949	7873	9545	406	9	6229	6871	Ξ	3320	4135	5926	6446	6/68	1380	2/60	4518	2897	6362	7405

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	ding protein 1 (SH3RP1) mRNA	Mus musculus expressed in non-melastatic cells 2 motein (NM/99R) (Nm-2) month	EST180120 Liver, hepatocellular carcinome Homo seniens cDMA 5' end	d/36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102.3' similar to contains MER10.t3 MER10 repetitive element:	V643e12.71 Scares infant brain 1NIR Homo sanians CONA clara 1946 CE 25E444 E	1943912.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE 35144.5	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes. complete cds	Gailus gailus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3 beta) genes, complete cda	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);contains L1.th	10 V D T440		METROVIRUS-KELATED GAG PULYFROTEIN (VERSION 1) M54c09.x1 NCI CGAP Kid11 Homo samiens child circum IMA CE 22 cancers	frontle rooting of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact of the fact 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Types Typessed III Healt		Homo sapiens SH3-domain binding protein 1 (SH3BP1) mBNA	Mus musculus expressed in non-metast	EST180120 Liver, hepatocellular carcing	of36c04x1 Soares_testis_NHT Homo s	va43e12 r1 Soares infant brain 1NIR Ho	yg43e12.r1 Soares infant brain 1NIB Ho	Gallus gallus rho-globin, beta-H globin, beta-A COR3'beta (COR3'beta) genes. complete cds	Gallus gallus rho-globin, beta-H globin, beta-A COR3'beta (COR3'beta) genes, complete cds	qc51c10.x1 Soares_pregnant_uterus_N gb:L02932 PEROXISOME PROLIFERA	Himan endonemore retrained LEDV D TATE	BETBOVIDI IS DEL ATED GAO DOLLAR	METROPICOS-RELATED GAG POLYPROTEIN (VERSION 1)	Homo saniens FRA3R common frantle re	Homo sapiens chromosome 21 segment HS3/Cn27	QV2-BT0258-261099-014-801 BT0258 Homo sardiens c DNA	EST178226 Colon carcinoma (HCC) cell macroglobulin	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797 P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.	Homo carians and a series of the	OF FACTORY RECEPTOR 514 (OF EACTORY)	2K27d02 s1 Soares prequent interns Ni	zk27d02s1 Soares pregnant interns Ni	Zi77e03.s1 Sogres fetal liver spleen 1N	RC0-CN0027-210100-011-601 CN0027 Homo sanlens CONA	CM2-TN0140-070900-372-401 TN0140 Hamp saniens cDNA	Home canions mond for VIA Anno 1
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	Top Hit Acession No.	11545732 NT	TN 7706799	AA309248.1	2.0E-11 AI150502.1		İ	2.0E-11 L17432.1	2.0E-11 L17432.1		-	T	7.1		2	2	۲-	2.0E-11 AA581028.1	2.0E-11 AF029308 1		-	-	-	-	-	
	Most Similar (Top) Hit BLAST E Value	4.0E-11	3.0E-11	3.0E-11	Ŀ	20E-11	20E-11	2.0E-11	2.0E-11	O OF 44 A14 28274	20E-11/	2 0F-11 P10263	20E-11/	2.0E-11	20E-11 AL163227	2.0E-11	2.0E-11 AA307331	20E-11 /	2.0E-11.4	20E-11 Q13606	2.0E-11 AA035369	2.0E-11	20E-11 A	20E-11	2.0E-11 BF377859.	20E-11
	Expression Signal	1.93	2.15	1.45	1.58	3.64	3.64	3.91	3.91	1 04	1	4 23	0.87	0.95	16.0	5.46	1.32	1.83	1.43	4.61	2.07	2.07	1.29	2.25	1.98	1.89
	ORF SEQ ID NO:		21245		20716	92602	20927	21359	21360	21365	22493	22889	23005				24604	25828		27989	28591	28592			25356	
	Exan SEQ ID NO:		11381	14079	10869	11080	11080	11500	11500	11505	12599	13085	13205	13368	14395	14732	14836	15715	17194	17750	18330	18330	19679	18927	18943	19103
	Probe SEQ ID NO:	9611	1478	4179	946	1168	1168	1596	1596	1600	2737	3160	3284	3452	4501	4851	4961	5810	7318	7900	8457	8457	9160	9192	9216	9477

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No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         &lt;</td><td>Exon         ORF SEQ         Expression Signel         (Top) Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Expression Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic Politic 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Top Hit Acession no.         Expression no.         Top Hit Acession no.         Top Hi</td><td>Exon SEQ ID ID NO:         CRF SEQ Signel Signel         Most Similar Lop Hit Acession Signel         Top Hit Acession No:         Top Hit Acession Source Source Source Source Source Source Source Source Source 19201           19201         2.38         2.0E-11 P08547         SWISSPROT 19401           19201         2.38         2.0E-11 P08547         SWISSPROT 195040           19401         2.054         2.68         1.0E-11 AL1321016.1         NT           11059         2.1862         2.0E-11 AL163279.2         NT           1138B         1.34         1.0E-11 AL163279.2         NT           1138B         1.34         1.0E-11 AL16374.1         NT           1158B         1.37         1.0E-11 AL163279.2         NT           1158B         1.37         1.0E-11 AL163279.2         NT           1158B         1.37         1.0E-11 AL163279.2         NT           1158B         1.32         1.0E-11 AL163279.2         NT           16552         25840         3.25         1.0E-11 AL163279.2         NT           16652         25840         1.32         1.0E-11 AL163279.1         EST HUMAN           17109         27301         1.32         1.0E-11 AL163279.1         EST HUMAN           17491         274         1.0</td><td>Exon NO:         CRF SEQ ID NO:         Expression Signal ID NO:         (Top) Hit Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Source Source Signal ID NO:         Top Hit Acession ID NO:         Top Hit Acession Source Source ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID
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Signel Signel         Most Similar Adue         Top Hit Acession Patheses         Top Hit Acession Source Adue           19201         1D NO:         Signel Signel         LASTE No.         No.         Source Source Source Source Source Source Source Source Source Adue           19201         2.38         2.0E-11         P08547         SWISSPROT 14100           19594         2.0412         1.24         1.0E-11         AL171066 NT           11388         2.0543         2.0E-11         AL1417966 NT           11389         2.0544         2.08         1.0E-11         AL1321016.1         NT           11380         2.1374         1.32         1.0E-11         AL163279.2         NT           11380         2.1050         1.34         1.0E-11         AL163247.2         NT           11591         2.2654         1.32         1.0E-11         AL163247.2         NT           11655         2.766         1.32         1.0E-11         AL163247.2         NT           11665         2.766         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         <td< td=""><td>Exon         ORF SEQ         Expression Signal         (Top) Hit Acession No.         Top Hit Acession Detabase Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source    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  Signal         2.38         2.0E-11         F08547         SWISSPROT           19504         2.042         1.24         1.0E-11 AL13279.2         NT         NT           11084         2.084         2.0E-11 AL13279.2         NT         NT           11089         2.0840         2.0E-11 AL13279.2         NT           11380         2.286         1.0E-11 AL13279.2         NT           11390         2.28640         3.25         1.0E-11 BE10347.1         NT           16856         2.7060         5.41         1.0E-11 BE1034315.1         EST HUMAN           17109         2.7300         1.32         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         5.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.22         1.0E-11 BF365119.1         EST HUMAN           19485         2.7041         2.706-12 AL132300.2         NT</td><td>Exon         ORF SEQ         Expression         Most Similar (Top) Hit (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top 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1.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.0</td><td>Exon         ORF SEQ         Expression Signed         (Top) Hit Top Hit Acession Value         Top Hit Acession Source Signed         Top Hit Acession Value         Top Hit Acession Source Source Signed         Top Hit Acession Value         Top Hit Acession Source Source Source Source Source Source Source Source Source Aceter Source Source Aceter Source Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter 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Ace In Acession No.         Ace In Acession No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         Ace In No.         &lt;</td> <td>Exon         ORF SEQ         Expression Signel         (Top) Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.         Top Hit Acession Politic Post No.    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Top Hi</td> <td>Exon SEQ ID ID NO:         CRF SEQ Signel Signel         Most Similar Lop Hit Acession Signel         Top Hit Acession No:         Top Hit Acession Source Source Source Source Source Source Source Source Source 19201           19201         2.38         2.0E-11 P08547         SWISSPROT 19401           19201         2.38         2.0E-11 P08547         SWISSPROT 195040           19401         2.054         2.68         1.0E-11 AL1321016.1         NT           11059         2.1862         2.0E-11 AL163279.2         NT           1138B         1.34         1.0E-11 AL163279.2         NT           1138B         1.34         1.0E-11 AL16374.1         NT           1158B         1.37         1.0E-11 AL163279.2         NT           1158B         1.37         1.0E-11 AL163279.2         NT           1158B         1.37         1.0E-11 AL163279.2         NT           1158B         1.32         1.0E-11 AL163279.2         NT           16552         25840         3.25         1.0E-11 AL163279.2         NT           16652         25840         1.32         1.0E-11 AL163279.1         EST HUMAN           17109         27301         1.32         1.0E-11 AL163279.1         EST HUMAN           17491         274         1.0</td> <td>Exon NO:         CRF SEQ ID NO:         Expression Signal ID NO:         (Top) Hit Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Source Source Signal ID NO:         Top Hit Acession ID NO:         Top Hit Acession Source Source ID NO:         Top Hit
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        AL171066 NT           11388         2.0543         2.0E-11         AL1417966 NT           11389         2.0544         2.08         1.0E-11         AL1321016.1         NT           11380         2.1374         1.32         1.0E-11         AL163279.2         NT           11380         2.1050         1.34         1.0E-11         AL163247.2         NT           11591         2.2654         1.32         1.0E-11         AL163247.2         NT           11655         2.766         1.32         1.0E-11         AL163247.2         NT           11665         2.766         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         <td< td=""><td>Exon         ORF SEQ         Expression Signal         (Top) Hit Acession No.         Top Hit Acession Detabase Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession 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2.28640         3.25         1.0E-11 BE10347.1         NT           16856         2.7060         5.41         1.0E-11 BE1034315.1         EST HUMAN           17109         2.7300         1.32         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         5.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.22         1.0E-11 BF365119.1         EST HUMAN           19485         2.7041         2.706-12 AL132300.2         NT</td><td>Exon         ORF SEQ         Expression         Most Similar (Top) Hit (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.      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Ace Hit Acession Sources No.         No.         Top Hit Acession Sources No.         No.         Top Hit Acession Sources No.         No.         Top Hit</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Value         Top Hit Acession<br/>Value         Top Hit Acession<br/>Surrise           19201         10 Co. 1<br/>19401         2.38         2.06-71<br/>2.38         2.06-71<br/>2.06-71<br/>2.38        
1.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.0</td><td>Exon 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        AL1321016.1         NT           11380         2.1374         1.32         1.0E-11         AL163279.2         NT           11380         2.1050         1.34         1.0E-11         AL163247.2         NT           11591         2.2654         1.32         1.0E-11         AL163247.2         NT           11655         2.766         1.32         1.0E-11         AL163247.2         NT           11665         2.766         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         <td< td=""><td>Exon         ORF SEQ         Expression Signal         (Top) Hit Acession No.         Top Hit Acession Detabase Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top 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17109         2.7300         1.32         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         5.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.22         1.0E-11 BF365119.1         EST HUMAN           19485         2.7041         2.706-12 AL132300.2         NT</td><td>Exon         ORF SEQ         Expression         Most Similar (Top) Hit (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top 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Similar (Top) Hit Top Hit Acession Potabase Publics         Top Hit Acession Potabase Source Publics         Top Hit Acession Potabase Publics         Top Hit Acession Potabase Publics         Top Hit Acession Potabase Publics         Top Hit Acession Potabase Publics         Top Hit Acession Potabase Publics         Top Hit Acession Public Publics         Top Hit Acession Public Publics         Top Hit Acession Public Publics         Top Hit Acession Public Publics         Top Hit Acession Public Publics         Top Hit Acession Public Publics         Top Hit Acession Public Public Public Publics         Top Hit Acession Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public Public 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       Signel Signel         LASTE No.         No.         Source Source Source Source Source Source Source Source Source Adue           19201         2.38         2.0E-11         P08547         SWISSPROT 14100           19594         2.0412         1.24         1.0E-11         AL171066 NT           11388         2.0543         2.0E-11         AL1417966 NT           11389         2.0544         2.08         1.0E-11         AL1321016.1         NT           11380         2.1374         1.32         1.0E-11         AL163279.2         NT           11380         2.1050         1.34         1.0E-11         AL163247.2         NT           11591         2.2654         1.32         1.0E-11         AL163247.2         NT           11655         2.766         1.32         1.0E-11         AL163247.2         NT           11665         2.766         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2         NT           11060         2.76         1.0E-11         AL163247.2 <td< td=""><td>Exon         ORF SEQ         Expression Signal         (Top) Hit Acession No.         Top Hit Acession Detabase Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession Detabase Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit 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       NT         NT           11084         2.084         2.0E-11 AL13279.2         NT         NT           11089         2.0840         2.0E-11 AL13279.2         NT           11380         2.286         1.0E-11 AL13279.2         NT           11390         2.28640         3.25         1.0E-11 BE10347.1         NT           16856         2.7060         5.41         1.0E-11 BE1034315.1         EST HUMAN           17109         2.7300         1.32         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         5.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.22         1.0E-11 BF365119.1         EST HUMAN           19485         2.7041         2.706-12 AL132300.2         NT</td><td>Exon         ORF SEQ         Expression         Most Similar (Top) Hit (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.       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Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         No.   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1.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.06-71<br/>2.0</td><td>Exon         ORF SEQ         Expression Signed         (Top) Hit Top Hit Acession Value         Top Hit Acession Source Signed         Top Hit Acession Value         Top Hit Acession Source Source Signed         Top Hit Acession Value         Top Hit Acession Source Source Source Source Source Source Source Source Source Aceter Source Source Aceter Source Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter 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Detabase           19201         1D NO:         Signal         2.38         2.0E-11         F08547         SWISSPROT           19504         2.042         1.24         1.0E-11 AL13279.2         NT         NT           11084         2.084         2.0E-11 AL13279.2         NT         NT           11089         2.0840         2.0E-11 AL13279.2         NT           11380         2.286         1.0E-11 AL13279.2         NT           11390         2.28640         3.25         1.0E-11 BE10347.1         NT           16856         2.7060         5.41         1.0E-11 BE1034315.1         EST HUMAN           17109         2.7300         1.32         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         5.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.41         1.0E-11 BF365119.1         EST HUMAN           19485         2.7060         6.22         1.0E-11 BF365119.1         EST HUMAN           19485         2.7041         2.706-12 AL132300.2         NT | Exon         ORF SEQ         Expression         Most Similar (Top) Hit (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         Top Hit Acession Sources No.         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1.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.06-71<br>2.0 | Exon         ORF SEQ         Expression Signed         (Top) Hit Top Hit Acession Value         Top Hit Acession Source Signed         Top Hit Acession Value         Top Hit Acession Source Source Signed         Top Hit Acession Value         Top Hit Acession Source Source Source Source Source Source Source Source Source Aceter Source Source Aceter Source Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source Aceter Source 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				Most Similar			
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7895	17745		4.67	5.0E-12	5.0E-12 AL163303.2	FN	Homo saplens chromosome 21 segment HS21C103
244	10211		3.42	4.0E-12	4.0E-12 AA700326.1	EST_HUMAN	274g11.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4606763'
245	10211	20027	3.55	4.0E-12	4.0E-12 AA700326.1	EST HUMAN	274g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4520	14413	24198	0.85	4.0E-12	4.0E-12 AI689984.1	EST_HUMAN	bz8h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE;
6797	16676		2.89	4.0E-12	4.0E-12 AF109907.1	LN	Homo saplens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8431	18305	28561	3.51	4.0E-12	1	TN	Homo saplens 959 kb config between AML1 and CBR1 on chromosome 21q22, segment 3/3
9520	19131		1.9	4.0E-12	4.0E-12 U78027.1	TN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
900	10536	20345	3.81	3.0E-12	3.0E-12 AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP:
900	10536	20346	3.81	3.0E-12	3.0E-12 AW341683.1	EST_HUMAN	hd13d01x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
8047	17938	28187	3.08	3.0E-12	3.0E-12 U37672.1	IN	Human prostate specific antigen gene, 5' flanking region
8047	17938	28188	3.08	3.0E-12	3.0E-12 U37672.1	LN	Human prostate specific antigen gene, 5' flanking region
3421	13338	23143	1.03	2.0E-12	6754495 NT	LN LN	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4025	13928	23704	1.04	2.0E-12		TN	Rat U3A small nuclear RNA
4025	13928	23705		2.0E-12	2.0E-12 J01884.1	TN	Rat U3A small nuclear RNA
4324	14221		1.8	2.0E-12	2.0E-12 BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4804	14688	24473		20E-12 O70306	070306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4804	14688	24474	0.78	2.0E-12 O70306	070306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
2898	- 1		. 2.22	2.0E-12	7.1		EST383946 MAGE resequences, MAGL Homo sapiens cDNA
6258	- 1		3.34	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
83.6	- 1	26552	2.07	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7367	17345		1.68	2.0E-12		NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
737	17587		8.13	2.0E-12		EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA
9175	18916		1.71	2.0E-12	AL163283.2	TN	Homo sapiens chromosome 21 segment HS21C083
9877	19041		1.52	2.0E-12	11418248 NT	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
		· 					hh90a09.x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2970040 3' similar to contains MER18.t1
	10095	19914	1.82	1.0E-12	1.0E-12 AW627674.1	EST_HUMAN	MER18 repetitive element;
1944	- 1		2.03	1.0E-12		EST_HUMAN	wm51f07.x1 NGI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element;
3032	12960	22752	1.16	1.0E-12	1.0E-12 AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
		•					

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Table 4
Single Exon Purhas Excension

Single Exon Probes Expressed in Heart	It Acession Top Hit Database Top Hit Descriptor		N	EST HUMAN	3.1 EST HUMAN	Ν	SWISSPROT	L.	EST_HUMAN		EST_HUMAN	3.1 EST HUMAN	64.1 EST_HUMAN	/ISSPROT	Į.	N	NT NT	EST_HUMAN	N.	Z	NT protein (naip) and survival motor neuron protein (smr.)	Homo saplens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), 144-like rithornman	Human germline T-cell receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair, T-central receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor heta chair receptor receptor heta chair receptor receptor heta chair receptor receptor heta chair receptor receptor heta chair receptor receptor receptor heta chair receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor receptor re	TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV6S8A2T, TCRBV6S8A3N2T, TCRBV6S6A2T TCPBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T TCPBV6S3	N	1 EST HUMAN		/ISSPROT	Homo sapiens chromosome 21 section (SALNAC-11)
Single Exon Probes Express	8		N	EST_HUMAN	3.1 EST HUMAN	Ν	SWISSPROT	L.	EST_HUMAN		EST_HUMAN	3.1 EST HUMAN	64.1 EST_HUMAN	SWISSPROT	Į.	N	NT NT	EST_HUMAN	N.	Z	L	TN	Human germline	TCRBV13S6A2T	N	1 EST HUMAN		SWISSPROT	Z INT
	Most Similar (Top) Hit BLAST E Value	4 NE 40 A FABRE	4 OF 42 A 142	1.0E-12/AU132248.1	4 OF 40 1100	1.0E-12 U82828.1	1.0E-12 Q9Y2G7	1.0E-12/AF196864.1	1.0E-12 AI248533.1		1.UE-12 AI24853	1.0E-12 AA782323.1	1.0E-12 AW9621	1.0E-12 P44836	0 0E 49 1 102	9.0E-13 AJZ/1735.1	0.0E-13 AB0Z8900.1	8.0E-13   120185 4	8 0F-13 1 2048E 4	001670 21	8.0E-13 U80017.1	8.0E-13 U78027.1		L	3.0E-13 U66060.1	7.UE-13 BE778223	7 05 40 040 475	6.0E-13 Q10473	
	Expression Signal	1.16			182	2 2	1707		9.11	77	1 24	3 2 8	250	272	1 13	1.18	2.37	5.05	5.05	1 5	06.1	2.13		2,0	10 33	3	1.33	18.51	
	ORF SEQ ID NO:		23496				26240		26256	26257	27119	29118				23570		20458	20459	21570		+		28079		-		21840	
-	SEQ ID NO:		13710	13710	15544	15591	16090		onror	16106	16928	18860	19728	19426	13489	13776	17388	10633	10633	11694		17688		18789	19149	_	19287	11944	
L	Probe SEQ ID NO:	3032	3798	3798	5630	5682	6224	8340	25	6240	7051	9085	9605	9963	3575	3865	7537	8		1796	1	3		8984	9550		8926	2054	

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Table 4

Probe SEQ ID NO: 3351 8234 1824 1824 1824 1824 2410 6601 8601 8601 8601 875 876 877 877 878 878 878 878 878 878 878	Exan SEQ ID ID NO: 13201 13271 18115 28367 11721 17721	
Exan SEQ ID ID NO: Signa 13201 13271 13271 12288 15350 25404	Signal 1.05 1.45 2.96 2.96	
13201     1.05       145     1.45       1 13271     1.45       1 1121     2.96       1 1228     1.58       1 156     25404     4.86       1 16142     26298     1.07	45 75 96	5.0E-13 F 5.0E-13 A 5.0E-13 P 4.0E-13 A 4.0E-13 A 4.0E-13 A
18115     28367     2.75       11721     2.96       12288     1.58       15350     25404     4.86       16142     26298     1.92	5.0E-13 P073 4.0E-13 AW37	4.0E-13 AW378614.1 4.0E-13 AW378614.1 4.0E-13 AF003529.1 4.0E-13 AF003529.1

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						200	Onigo Expire Typiessed III neall
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4019	13923		1.72	2.0E-13	2.0E-13 AL163278.2	N-	Homo sapiens chromosome 21 segment HS21C078
5722	15629	•	3.87	2.0E-13	2.0E-13 Q06852	SWISSPROT	OELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6078	16061	26209	6.32	2.0E-13	X16912.1	¥	Human PFKL gene for liver-two Sonhosphorfrieto/hingso/FC 2 7 4 41)
7976		28067	3.97	2.0E-13	2.0E-13 5031896 NT	N	Homo sapiens mab-21 (C. elegans Hilke 1 (MAR241 1) mRNA
9251			7.42	2.0E-13	Į	EST HUMAN	CM0-NN0001-100300-274-e11 NN0001 Home sanions (1971)
288	·		1.37	1.0E-13		N.	FGF-1=fibroblast growth factor 1 fruman kichey Genomic 342 nt somment 2 25 or
870	10796	20646	4.39	1.0E-13	7	L	Homo sapiens LGMD2B gene
1314	11220	21077	1.27	1.0E-13	1.0E-13 X87344.1	ŢN	H.sepiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1976	11869	21761	2.16	1.0E-13	1.0E-13/AA720574.1	EST HUMAN	nw2/g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element
4488	14382	24169	1.48	1.0E-13	Γ	EST HUMAN	602038009F1 NCI CGAP Bm64 Homo sapiens cDNA clane WAACE:418Eees F
8684	18572	28855	13.83	1.0E-13		EST HUMAN	745e/0.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MFR29 b2 MFR29 renefitine element.
9026			1.62	1.0E-13		EST HUMAN	AV715377 DCB Homo saniens cDNA clone DCB Alena Er
9714	19255		1.6	1.0E-13		NT	Homo sapiens Xa oseudoautosomal region: segment 1/2
330	10289	20105	2:92	9.0E-14	9.0E-14 AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.r1 MER19 repetitive element;
331	10290	20106	2.85	9.0E-14	9.0E-14 AA781159.1	EST HUMAN	el/24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19;11 MER19 repetitive element:
2451	- 1		4.04	9.0E-14	9.0E-14 AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo saniens cDNA
2725	-	22482	4.62	9.0E-14	Γ	Z	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3073	13000	22790	3.74	9.0E-14	9.0E-14 AW513296.1	EST_HUMAN	xo54h05x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2707833 3
3200	10289	20105	0.98	9.0E-14	9.0E-14 AA784159 4	EST HIMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
3728	13640	23426	5.22	9.0E-14 D14547.1		Т	Human DNA SINF renefitive element
4650	14536	24325	1.93	9.0E-14	2.7		Sadulnus pediatis gene for seminal vasiria a construction
3453	13369		1.57	8.0E-14	5	T HUMAN	hz71c09.x1 NCI CGAP Lu24 Home saniers c NNA clara MA CE 2242424 21
3872	13783		2.77	8.0E-14 R76269.1		HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sepiens cDNA done IMAGE-144706.9
\$ \$	16447	26637	69.09	8.0E-14 X89211.1			H.sapiens DNA for endogenous retroviral like element
7515	17303	27510	3.49	8.0E-14	8.0E-14 AA219316.1	Г	2417c10.s1 Strategene fetal retina 937202 Homo saniens cinna chare INA CE:espeza si
8732	18588		4.39	8.0E-14	8.0E-14 BE062558.1	Т	QV2-BT0258-261099-014-e01 BT0258 Homo septens oDNA
						1	

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		<del></del>	_								_												
Top Hit Descriptor	xf67e10x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:26231463' similar to contains MER10.t2 MER10 repetitive element;	Homo sapiens FRA3B common fracile recion diadenceire trinhosnicate hudological curry	Homo sapiens hypothetical protein FI. (20585/FI. 120585) mPNA	Homo saplens hypothetical protein FLJ20585 (FLJ20585), mRNA	Homo sepiens FRA3B common fregile region, diadenosine triphosphate hydrolase (FHIT) neme even 5	Homo sapiens FRA3B common fracile region clademosine frinhosnhete hadronee (EUIT) and	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTISPECIFIC ORGANICAL MULTIPLICAL MULTIPLICAL REPORTER 1 (MULTIPLICAL RESISTANCE) ASSOCIATED PROTEIN 2) (CANALICULAR MILTIDELIC RESISTANCE PROTEIN)	xb03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.t2 L1	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	S-ANTIGEN PROTEIN PRECURSOR	Homo sapiens LGMD2B gene	2467a06.11 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMACE: 487888 81	W/3c12s1 Scares_multiple_sclerosis_2NbHMSP Homo sepiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element:	wm08c03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu	R.norvegicus mRNA for CPG2 protein	xp45f12.x1 NCI_CGAP_HN11 Homo saplens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element contains element MFR0 condition element.	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM20)	hx84f11xf NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:31955013' similar to contains MER4.b2 MER4 receitive element	CIRCUMSPOROZOITE PROTEIN PRECLIRSOR (CS)	xp45f12x1 NCI_CGAP_HN11 Homo sapiens cDNA close IMAGE:2743343 3' similar to contains Alu repetitive element contains element MFRO repositions and all properties elements.	Homo sapiens Xa oseudoantosamal region: serment 2/2	Homo sapiens Xg pseudoautosomal region; segment 2/2	Homo sapiens chromosome 21 segment HS21C103
Top Hit Database Source	EST_HUMAN	Ę	Z	LN	TN	LN	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	TN.	EST HUMAN	EST HUMAN	EST HIMAN	IN	$\Box$		T HUMAN	Т		Ţ		
Top Hit Acession No.	7.0E-14 AW151673.1	6.0E-14 AF020503.1	8923548	8923548 NT	6.0E-14 AF020503.1	6.0E-14 AF020503.1	263120	5.0E-14 AW073791 1			4.0E-14 AJ007973.1	2		-		3.0E-14 AW265354.1	3864	3.0E-14 BE466372.1		3.0E-14 AW265354,1			2
Most Similar (Top) Hit BLAST E Value	7.0E-14,	6.0E-14	6.0E-14	6.0E-14	6.0E-14	6.0E-14	5.0E-14 Q63120	5.0E-14	5.0E-14 P08547	4.0E-14 P04928	4.0E-14/	4.0E-14	4.0E-14 N46328.1	4.0E-14 Al886224	3.0E-14 X95466.1	3.0E-14 A	3.0E-14	3.0E-14 B	3.0E-14 P02894	3.0E-14 A	2.0E-14 A	2.0E-14 A	2.0E-14 AL163303
Expression Signal	3.07	10.2	1.02	1.02	2.56	2.56	3.92	1.09	5.12	1.77	6.5	0.94	+	2.31	2.13	0.82	1.1	1.23	1.5	7.59	3.98	3.98	6.35
ORF SEQ ID NO:			24756	24757	27725	.27728	20348	24628	25363		21608		23873		20705	24505	24507		24791	24505	20154	20155	20428
Exon SEQ ID NO:	12699	10319	14982	14982	17502	17502	10538	14860	15316	12685	11732	13607	14094	19760	10859	14722	14725	14972	15024	14722	10331	10331	12673
Probe SEQ ID NO:	1611	363	5114	5114	7652	7652	602	4985	5397	1107	1835	3693	4194	7776	934	4841	4844	5104	5157	8563	384	384	675

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2339	12219		1.36	2.0E-14	2.0E-14 AW372868.1	EST HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2416	12293		1.09	2.0E-14	7657529 NT	N	Homo saplens rhabdoid fumor deletion region protein 1 (RTDR1), mRNA
2479	12355	22246	1.24	2.0E-14	2.0E-14 AL163209.2	N	Homo sapiens chromosome 21 segment HS21C009
2640			0.95		P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5505		25485	2.96	2.0E-14		N	Human beta globin region on chromosome 11
6114	16008		2.18	2.0E-14	7.	EST HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
6432		26454	19.91	2.0E-14	2.0E-14 BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0387 Homo sepiens cDNA
6432		26455	19.91	2.0È-14		EST HUMAN	L2-HT0397-071299-024-D04 HT0387 Homo sapiens cDNA
8160		28300	4.76	2.0E-14	2.0E-14 AW139800.1	EST HUMAN	UI-H-BI1-adw-a-10-0-UI.s1 NCI CGAP Sub3 Homo saplens cDNA clone IMAGF-7718234 31
8791	15423	25485	1.81	2.0E-14	2.0E-14 U01317.1	IN	Human beta globin region on chromosome 11
1051	10968	20810	1.31	1.0E-14		IN	Homo sapiens chromosome 21 segment H321C046
1384	11289	21143	7.67	1.0E-14	1.0E-14 AL163268.2	LN	Homo sapiens chromosome 21 segment HS21C068
1384	11289	21144	7.67	1.0E-14		LN	Homo sapiens chromosome 21 segment HS21C068
1956	11851	21738	21.54	1.0E-14	1.0E-14 L44140.1	IN	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene complete cyc.'s
2137	12025	21921	6.17	1.0E-14	3.2	NT	Homo sapiens chromosome 21 segment HS21C103
2358	12238	22134	6.43	1.0E-14	_	N	Homo sapiens ribosomal protein [234 (RPI 234) gene complete ode
2914	12841	22641	1.38	1.0E-14 P05227		SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PEHRP-II)
3130	13055	22854	4.67	1.0E-14	1.0E-14 BF335227.1	EST HUMAN	RC2-CT0432-310700-013-a09 1 CT0432 Homo sapiens cDNA
3130	13055	22855	4.67	1.0E-14	-	EST_HUMAN	RC2-CT0432-310700-013-e09_1 CT0432 Homo sepiens cDNA
3811	13723	23512	2	1.0E-14		EST_HUMAN	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350.3'
4374	14270	24051	1.74	1.0E-14	1.0E-14 AW275852.1	EST HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5550	15466	25536	1.97	1.0E-14	1.0E-14 AF126145.1	LN L	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6012	1	26045	10.41	1.0E-14	7150	Į.	Hamo sapiens prominin (mouse)-like 1 (PROML1) mRNA
6012	ı	26046	10.41	1.0E-14	11437150 NT	N	Homo sepiens promínin (mouse)-like 1 (PROMI.1), mRNA
1558	11463	21320	2.85	9.0E-15	7427522 NT	LN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
			!				Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,
2126	12014		1.64	9.0E-15/	9.0E-15/AF196779.1	LN	JUNIU protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds: and L-type calcium channel a>
6427	16288	26449	4.28	9.0E-15 P21416		SWISSPROT	GAG POLYPROTEIN ICONTAINS: CORE PROTEINS P15 P12 P20 P40 P401
6673	16553	26748	1.53	9.0E-15	9.0E-15 BE903559.1	Π	601677750F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5:
2780	10415		1	8.0E-15	8.0E-15 BE261482.1	Γ	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5
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Single Exon Probes Expressed in Heart

						-	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7963	. 17813		2.83		7.0E-15 AW241958.1	EST HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2700483 3' similar to contains THR:2 THR repetitive element:
826	10901	20748	6.12		6.0E-15 AJZ71736.1	- LN	Homo sapiens Xa oseudoautosomal renion: semment 2/2
8622	19770		1.86		6.0E-15 AW836843.1	EST HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo satiens cDNA
9948			1.57		BF432200.1	EST HUMAN	nab81c12x1 Soares NSF F8 9W OT PA P S1 Homo sabiens cDNA clone IMAGE: 3'
404	10350	20177	5.79		5.0E-15 AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2733	12595	22490	1.38		5.0E-15 U91328.1	LΝ	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transmitter (NDT3) recessored to the complete and
3423	13340		-	6.0E-16	6.0E-15 AW296817.1	EST HUMAN	UI+FW0-aib-q-(0-0-II) st NC  CGAP Subst Home campions of Na close IMA CE-272 222 2
8063	17954		222	5.0E-15	5.0E-15 AV730056.1	EST HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVENE 5:
421	8866	19779	2.6	L	4.0E-15 AL163303.2	1 _N	Homo sexiens chromosome 21 secrete HS21C103
4039	13942	23720	0.78		4.0E-15 AL118596.1	EST HUMAN	DKFZp761C0810 r1 761 (synonym: hamy2) Home seniens cDNA close DKFZp761C0840 E
8414	16438	26623	2.38		4.0E-15 AJ130894.1	N.	Homo saplens mRNA for transcription factor
8414	16438	26624	2.38		4.0E-15 AJ130894.1	N	Homo sapiens mRNA for transcription factor
4123	14023		5.93		3.0E-15 N89452.1	EST HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
4843	14724		1.41		3.0E-15 P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
4955		24599	0.88		3.0E-15 AA078097.1	EST HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo saniens cDNA clane 7D04Enz
4955		24600	0.88		3.0E-15 AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01Fn3
6314	_	26335	2.86		3.0E-15 M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6314	16177	26336	2.86		3.0E-15 M27685.1	Z	Mus musculus ultra high sulfur keratin gene, complete cds
7709	17559		1.87	3.0E-15	3.0E-15 AA807128.1	EST_HUMAN	oc36a07.s1 NCI_CGAP_GCB1 Hamo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repetitive element;
8173	18061	28311	271	3.0E-15	3.0E-15 AB026898.1	TN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
250	10216	20033	3.29	2.0E-15	2.0E-15 AF223391.1	TN	Homo sapiens calcium charnel alpha1E subunii (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced.
364	10320	20141	3.23	2.0E-15	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	10320	20142	3.23		AF22336	LN.	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1512	11417		1.14	2.0E-15	8923201 NT	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA

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Fig. 2   1986   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586   1586						_			_					_	_												
Exon         ORF SEQ         Expression         (Top) Hit Top Hit Accession         Top Hit Top Hit Accession         Top Hit Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         Top Hit Accession         <	bes Expressed III near	Top Hit Descriptor	Homo sepiens calolum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINFIN	REPETITIVE PROLINE RICH CELL MALL DECITEM SENTALISASE	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17	2/7/903.51 Soares fetal liver spieen 1NEIS St Homo company All All St. 1995 Constant	Za78d10.r1 Scares_fetal_lung_NbHz News sapiens cDNA clone IMAGE:298675 5' similar to	Human DNA SINE ranatiting along the	CMO-HT0244-201099-078-a12 HT0244 Home contains CDNA	CMO-HT0244-201099-078-812 HT0244 Hpmo seriens cDNA	Homo sabiens Xg pseudoautosomal region: segment 1/2	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	bZ6h05.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINFR TRANSPOSACE	hk40e02 vi NCI OGAP Ovad Homo emicro - DNA -1 II na OE 2000.	LINE-1 REVERSE TRANSCRIPTARE HOMAN CO.	RC3-HT0649-100500-072-b08 HT0849 Home seeing and	w86e04.x1 NCI CGAP Kid11 Homo saniens cDNA clone IMAGE:2302500 21	940e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens GDNA clone IMAGE:120234 3' similar to contains	OV3-BT0569-270100-074-06 BT0569 H.	Homo sapiens chromosome 24 segment Licot Coop	offshoe of some batte NHT Home salans about the NIACE Consession	df88h06.xf Spares festis NHT Home canans ADMA June 1878 Carastal	Homo sapiens spermidine synthase (SRM) mRNA
Exon No:         CRF SEQ Expression Signal No:         Most Similar Noil No:         Most Similar Noil Noil Noil Noil Noil Noil Noil Noil	שוה ביפו		IN.	ħ	EST HUMAN	SWISSPROT	SWISSPROT	<u> </u>	EST HUMAN	EST HUMAN	LN	EST HUMAN	EST HUMAN	IN.	Þ	Ę	EST HUMAN			EST HUMAN	EST HUMAN	EST HIMAN	EST HIJMAN	Į.	T HUMAN	Т	
Exan NO:         ORF SEQ ID NO:         Expression Signal         (T Signal         Mos Signal         Mos Signal <th< td=""><td></td><td>Top Hit Acessian No.</td><td>AF223391.1</td><td>AF223391.1</td><td>5.1</td><td></td><td></td><td>AJ400877.1</td><td>AA704195.1</td><td>W05064.1</td><td>D14547.1</td><td>AW379465.1</td><td>AW379465.1</td><td>AJ271735.1</td><td>AF223391.1</td><td>AF223391.1</td><td>Al689984.1</td><td>BE043584.1</td><td>P08547</td><td>3E182696.1</td><td>Al984928.1</td><td>95763 1</td><td></td><td></td><td></td><td></td><td>07208</td></th<>		Top Hit Acessian No.	AF223391.1	AF223391.1	5.1			AJ400877.1	AA704195.1	W05064.1	D14547.1	AW379465.1	AW379465.1	AJ271735.1	AF223391.1	AF223391.1	Al689984.1	BE043584.1	P08547	3E182696.1	Al984928.1	95763 1					07208
Exon SEQ ID NO:         ORF SEQ Express Signa NO:         Express Signa NO:           13381         23186         24741           14416         24742         24742           16089         24742         26397           16173         26397         6           17277         27485         1           17277         27486         1           17277         27486         1           17277         27486         1           17209         23186         2           13381         23187         2           12806         22706         0           13029         22825         0           14161         23939         1           14656         24731         1           15750         25864         1           16078         26862         1           16773         26892         1           16773         26976         4           16773         26977         4           17104         27293         1		Most Similar (Top) Hit BLAST E Value	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	1.0E-15	1.0E-15	1.0E-15	1.0E-15	1.0E-15	1.0E-15	1.0E-15	1.0E-15/	1.0E-15	1.0E-16/	1.0E-15
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		ORF SEQ ID NO:								26397	27232	27484	27485		23186	23187		22706	22825	23939	24731	25864		26862	26976	26977	27293
Probe SEQ ID NO: NO: 3465 3465 3465 3465 3465 3465 3465 37103 7410 7410 7410 7410 7410 7410 8212 2979 9799 9799 9799 9799 9799 9799 9		Exon SEQ ID NO:	_ }	j		14966	14966		_ ]	16237	17040	17277	17277	18096	13381	13381	12609	12906	13029	14161	14956	15750	16068	16870	16783	16783	17104
		Probe SEQ (D NO:	3465	3465	4522	5097	2097	6223	8310	6375	7163	7410	7410	8212	9799	9799	2747	2979	3103	4262	5086	5844	6182	6791	6905	6905	7227

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Table 4
Single Exon Probes Expressed in Heart

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onge that I have the second in heart	Top Hit Descriptor	Homo sapiens major histocompatibility locus class III region	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912.3' similar to contains Alu repetitive element	Homo sapiens cut (Droscophila) libe 4 (OCNAT 4)c-1	HSC28F051 normalized infant brain cDNA Home saniens cDNA class a 2350s	PROTEIN ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE AI (PHA)	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)	NPORTO 1 Stratograms (mg (#027248))	EST384702 MAGE resequences, MAGL Homo seniens cDNA	Mus musculus olfactory recenter clineter OP278 OP279 OP279	ot80c04.s1 Sources_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to	Homo cariono obtambano 22	60/18857375 MILINGS 671	Homo sariens GTP hinding produkt 4 /CTDPD 1 - 1114	Homo sariens gene for TMEMA and DIMPS complete and and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete and DIMPS complete	OV1-UM0036-200300-115-002 UM0786 Home Amilian Cas	QV1-UM0036-200300-115-002 UM0036 Home series collid	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN DRECHISCOR	PM4-BT0650-010400-002-409 BT0650 Homo saniems CNNA	PM4-BT0650-010400-002-909 BT0650 Homo sapiens cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens hypothetical protein FL J10024 (FL J10024), mRNA	AV730030 HTF Homo saplens cDNA clone HTFAWA03 5'	LINE-1 REVERSE TRANSCRIPTASE HOMO! OG	C05947 Human pancreatic islet Homo sapiens CDNA close the R255	Homo sapiens Grb2-associated binder 2 (KIAA0571) mRNA	df45c01.v1 Morton Fetal Cochlea Home saniens cDNA clane IMAGE:2/962375 51	df45c01.v1 Morton Fetal Cochlea Homo saniens cDNA clans INA CE 2200370 5	DVFT ASSESSED TO SEPTICAL COLOR GIOTE IN A CE ZA 803 / 6 5
אום דעמון ג ומי	Top Hit Database Source	NT	EST HUMAN	L	EST HUMAN	SWISSPROT		Т	Т	IN	LI RAAN	Т	T HI IMAN		LN	T HUMAN	7	Т	T		SWISSPROT			EST_HUMAN	SWISSPROT	EST HUMAN		EST HUMAN	Τ	T
	Top Hit Acessian No.	1.0E-15 AF044083.1	-	9.0E-16 4503168 NT				-	17	5.0E-16 AJ251154.1		T	5.0E-16 BF217368 1	8127	4.0E-16 AB001523.1				75.1	75.1		4.0E-16 AL163284.2	11423191 NT	30.1			2459	Γ	2.1	Ī
	Most Similar (Top) Hit BLAST E Value	1.0E-15	1.0E-15	9.0E-16	9.0E-16 F08688.1	7.0E-16 O88807	7.0E-16 O88807	7.0E-16	6.0E-16	5.0E-16	5 OF-16	5.0E-16/	5.0E-16	5.0E-16	4.0E-16/	4.0E-16/	4.0E-16	4.0E-16 Q16853	4.0E-16	4.0E-16	4.0E-16 P08548	4.0E-16	4.0E-16	4.0E-16 AV730030	4.0E-16 P08548	4.0E-16 C05947.1	4.0E-18	3.0E-16	3.0E-16	3 OF 18 AL 04844F
	Expression Signal	6.81	3.71	1.03	2.6	1.5	1.5	6.8	8.32	1.09	1.79	1.69	3,33	8.34	1.27	1.32	1.32	3.85	3.55	3.55	-	33.8	122	1.74	1.64	5.94	2.04	1.59	1.59	1 47
	ORF SEQ ID NO:	28331	25131	24082	28486	26368	26369	-		21246	22404	27867	28914	-		22107	22108	23129	23728	23729	24737	26575	27425	28691			25319	19924	19925	_
	Exon SEQ ID NO:	18079	19492	14298	18238	16206	16206	19585	11983	11382	12514	17634	18623	19381	12079	12209	12209	13328	13952	13952	14962	16396	17226	18421	18906	18957	18964	10102	10102	10402
	Probe SEQ ID NO:	8183	9867	4404	8361	6343	6343	9816	2094	1477	2647	7784	8809	9904	2192	2328	2328	3411	4050	650	2000	6538	7358	200	9156	9244	9255	128	138	458

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Perco								_	,		_		_			_												
Exon NO::         ORF SEQ ID NO::         Expression Signal         (Top) Hit Paces         Top Hit Aces           100::         10 NO::         Signal         (Top) Hit Paces         Top Hit Aces           104:0         10 NO::         Signal         (Top) Hit Paces         No.           134:1         21207         2.01         3.0E-16 AF135448.1           13785         22670         4.05         3.0E-16 AF020503.1           13785         22671         2.01         3.0E-16 AF020503.1           15373         25431         1.41         3.0E-16 AF020503.1           16508         27922         3.08         3.0E-16 AF020550.1           1754         27922         3.08         3.0E-16 AF0023529.1           1754         1.27         3.0E-16 AF0023529.1           1754         1.27         3.0E-16 AF0023529.1           12524         1.71         2.0E-16 AF0023529.1           12524         1.71         2.0E-16 AF0023529.1           12524         1.33         2.0E-16 AF002719.1           16526         2.55         1.0E-16 AF200719.1           16526         2.55         1.0E-16 AF200719.1           16526         2.55         1.0E-16 AF200719.1           17217 </td <td>bes Expressed in Heart</td> <td>Top Hit Descriptor</td> <td>Homo saniene TSX (TSX) pseudoceno come E</td> <td>ZONADHESIN PRECURSOR</td> <td>ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]</td> <td>Lower control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the</td> <td>Trunio Sapiens FrA3B common tragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5</td> <td>AV68/393 QLC Home emigra aDNA - Land Cl. Colored Al</td> <td>Homo saciens divinicen 3 (GPC3) mane martial and standards.</td> <td>am98h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMACE:1684185 3' similar to contains THR h2 THP constitue element</td> <td>60724653RE1 NIH MGC 621</td> <td>Homo sapiens A DPIA TP corries across A Nation And Services (ANT 2)</td> <td>Home saciens chromesome 21 reamont 10 24 2020</td> <td>af06d04.s1 Spares Pestis NHT Home semiser COMA 11.1.111.001</td> <td>Human SSAV, related and communic refraince 1 TD III.</td> <td>H. Sapiens ONA for endopendity retroited life along a legion of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of th</td> <td>TUBLUE I STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF T</td> <td>nz47f06.x5 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:054849 054849</td> <td>Homo saviers with item times from formal in 12 IR:008905 ; contains MER7.11 MER7 repetitive element;</td> <td>af39911:S1 Some solution was shall like a NozHFB gw Homo sapiens cDNA clone IMAGE:1034084 3' similar to</td> <td>ONA BRIDA &amp; OZOZO 200 240 BRIDA 2011</td> <td>Homo sapiens CCR8 chemokine recently (AMADDA)</td> <td>MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN</td> <td>NIMASE MS I</td> <td>OV2-PT0012-04040-124-05 BT002-1</td> <td>CM1-NN1003-200300-153-601 NN1003 Home contains only</td> <td>tg22c11.x1 NCI_CGAP_CL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element:</td> <td>xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element;</td>	bes Expressed in Heart	Top Hit Descriptor	Homo saniene TSX (TSX) pseudoceno come E	ZONADHESIN PRECURSOR	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]	Lower control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the	Trunio Sapiens FrA3B common tragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	AV68/393 QLC Home emigra aDNA - Land Cl. Colored Al	Homo saciens divinicen 3 (GPC3) mane martial and standards.	am98h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMACE:1684185 3' similar to contains THR h2 THP constitue element	60724653RE1 NIH MGC 621	Homo sapiens A DPIA TP corries across A Nation And Services (ANT 2)	Home saciens chromesome 21 reamont 10 24 2020	af06d04.s1 Spares Pestis NHT Home semiser COMA 11.1.111.001	Human SSAV, related and communic refraince 1 TD III.	H. Sapiens ONA for endopendity retroited life along a legion of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of th	TUBLUE I STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF THE STOCK BOTTON OF T	nz47f06.x5 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:054849 054849	Homo saviers with item times from formal in 12 IR:008905 ; contains MER7.11 MER7 repetitive element;	af39911:S1 Some solution was shall like a NozHFB gw Homo sapiens cDNA clone IMAGE:1034084 3' similar to	ONA BRIDA & OZOZO 200 240 BRIDA 2011	Homo sapiens CCR8 chemokine recently (AMADDA)	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN	NIMASE MS I	OV2-PT0012-04040-124-05 BT002-1	CM1-NN1003-200300-153-601 NN1003 Home contains only	tg22c11.x1 NCI_CGAP_CL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element:	xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element;
Exon NO:         CNF SEQ ID NO:         Expression Signal         (Top) Hit Value         Top Hit Acess No.           10410         1D NO:         Signal Signal         (Top) Hit Value         Top Hit Acess No.           11341         21207         2.01         3.0E-16 AF735446.1           13785         2.2670         4.05         3.0E-16 AF735446.1           13786         2.2671         2.01         3.0E-16 AF73546.1           14771         24521         1.01         3.0E-16 AF020503.1           14773         25431         1.41         3.0E-16 AF0205329.1           17541         27922         3.08         3.0E-16 AF0205329.1           17578         27922         3.08         3.0E-16 AF0205329.1           12524         1.27         3.0E-16 AF0205329.1           12524         1.71         2.0E-16 AF020571.1           12524         1.77         2.0E-16 AF200719.1           12524         1.33         2.0E-16 AF200719.1           16526         2.55         1.0E-16 AF3923.1           16526         2.55         1.0E-16 AF3929.2           16526         2.55         1.0E-16 AF3929.2           16528         2.55         1.0E-16 AF3929.2           16783         <	gie Exon Pro		LN	SWISSPROT	SWISSPROT	<u>L</u>	Z P	EST HIMAN	-7	EST HIMAN	EST HIMAN	LN	NT	EST HUMAN	LN	LN		10 HANNI	NT NOWAY	FOT LIBADE	EST HIMAN	L L	TOGGOW	I DA POSITIVO	EST HIMAN	EST HUMAN	EST HUMAN	
Exon NO:         ORF SEQ Expression (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)         Mossignal (Total)	Sim	Top Hit Acession No.	AF135446.1	028983	P03200	AE020503 4		AV661393.1	AF003529.1	A1002836.1	BF690617.1	L78810.1	AL163279.2	1.1		X89211.1		A1723837 4						-			_	1.7
Exon SEQ ID         ORF SEQ Expression Signal NO:         Company of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t		Most Similar (Top) Hit BLAST E Value	3.0E-16	3.0E-16	3.0E-16	3 0E-46	3.0F-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16		2 OF-16	1.0E-16	1.0F-16	1.0E-16	1.0E-16	4 OF-46	10F-16	1.0E-16	9.0E-17	9.0E-17	9.0E-17
Exon ORI SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	1.6	201	4.05	87	66.0	1.01	1.41	4.72	1.27	3.08	1.18	0.96	1.71	1.33			2.55	22.41	244	23.72	2.84	6.59	1.31	254	202	4.87
		ORF SEQ ID NO:						24521	25431	27098		27922				23764		26720	19963		21704		25987		27416	23379		
Probe SEQ ID NO: NO: 1436 1436 1436 1436 1438 1728 1646 1646 1646 1646 1646 1646 1646 164		Exon SEQ ID NO:	Ш		_	L	L	14741	15373	16908	17541	17678	10880	12217	12524	13987		16526	10149	10361	11823	15783	15865	15783	17217	13593	15938	18600
		Probe SEQ ID NO:	467	1436	2946	3874	3875	4861	5452	7031	7691	7828	926	2337	2657	4087		6646	178	377	1928	5877	5960	6458	7349	3679	6035	6720

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C080	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'	Mus musculus apolipoprotein B editing complex 2 (Apobec 2), mRNA	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown nene	RC1-HND003-220300-021-b04 HN0003 Horno sapiens cDNA	hi81404.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695.3' sImilar to contains L1.t2 L1 repetitive element	vc05h08.r1 Stratagene lung (#937210) Homo saniens CDNA clone IMACE: 70930 F.	yd26b04.r1 Soares fetal Iver spleen 1NFLS Homo saplens cDNA clone IMAGF-10937 5'	Homo sapiens chromosome 21 segment HS21C047	ov45e04.xt Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element :	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 31	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG	hw05b04.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3181999 3'	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens SEC14 (S. cerevisiae) Hike 2 (SEC14L2), mRNA	AV720204 GLC Homo sapiens cDNA clone GLCDIF08 51	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu	repetitive element,	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'	NADHESIN PRECURSOR	ZONADHESIN PRECURSOR
אסוון וחסיין אול	Top Hit Database Source	E	EST HUMAN Q		EST HUMAN M	Г		NT	₩ 8	T HUMAN		T	Т	Γ	EST HUMAN Q	Т	Π	EST HUMAN hv	EST_HUMAN hy	H S		THUMAN	EST HUMAN re	Γ		[ _		SWISSPROT
3	Top Hit Acesston No.	9.0E-17 AF200719.1	8.0E-17 AW880701.1	8.0E-17 AL163280.2	8.0E-17 BE172081.1	8.0E-17 AV730759.1	TN 200579	7.0E-17 AF216650.1	7.0E-17 AF229843.1		6.0E-17 AW682772.1			4.0E-17 AL163247.2	_	7.	3.0E-17 P35410	-	3.0E-17 BE326522.1	3.0E-17 AB026898.1	11417968 NT	3.0E-17 AV720204.1	2.0E-17 AIZ70080.1			32.1		
	Most Similar (Top) Hit BLAST E Value	9.0E-17	8.0E-17	8.0E-17	8.0E-17	8.0E-17	7.0E-17	7.0E-17	7.0E-17	6.0E-17	6.0E-17	5.0E-17	5.0E-17	4.0E-17	4.0E-17	3.0E-17	3.0E-17	3.0E-17	3.0E-17	3.0E-17	3.0E-17	3.0E-17	2.0E-17		2.0E-17	2.0E-17	2.0E-17 Q28983	2.0E-17 Q28983
	Expression Signal	2.18	1.7	0.87	3.56	1.36	3.18	3.05	6.83	4.78	1.61	231	2.07	2.12	1.98	1.35	1.31	1.14	1.14	4.72	3.16	15.82	2.81	-	2	1.27	2.6	2.6
	ORF SEQ ID NO:				25402				26052	19986	25830	19773	26502	28887		21836	-	23293	23294	27680			20127		20127		22170	22171
	Exan SEQ ID NO:	17720	10919	13729	19444	16174	11347	15184	15921	10168	15717	9982	16335	18598	18914	11941	13082	13504	13504	17445	18890	19386	10309		10309	10896	12275	12275
	Probe SEQ ID NO:	7870	1001	3817	5427	6311	1442	5262	6017	198	5812	415	6476	8783	1716	2051	3157	3290	3280	7594	9134	6086	350		321	972	2397	2397

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT PROTEIN)	Mus misculus ulta hida entire baratin and a second of the	Mus musculus titta high suifur berefin dans committee as	Homo sapiens MHC class 1 region	OLFACTORY RECEPTORJ IKE PROTEIN OF E2	EST13504 Testis tumor Homo saniens CDNA Fi and climitant committees.	Homo sapiens chromosome 21 segment HS217047	Horno sapiens chromosome 21 segment HS24Cn47	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting	denscriptional regulatory elements)	INOLITICATOR RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	Figure Septembries and Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries of Septembries o	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR	Inoπo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes. complete cde.	W30e07 1 Spares fertal live solom AMEI S. Learning	he38e05x1 NCI_CGAP_CML1 Homo sepiens cDNA clone IMAGE:128388 5' renefitive element-contains 1 TDs 41 1 TDs 41 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 1 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TDs 11 TD	de65b05 x1 Spares fetal time NIAHI 10M Home	ge55b05 x1 Spares fetal ling NhH 19M Homes appears con line in NhH 19M Homes	URIDINE PHOSPHORYLASE (LIDREASE)	MYOSIN LIGHT CHAIN KINASE SMOOTH MISO E MI CO KOSHITATIS	2018012.51 Strategrene festa retine 937202 Home continues of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of t	ti86403.x1 Soares NSF F8 9W OT DA D 64 USES	Homo sapiens protein tyrosing phosphatase non recent.	xx10b04.x1 NCI_CGAP_PartH Homo saplens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN 14 (HI IMAAN).	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 GOS RIBOSOMAL PROTFIN 14 (HI IMAAN).	ya49c07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53285 3' similar to contains L1 repetitive element;
מוס בעמווי וס	Top Hit Database Source	SWISSPROT	TN	LN LN	N	SWISSPROT	EST HUMAN	IN	Ā	LIV	TOGGEDOT.	DATE OF THE	CMICCODAT	OWIGOTAG	I NI		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	
5	Top Hit Acession No.	2.0E-17 P12036	2.0E-17 M27685.1	2.0E-17 M27685.1	2.0E-17 AF055066.1	2.0E-17 Q95156	_		2	2 0E-47 D43304 4	P08183	1.0F-17 AI 163207 2	!	-	Ì	1.0E-17 AF224669.1	1.0E-17 R09942.1	1.0E-17 AW468468.1	1.0E-17 AI185642.1	1.0E-17 AI185642.1	216831		9.0E-18 AA174078.1	9.0E-18 AI472167.1	4758977 NT	7.0E-18 AW316976.1	7.0E-18 AW316976.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-17	20E-17	20E-17	2.0E-17	2.0E-17	2.0E-17	20E-17	2.0E-17	2.0E_47	1 0F-17 P08183	1.0F-17	1.0F-17 P02464	1 0F-17	11.77	1.0E-17	1.0E-17	1.0E-17	1.0E-17	1.0E-17	1.0E-17 Q16831	1.0E-17 Q28824	9.0E-18	9.0E-18	8.0E-18	7.0E-18	7.0E-18	7.0E-18 R16220.1
	Expression Signal	5.62	1.95	1.95	2.07	1.44	1.38	2.72	2.72	53	337	2.45	1,68	146	2	1.01	71.17	4.7	1.44	1.44	1.32	2.01	0.96	3.26	1.75	8.39	8.39	0.85
	ORF SEQ ID NO:	22621		25018		26779			27773	27981					L				26037	26038	26232	28821	22196		23415	20121	20122	24774
	Exan SEQ ID NO:	12826	15216	15216		_			17549	17737	10665	11630	11959	12170		l	13947	ſ	15911	15911	16082	18536	12299	17328	13630	10305	10305	15003
	Probe SEQ ID NO:	2899	5295	5235	5790	6711	6925	7699	7699	7887	733	1729	2069	2287		3519	4045	5885	9009	9009	6216	8719	2422	7468	3718	346	346	5136

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				Mont Cimilor			
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5293	15214	25015	2.55		4.0E-18 AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8370	18247	28499	7.12		4.0E-18 AA371807.1	EST HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) Il Homo sapiens cDNA 5' end similar to EST containing O family repeat
831	10758		2.38		3.0E-18 AA814196.1	EST HUMAN	ob23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RSE_HUMAN P46782 40S RIBOSOMAL PROTEIN S5.;
914	10838	20686	2.41		3.0E-18 BE088634.1	EST_HUMAN	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
3867	13778	23571	1.19		3.0E-18 AL163247.2	FN.	Homo sapiens chromosome 21 segment HS21C047
6084	16029		5.2	į	3.0E-18 BE001671.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sepiens cDNA
9642	19210		4.92		3.0E-18 AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5
251	10217	20034	2.83		2.0E-18 AW836820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1135	11049		47.22		2.0E-18 BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5
6432	15242		66		2 0E_18 A 4 8 6 8 6 1 0 1	INAMIL TOO	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652.3' similar to TR:014577
5380	L				2 0F-18 D14547 1	LN LN	Human DNA SiNF renetitive element
5380	1	25150			2 OF 18 D14547 1	-N	Human DNA SINE renetitive element
5585	1				2.0F-18 BF347229 1	EST HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5
	1						HIGHMAN SPACES NET T CRC St Down control Hard MACE STOCKED 19 in 11-44 contains
5814	15720	26834	3.53		2.0E-18 AW665853.1	EST_HUMAN	Institut. Sociales in P. 1. Godo. 3 Franta sapiens curva cione invalor. 2979994 3 similar to contains MER19.12 MER19 repetitive element;
							xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2
- 33	17629	27861	1.53		2.0E-18 AW151673.1	EST_HUMAN	MER10 repetitive element ;
9777	17629	27862	1.53		2.0E-18 AW151673.1	EST HUMAN	x/67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element;
							ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
8340	18217	28469	5.32		2.0E-18 AW470791.1	EST_HUMAN	THR repetitive element;
							xg47e09.x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
8968	18774	29065	4.44		2.0E-18 AW151299.1	EST_HUMAN	MER8 repetitive element;
9325	11049		3.15		2.0E-18 BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
							ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains
4318	14215		1.02		1.0E-18 T95406.1	EST_HUMAN	L1 repetitive element;
5286	15208		2.38		1.0E-18 AV653405.1	EST_HUMAN	AV653405 GLC Homo saplens cDNA clone GLCDKE113'
5419	. '		1.97		1.0E-18 D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5419					1.0E-18 D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5883	15790	25912	1.32		1.0E-18 AL163280.2	ΝΤ	Homo sapiens chromosome 21 segment HS21C080

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			-		7	_	-	-	_	_	_		_	_	_,	٠,	_		_			<del></del>			
Single Exon riodes Expressed in Heart	Top Hit Descriptor	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and socialm phosphate transporter (NDT3) gene, percentary haemochromatosis	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking reneat regions	zf11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element:	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone iMAGE:712811 5' similar to contains MER19.t2	HSC23F051 normalized infant brain cDNA Homo seniors cDNA class c 23695	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens chromosome 21 segment HS21C003	Homo saplens mRNA for KIAA1143 protein, partial cds	#11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element	EST387007 MAGE resequences, MAGN Homo sapiens cDNA	Homo sabiens DEAD/H (Asp-Gli-Ala-Asn/His) hrv notmentide & /DNA hall as a second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of se	Rattus novecicus co151 mRNA partial cds	Zi60b01.51 Soares fetal liver splean 1NFI S S1 Homo conione - DNIA plane 1848 CE 10054.25 of	PM0-CT0248-131099-001-001 CT0248 Home sapiens cDNA	OLFACTORY RECEPTOR 6 (M50)	OLFACTORY RECEPTOR 6 (M50)	Homo sapiens Xq pseudoautosomal region; segment 1/2	DKFZp762F192_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)	%87b02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2864171 3' similar to contains element the solution of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6SBAZT, TCRBV5S6A3N2T, TCRBV13S6AZT, TCRBV6S9P, TCRBV5S3AZT, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6AZT, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4AZT, TCRBV6S4A1	TCRBV23S1A2T, TCRBV12>	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
gle Exuli Pio	Top Hit Database Source	Ę	Į.	EST HUMAN	EST HUMAN	EST HUMAN	NT	LN	N	EST HUMAN	EST_HUMAN	IN	F	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	TN	EST_HUMAN	SWISSPROT	EST_HUMAN		TN.	LN	EST_HUMAN
	Top Hit Acession No.	1.0E-18 U91328.1	1.0E-18 AF003529.1	9.0E-19 AA281961.1	9.0E-19 AA281961.1	9.0E-19 F08688.1	9.0E-19 AL163203.2	9.0E-19 AL163203.2	9.0E-19 AB032969.1	9.0E-19 AA281961.1	8.0E-19 AW974902.1	4758139 NT	7.0E-19 AF092090.1	7.0E-19 AA705684.1	6.0E-19 AW852930.1	P34986	234986	6.0E-19 AJ271735.1	AL120817.1	200193	4W183725.1		166060.1	3B007970.1	4.0E-19 BF697362.1
	Most Similar (Top) Hit BLAST E Value	1.0E-18	1.0E-18	9.0E-19	9.0E-19	9.0E-19	9.0E-19	9.0E-19	9.0E-19	9.0E-19	8.0E-19	7.0E-19	7.0E-19	7.0E-19	6.0E-19	6.0E-19 P34986	6.0E-19 P34986	6.0E-19	6.0E-19	5.0E-19 Q00193	5.0E-19 AW1837	· [	5.0E-19 U66060.1	4.0E-19 /	4.0E-19 E
	Expression Signal	4.4	2.53	4.28	3.19	5.21	2.46	2.46	3.88	8.69	1.54	1.58	2.15	2.95	1.02	1.36	1.36	1.18	1.09	5.24	7.19		1.52	1.45	1.39
	ORF SEQ ID NO:	27769	25324	20289	20289		27110	27111	28608	20289		21987	25913			24041	24042		24595	25562	28921		20000	20230	22406
	Exon SEQ ID NO:	17546	18980	10475	, 10475	16464	1		18343	10475	10950	12085	15791	19742	13626	14256	14256	14580	14829	15486	18637	40405	10/83	3 3	12516
	Probe SEQ ID NO:	7696	9277	533	534	6584	7042	7042	8470	9042	1032	2198	5884	9179	3713	4360	4360	4694	4952	5571	8824	00,00	542	7 0	2649

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Table 4

Single Exon Probes Expressed in Heart	Top Hit Descriptor	100 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1	00 1441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5	AVIZULZA DI UNIONO Sapiens CDNA clone HTCBTA01 5' Zh78408.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to	zunanıs Michaelt Michael Epetitive element; zh78408.st Soares_feta_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE-318101 3's similar to	contains MER30.tf MER30 repetitive element;	Mus musculus MMAN-g mRNA, complete cds	Ivius rijusculus MiMAN-g mRINA, complete cds	L24gus.x1 NCI_CGAP_Ov35 Homo saplens cDNA clone IMAGE:2293396 3'	AVS-D 1004S-USUCLUL-USU-C04 D 10043 Home sapiens cDNA	Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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TRANSCRIPTASE :	SOME AND THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF 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ZONADHESIN PRECURSOR	ZUNAUHESIN PRECURSOR	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA	Homo saplens KGH1 gene, retrovirus-like element	oe35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMACE-1120e025.21	MER4 repetitive element;
gle Exon Pro	Top Hit Database Source	ECT (11114AN)	EST HIMAN	EST HIMAN	100	FO HOMAN	Z LV	EST DIMEN	EST LIMAN	NO.	SWISSPBOT		ESI HUMAN	Z	TORISSIMS	Т			T	EST_HUMAN		TOGGSOWS	7	DARGE				EST HUMAN N
<u>.</u>	Top Hit Acession No.	8 0F-20 RE622434 4	5.0E-20 AV725123.1	5.0E-20 W90525.1	5 0E-20 Wook2E 4	7,	¥ 4	T	4.0E-20 AW937469 1	Τ						22.1				Z.UE-ZU AA516335.1	2.0E-20 AW303868.1			E474E90	000+710			
	Most Similar (Top) Hit BLAST E Value	8 OF-20	5.0E-20	5.0E-20	5.05-20	50F-20	5.0E-20	4.0E-20	4.0E-20	3.0E-20	3.0E-20 P23273	3 OE 30	2 DE 20	3.0E-Z0	3.0E-20 P11369	3.0E-20	2.0E-20	2.0E-20	100	Z.UE-20)	2.0E-20/	2.0E-20 028983	2.0E-20 028983	20F-20	2.0F-20 D10083 4	20E-20 D10083 1	000	2.UE-2U AA / 66 / 55.
	Expression Signal	2.55	1.17	4.66	4.68	4	1.44	6.03	1.17	1.04	1.69	98.0	3,8		2.08	5.37	4.52	2.03	200	2.03	2.72	4.32	4.32	11.35	2.95	2.95	40	106.1
	ORF SEQ ID NO:	23850		26704	26705	27197	27198		28087	21876	23795	24201				25352		20852	20853			24525	24526		27378	27379	29089	
	Exon SEQ ID NO:	14075	14385	16514	16514	17005	17005			11981	14015	14417	17049		17946	18929	10741	11011	11011		10741	14746	14746	14960	17177	17177	18797	
	Probe SEQ ID NO:	4175	4491	6634	6634	7128	7128	6624	7995	2092	4115	4524	7172		8055	9185	813	1095	1095		2786	4866	4866	2090	7301	7301	8993	

Page 181 of 413 Table 4 Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2 MER4 repetitive element;	CHR220310 Chromosome 22 exon Hamo sapiens cDNA clane C22_391 5'	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element;	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.t2 L1 repetitive element;	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	nc60d08.rt NCI CGAP Pr1 Homo sapiens cDNA done IMAGE:745694 similar to contains L1.t3 L1	repetitive element;	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpf12-8J21	RC3-NN0068-090500-021-b03 NN0068 Hamo saplens cDNA	bb30a02.y1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN 095169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR;	ob71f06.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1336835 3'	ATP SYNTHASE A CHAIN (PROTEIN®)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'	Homo sapiens dNT-2 gene for mitochondrial 5(3) deoxyribonucleotidase (dNT-2 gene), exons 1-5	Human chromosomal protein HMG1 related gene	2g73403.s1 Soares_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR	repetitive element;	Homo sapiens PTD013 protein (PTD013), mRNA	601304123F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA	om23g03.s1 Soares_NPL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:002711   002711 PRO-POL-DUTPASE POLYPROTEIN;	601649871F1 NIH_MGC_74 Homo septens cDNA clone IMAGE:3933880 5'	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
יייייייייייייייייייייייייייייייייייייי	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	F	Ę		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	TN	TN		EST_HUMAN	NT	EST_HUMAN	IN	EST HUMAN	EST_HUMAN	M
Signio	Top Hit Acessian No.	\A766755.1	155371.1	1.0E-20 AA281961.1	3F115158.1		E0000004 4	1.UE-20 AF 223391.1	1.0E-20 AA420453.1	9.0E-21 AJ003514.1	4W898189.1	8.0E-21 AW674891.1	8.0E-21 AA809411.1	021330	215800	715800	7.0E-21 AA046502.1	7.0E-21 AJ277557.1	7.0E-21 D14718.1		7.0E-21 AA723404.1	7706668 NT	6.0E-21 BE408611.1	5902031 NT	AA928194.1	BE968839.1	· 4885474 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-20 AA7667	2.0E-20 H55371	1.0E-20 A	1.0E-20 BF1151	1.0E-20	100	1.02-20.1	1.0E-20/	9.0E-21	9.0E-21 AW8981	8.0E-21	8.0E-21	8.0E-21 O21330	7.0E-21 P15800	7.0E-21 P15800	7.0E-21	7.0E-21	7.0E-24		7.0E-21	7.0E-21	6.0E-21	5.0E-21	5.0E-21	5.0E-21	5.0E-21
	Expression Signal	1.95	1.5	5.25	-	2.42	700	701	1.84	1.08	235	1.74	3.42	4.02	2.07	2.07	4.96	1.43	6.84		2.94	2.37	0.94	1.6	1.08	2.65	5.98
	ORF SEQ ID NO:	29090	25129					04807					28922			21804		26962	27102		28220			20678			24375
	Exan SEQ ID NO:	18797	19482	<u> </u>			1	76081	19011	12810	18830		1		L	11914	14061	16766	16913		17971	<u> </u> _	13920	10831	12119		Ш
	Probe SEQ ID NO:	8993	9574	1967	4338	7285	300	8838	9321	2883	9045	7115	8825	9207	2023	2023	4161	6887	7036		8080	8590	4014	807	2234	4266	4696

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Table 4
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	Homo sapiens DNA for emylaid precursor motein complets of	0086e08.51 NCI_CGAP_KId5 Home sepiens cDNA clone IMAGE:1573094 3' similar to TR:Q16630 Q16530	Raffus nonvericus mRNA for TIM completed	Homo sapiens chromosome 24 sectional USAs Const.	Homo sapiens I GMD/8 gane	601844465F1 NIH MGC 54 Homo senions of NA - 1. 114.0F 400.5	RC1-070083-100800-019-018 OTIONS Home content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the 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Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and all Contract and 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Soares, testis, NHT Homo:sapiens cDNA clone IMAGE:1838338 3' similar to gb:M64241 QM	iono sapiens SET domain and marines trans-	1294803 X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT
Top Hit Database Source	IN	EST HI IMAN	L	Į.	<u>k</u>	EST HUMAN	EST HUMAN	EST HUMAN	N	EST HUMAN	N	N.	EST HUMAN	SWISSPROT	SWISSPROT	HAMI IL	EST DIMAN	EST HUMAN	COT LINAAN	EST HIMAN	Г	Г	EST HIMAN	Т	Т			T_HUMAN
Top Hit Acession No.	5.0E-21 D87675.1	4.0E-21 AA970713.1		3.0E-21 AL163201.2	3.0E-21 AJ007973.1	3.0E-21 BF184739.1	3.0E-21 BF361093.1	3.0E-21 AW897760.1	3.0E-21 AL163213.2		2.0E-21 AB007857.2				Q28983	2.0E-21 AI6245R2 1	BE141785 1	2.0E-21 AU136779.1	l	: -		2.0E-21 AF176815.1	1.0E-21 AA557657 1	1.0E-21 AI601264.1	1.0E-21 AL079752.1	1.0E-21 AI223104.1	5730038 NT	11702438.1
Most Similar (Top) Hit BLAST E Value	5.0E-21	4.0E-21	4.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21 Q28983	2.0E-21 Q28983	2.0E-21	2.0E-21	2.0E-21	2.0E-24	20E-21	2.0E-21	20E-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	9.0E-22 AI702438.
Expression Signal	96'0	1.24	3.06	1.06	4.04	1.72	4.79	1.55	1.32	14.75	0.85	0.85	2.09	2.89	2.89	1.77	4.66	3.43	1.98	1.92	1.92	5.13	1.68	2.46	2.43	4.43	1.46	2,55
ORF SEQ ID NO:		21473	26138	22015	22762		26100	27656	24992		20688	20689		22361	22362	25126	26944	27190		28776	28777	1	20394			26289		23993
Exan SEQ ID NO:	14977	11602	16000							10114	10843	10843	11106	12468	12468	15290	16749	16999	18287	18501	18501	19072	11142	11286	15813	16134	17871	14209
Probe SEQ ID NO:	5109	1701	6106	2228	3041	5749	6206	7589	8684	5	919	919	1196	2599	2599	5370	0289	7122	8412	8636	8636	9425	1235	1381	2907	6229	8021	4312

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Table 4
Single Exon Probes Expressed in Heart

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Single Lyon riones Capressed in Rear	, Top Hit Descriptor	Homo sapiens chromosome 21 seament HS24Cn04	Homo sabiens chromosome 21 segment HS21C001	AV761874 MDS Homo sablens cDNA clone MDSCCCop F	AU140358 PLACE2 Home saniens cDNA clans DI ACESSASSES	Mus musculus TE-1 cell anomineis related markets 45 (Televisis - Days	CM0-HT0179-281099-076-h05 HT0179 Home canions ANIA	2k67a06,r1 Sogres pregnant utents NHHDI Home annions and Alexander Areas an	Homo sapiens chromosome 21 segment HS210046	ALPHA-2-MACROGLOBULIN PRECIRSOR (AI PHADAM)	Homo sabiens gene for activity recentor two IIR commissions	Homo sapiens HSPC220 mRNA, complete cris	EST00738 Fetal brain. Stratagene (cattlegalance) Homo september Child Alone Lieb Andre	Homo sapiens T cell receptor beta locus TCRBV75345 th Trop14555	WX05g07.x1 NCI CGAP Gas4 Homo saniens CDNA close (NA GE : 252.794.2.2)	Homo sapiens chromosome 21 segment HS21C402	Human dystrochin (DMD) rene avvne 7 8 and 0 and and 4 d 2	naa27b06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu	repeative element;	Homo saplens Xq pseudoautosomal region; segment 1/2	rouns septens circonosome 21 segment HS21C002	001862813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5	Induito sapiens ciromosome 21 segment HS21C009	AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN) contains L1 #11 reposition demonstration	WIG6b04.X1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN 1.21	Human chromosomal protein HMG1 related gene	db28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to	RCS-BT0707-150300-031-H10 BT0707 United Control Control	VX730D5 s1 Spares melanovide 2NHMM Home conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the conjunction in the 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מום דייטיין בו וס	Top Hit Database Source	LN L	FX	EST HUMAN	EST HUMAN	IN	EST HUMAN	EST HUMAN	N TN	SWISSPROT	F	LN L	EST HUMAN	TN	EST HUMAN	IN IN	Į.	144111111111111111111111111111111111111	EST FIUMPIN		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ESI_HUMAN		EST_HUMAN	EST HUMAN	LN	EST HUMAN	EST HIMAN	EST HUMAN	SWISSPROT	TN	T HUMAN
5	Top Hit Acession No.	9.0E-22 AL163201.2	9.0E-22 AL 163201,2	9.0E-22 AV761874.1	9.0E-22 AU140358.1	9790256 NT	8.0E-22 BE144748.1	l	ŀ		7.0E-22 AB008681.1	7.0E-22 AF151054.1	M78590.1	7.0E-22 AF009660.1	6.0E-22 AW029123.1		5.0E-22 U60822.1	DE476644 4	10211.1	4.0E-22 AJZ/1/35.1	) ; !	-	1	3.0E-22 AI469679.1	3.0E-22 Al859038.1		3.0E-22 Al090125.1				8394043	2.0E-22 AW817794.1
	Most Similar (Top) Hit BLAST E Value	9.0E-22	9.0E-22	9.0E-22	9.0E-22	9.0E-22	8.0E-22	8.0E-22	7.0E-22	7.0E-22 Q61838	7.0E-22	7.0E-22	7.0E-22 M78590.	7.0E-22	6.0E-22	5.0E-22	5.0E-22	5 0E-22 DE476E4	100	4.0E-22	20.7	4.0E-22		3.0E-22	3.0E-22	3.0E-22 D14718.1	3.0E-22	3.0E-22 BE08984	2.0E-22 N24942 1	2.0E-22 P24916	2.0E-22	2.0E-22/
	Expression Signal	1.26	1.26	3.65	2.92	2.39	4.55	3.8	4.23	2.32	1.18	1.34	2.63	1.86	1.82	2.53	3.97	203	200	0.00	100	1.51		1.2	1.86	1.49	2.72	2.75	2.86	1.33	4.06	1.26
	ORF SEQ ID NO:	27070	17072	28309	29048					23861	24613		27196	27599		25955	28001				AACRC				22288		24374	26864		22244	23091	23808
	Exon SEQ ID NO:	16879	16879	18059	18753	18800	1	1	_1			_ {			- 1	15832	17762	19213	L	1	L	1		10868	12397	13534	14581	16672	11805	12352	13292	14033
	Probe SEQ ID NO:	7002	7002	8171	8945	8997	933	6099	949	4186	4969	704	7127	7538	8796	5927	7912	9645	35BA	6902	8105	9803		943	2523	3820	4695	6793	1910	2476	3373	4133

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Fig. 2   Exp. 1   Copp. 552   Expression   Copp. 187   Copp. 18   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187   Copp. 187			_	_							_	_,																	
Exan         ORF SEQ         Expression         (Top Hit Acession Value Seq In 1.44         Cop Hit Acession Source Signal         Top Hit Acession Source Signal         Top Hit Acession Source Signal         Top Hit Acession Source Signal         Top Hit Acession Source Signal         Top Hit Acession Source Source Signal         Top Hit Acession Source Source Source Source Source Signal         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source So	bes Expressed in Heart	Top Hit Descriptor	202001.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 6' similar to db:X72308 MONOCYTE CHEMOTACTIC PROTEIN 9 PDE CHESCO A ILLIAMAN	RC0-TN0079-150900-025-h12 TN0079 Homo saniens cDNA	ql76h06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains	MOGANTAL STANCE CONTROLLY	INO4h11.s1 NCI CGAP Pr22 Homo sanians cDNA clone IMAGE:12192693	ha24f04 x1 NCL CGAP Kidto Homo seniene cONA class HA CE 12 19209 3	Home sapiens chromosome 21 serment HS21Chan	PM4-SN0020-010400-009-b02 SN0020-0-000-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	Human familial Alzheimer's disease (STM2) none complete add	Human DNA SINF renefitive derrent	WR0-BT0659-220200-002-002-00-002-00-00-00-00-00-00	IL2-UM0076-070400-061-F11 IM0076 Home emisse ablive	Gallus gallus Dach2 protein (Dach2) mBNA complete de	HA2340 Human fetal liver cDNA library Homo conjunctions	HA2340 Human fetal liver CDNA library Home continued only	AV647246 GI C Home september 2011 Average Control	Homo sapiens DKFZP56400463 protein (DKFZP56400483) ENIA	Homo saplens Not56 (D. melanoraster-like protein (NOT561) - DNA	Rattus horveoleus RIM1B (RIM1B) mRNA complete ada	Homo saplens chromosome 21 segment HS21C049	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo saptens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds.	9959c03.x1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin	Pondo piermaens offentant recents (PDV445)	Pondo pyomaeus offaction recentiv (DDV/16)	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
Exon         ORF SEQ         Expression Signal         (Top) Hit Top Hit Acess No.         Top Hit Acess No.           19447         25661         1.44         2.0E-22 W39456.1           17446         27710         1.44         2.0E-22 BF092116.1           17490         27711         7.07         2.0E-22 AA715315.1           17490         27711         7.07         2.0E-22 AA715315.1           18779         2.9071         2.04         2.0E-22 AA715315.1           18779         2.9071         2.04         2.0E-22 AA715315.1           18779         2.500         1.78         2.0E-22 AA715315.1           18779         2.500         1.78         1.0E-22 AA715316.1           18779         2.500         1.78         1.0E-22 AA715376.1           18779         2.500         1.0E-22 AA715376.1           18741         2.6589         1.49         1.0E-22 AA715376.1           18411         2.6589         1.48         8.0E-22 AA715376.1           1841         2.4936         1.48         8.0E-23 AA715376.1           15165         24936         1.48         8.0E-23 AF198349.1           14649         2.4438         1.04         7.0E-23 AF198349.1           14656	gie Exon Proi		EST HUMAN	EST HUMAN	EST HIMAN	EST HIMAN	EST HUMAN	EST HUMAN	TN	EST HUMAN	N-	Į.	EST HUMAN	EST HUMAN	L	EST HUMAN	EST HUMAN	EST HUMAN	N	L	Ł	LN	Į.	TA	Ī				
Expn NO:         ORF SEQ ID NO:         Expression Signal         Mos Bignal         Mos Bignal <t< td=""><td>Uio</td><td></td><td>W39456.1</td><td>BF092116.1</td><td>A/276522.1</td><td>AA715315.1</td><td>AA715315.1</td><td>AW418960.1</td><td>AL 163280.2</td><td>AW865517.1</td><td>J50871.1</td><td>014547.1</td><td></td><td></td><td></td><td></td><td>AM33716.1</td><td>1,0647246.1</td><td>10092626</td><td>5031952</td><td>NF199333.1</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	Uio		W39456.1	BF092116.1	A/276522.1	AA715315.1	AA715315.1	AW418960.1	AL 163280.2	AW865517.1	J50871.1	014547.1					AM33716.1	1,0647246.1	10092626	5031952	NF199333.1								
Expn         ORF SEQ         Express           SEQ ID         ID NO:         Signe           19447         25561         Signe           19447         25561         Signe           17490         27710         27711           17490         27771         25071           18779         29071         2500           18304         2500         2500           1343         23236         24036           1342         2303         24386           1345         24936         24936           13192         24936         24936           13192         24936         24936           13007         23846         25038           14649         25339         25338           18899         25339         18899           19021         25297         2508           19454         25797         3           19454         25797         3		Most Similar (Top) Hit BLAST E Value	2.0E-22	20E-22	2.0E-22	20E-22	20E-22	2.0E-22	2.0E-22	1.0E-22/	1.0E-22	1.0E-22	1.0E-22	9.0E-23	8.0E-23/	8.0E-23/	8.0E-23/	7.0E-23/	7.0E-23	7.0E-23	6.0E-23	6.0E-23	6.0E-23 A	6.0E-23	6.0E-23 A	5.05-231	5.0E-23	6.0E-23 A	
Exan ORI 19447 19447 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 19454 194		Expression Signal	1.44	3.39	1.49	7.07	7.07	2.04	1.85	1.78	2.65	1.74	1.49	4.71	0.84	1.48	1.48	1.45	1.04	3.51	1.62	3.12	1.99	1.99	2.18	3.51	3.51	3.04	
		ORF SEQ ID NO:										23084	26589		23236	24935			24438	28526		23846	25338	25339	25297	25088	25797	25797	
Probe SEQ ID NO: NO: 7640 8874 88974 8898 8898 8898 8898 8898 889		Exon SEQ (D NO:	19447	15655	17446	17490	17490	18779	19304	11733	12413	13284	16411	19342	13439	15165	15165	13192	14649	18274	13305	14071	18899	18899	19021	15262	19454	19454	İ
		Probe SEQ ID NO:	5570	5747	7595	7640	7640	8974	6006	1836	2539	3365	6553	9844	3523	5241	5241	3271	4764	8398	3387	4171	9146	9146	8341	5341	5781	6397	

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Table 4
Single Exon Probes Expressed in Heart

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Single Exort Probes Expressed in Heart	Top Hit Descriptor	235g09.r1 Soares, pregnant uterus. NbHPU Homo sapiens cDNA clone IMAGE:503968 5' stmilar to	Himan endocember extension of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of	Human endorence setsoinal element HC2	Home contant KIAAA884 American Media	Human matrix Gla protein (MGP) news commits and LZTFL1 gene	TENASCIN-X PRECURSOR (TALX)/HEYABBAALION 1 1273	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	qs73f11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537	MB3-HT0487-15/200-113 201 UTA-22 U-	Various fatel line and a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens con a feet of the sapiens	yr16a02.r1 Soares fetal liver spleen 1NFLS Home seriese ANA April 114.0F 205418 5	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	1 (CH 3A4) and cyconrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds.	Human alcohol dehinfronensee gemen enkimis (ADLIA)	Homo saplens T cell recentor heta focus. TODAVICE A CONTROLLE	AU133931 OVARC1 Homo saniens cDNA clare OVARC52 region	Homo sablens chromosome 21 segment HS21 Ones	Hamo sablens chromosome 21 segment HS21 Coso	601236455F1 NIH MGC 44 Home sapiens cDNA chare IMA CE 25025F2 F1	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA done IMAGE.782698 5 similar to contains PTR5.r2 PTR5 repetitive element	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to	NE ENCTORY DECEDED IN THE PROPERTY.	OF FACTORY RECEPTOR 1 (VE PROTEIN 13	ONO DITORA 1 100-LINE PROTEIN IS	Macaca filedon mBNA F T C T C	Homo capiene chromosoco 24	Homo sapiens 959 kh contin between AMI 4 and OPE4	nn31h05.s1 NCI_CGAP_Gas1 Homo saplens cDNA clone IMAGE:1086529 3' similar to SW:POL_MLVRK
פום באטוו רונס	Top Hit Database Source	EST HIMAN	NT	Ę	5	Į.	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN		TN	Į.	TN	EST HUMAN			EST_HUMAN	EST_HUMAN		T	T	Т	Т		IN	EST_HUMAN
5	Top Hit Acession No.	3.0E-23 AA130165.1	3.0E-23 Z70664.1	3.0E-23 Z70664.1	2.0E-23 AJ289880.1	2.0E-23 M55270.1	P22105	P22105	2.0E-23 AI201458.1	2.0E-23 BE165980.1	2.0E-23 H59931.1	2.0E-23 H59931.1		5	2.0E-23 M32658.1	7	Ξ	2	2	1.0E-23 BE378471.1	1.0E-23 AA448097.1	9.0E-24 AA663213.1	T		954.1	Γ	2	-	_
	Most Similar (Top) Hit BLAST E Value	3.0E-23	3.0E-23	3.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23 P22105	2.0E-23	2.0E-23	2.0E-23	2.0E-23		2.0E-23	2.0E-23	2.0E-23 AF009660	2.0E-23 AU13393	1.0E-23	1.0E-23 /	1.0E-23	1.0E-23	9.0E-24	8.0E-24 P23269	8.0E-24 P23269	7.0E-24	6.0E-24 AB001421	6.0E-24 AL 163249	5.0E-24 AJ229043	4.0E-24 AA594178.
	Expression Signal	3.56	3.61	3.61	4.38	2.77	1.06	1.06	1.46	3.03	2.98	2.98		5.62	2.69	2.47	2.02	1.6	4.49	2.91	4.54	1.88	1,08	1.08	1.31	2.4	10.14	7.18	3.06
	ORF SEQ ID NO:	26653	27435		20402			22520			23589	23590						24110			26937		24225	24226			20595	23585	25609
	Exon SEQ ID NO:				_			12627			13804	13804		16475	18888	19218	19676	14323	14543	15937	16744	10481	14442	14442	13708	10623	10748	13800	15526
	Probe SEQ ID NO:	6580	7329	7329	650	1126	2765	2765	3325	3655	3894	3894		6595	9131	9656	9774	4428	4657	b034	6865	540	4549	4549	3796	8	820	3880	5611

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens mRNA for KIAA1093 protein, partial cds	Homo saplens G-2 and S-phase expressed 1 (GTSE1), mRNA	hh68c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2. MER29 repetitive element:	Homo sapiens chromosome 21 segment HS21C052	601810449F1 NIH_MGC_48 Hamo sapiens cDNA clone IMAGE:4053396 5'	zp11f09.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:609161 5'	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5	Human O family dispersed repeat element	Homo sapiens CGI-127 protein (LOC51646), mRNA	QV0-ST0294-100400-185-c10 ST0294 Homo saplens cDNA	Mus musculus mRNA for HGT keratin, partial cds	Homo sapiens PTEN (PTEN) gene, exon 2	Homo sapiens chromosome 21 segment HS21C103	CMD-NN1010-130300-281-d07 NN1010 Homo saplens cDNA	ne92e10.s1 NOI_CGAP_Kld1 Homo saplens cDNA clone IMAGE:911754 similar to contains MER1.b2	IMEN I repetuve element;	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR	repetuve eletrent	m25n05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.;	zh65h07.r1 Soares_fetal_fiver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5	Mus musculus ctogelin (Otog), mRNA	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA	EST391217 MAGE resequences, MAGP Homo sapiens cDNA	ye58h04.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:121783 5'	PM3-OT0093-280200-001-g07 OT0093 Homo saplens cDNA	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)	Homo sapiens chromosome 21 segment HS21C010
	Top Hit Database Source	IN	N F	EST HUMAN	R	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	INT	EST_HUMAN	N	TN	IN	EST_HUMAN	144.6	ESI_HUMAN	: :	ESI HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	M	ᅜ	SWISSPROT	NT
	Top Hit Acesslon No.	AB029016.1	11418318 NT	3.0E-24 AW614871.1	AL163252.2	BF127762.1	2.0E-24 AA167539.1	2.0E-24 AW898189.1	AL119158.1	M28877.1	7706340 NT	1.0E-24 AW820194.1	D86423.1	1.0E-24 AF143313.1	1.0E-24 AL163303.2	AW901164.1	7 7 7 0007 1	7.0E-25 AA483944.1		7.0E-25 AA468645.1	AA583540.1	ď	7305360 NT	AW838171.1	5.0E-25 AW979107.1	T98107.1	AW887671.1	BE170957.1	8923321 NT	8923321 NT	P29622	AL163210.2
	(Top) Hit BLAST E	4.0E-24 AB0290	4.0E-24	3.0E-24	3.0E-24 AL1632	3.0E-24 BF127	2.0E-24	2.0E-24	2.0E-24 AL 1191	2.0E-24 M2887	1.0E-24	1.0E-24	1.0E-24 D8642;	1.0E-24	1.0E-24	1.0E-24 AW901	10 10	7.05-25		/.UE-25	7.0E-25 AA583	6.0E-25	6.0E-25	5.0E-25 AW838	5.0E-25	4.0E-25 T98107	4.0E-25 AW887	4.0E-25 BE170	3.0E-25	3.0E-25	3.0E-25 P2962	3.0E-25/AL163;
	Expression Signal	2.12	1.53	3.02	4.12	5.14	2.33	1.01	3.14	6.55	2.18	1.87	0.91	1.63	4.07	1.98		2.32	. !	3.70	7.46	4.32	11.44	96.0	3.61	2.08	2.78	3.02	2.66	2.66	0.85	2.47
	ORF SEQ ID NO:	25293	25203	1	27463		22078		27146		21438		22710		26484	26703		245/5		CCROZ	29045		26580			21201			22999	23000		26926
	Exan SEQ ID NO:	19121	19309	16784	17258	19171	12180	13641	16952	19717	11572	12505	12915	14073	16317	16513	100,	14805		10004	18750	15131	16401	15032	18499	11335	13275	14119	13199	13199	14683	16733
	Probe SEQ ID NO:	9206	9748	9089	7449	9587	2298	3729	7075	9433	1670	2638	2987	4173	6456	6633	000,	4926		6/8/9	8942	6174	6543	5166	8634	1430	3356	4221	3278	3278	4798	6854

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Table 4

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	nf30h10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.t1 L1	Homo sapiens transducin (hear) illo 4 (TD) 41 - Entra	1 BOTS 11530E1 NIH MCC 71 H	40S RIBOSOMAI PROTEIN S48	40S BIBOSOMAL DEOTEIN SAS	40S RIBOSOMAI PROTEIN SAS	AI 449573 Homo sanions Tartis (Standard - CON)	DKFZ0434H0313 11 434 (surcement Hence) 11.	Human endocency settowing complete and sequence CUNA clone DKFZp434H0313 5	A TP SYNTHASE UPID BINDING DEGTEN BY PRESURES	PM4-HT0454_0R0100_002-boot UT045411-	nn54h11s1 NCI CGAP Kidi Home septemb cDNA	296g04.s1 Soares thear UbHH19W Homo sapiens cDNA clone IMAGE:1087749 3: PTR5 t3 PTR5 renefiting along the contains	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	(whice bil) genes, complete cds	Turnari Divik, Silve repetitive element	numen Diva, sine repetitive element	runnan tannoa-unmunoglobulin constant region complex (germline)	House sapiens on one of segment HS21C018	Human DNA, SINF repairing algebra (1921)	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	Spirits J. conform DNA fa-	hdroadowy Spara NET T CEC Service like element	2030408.r1 Strategene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5	EST366629 MAGE resentences MAGC Homo control Protein S PRECURSOR (HUMAN);	ANIOS SEDIENS COLORA	riomo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	Homo sapiens chromosome 21 segment HS21C010
gle Exon Prol	Top Hit Database Source	EST HIMAN	NT	EST HIMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	N F	SWISSPROT	EST HUMAN	EST HUMAN	1	$\Box$	MT						Į.		T HI MAN	T			EST LINAM	П
Sin	Top Hit Acession No.	AA579013.1	5032158 NT	2.0E-25 BE888016.1	P17008	P17008	217008	2.0E-25 AL449573.1	1.0E-25 AL040229.1	9635487 NT	206055	1.0E-25 BE162737.1	1.0E-25 AA582690.1						5	110	Γ	7.0E-26 AF003528 1		) 123	r.				
	Most Similar (Top) Hit BLAST E Value	3.0E-25 AA5790	2.0E-25	2.0E-25	2.0E-25 P17008	2.0E-25 P17008	2.0E-25 P17008	2.0E-25	1.0E-25	1.0E-25	1.0E-25 Q06055	1.0E-25	1.0E-25	1.0E-25	1.0E-25 193163	1.0E-25 D14547	1.0E-25	1.0E-25/X51755 1	9.0E-26	9.0E-26	8.0E-26 D14547.	7.0E-26 A	7.0E-26 X89211.1	7.0E-26 AW3401	7.0E-26.A	7.0E-26 A	A OF 30	6.0E-26 A	6.0E-26 AL16321
	Expression Signal	203	3.37	7.11	4.32	1.91	1.91	2.25	1.61	1.21	2.79	2.71	2.85	3.15	3.5	1.45	1.45	1.32	194	1.73	1.56	1.44	1.35	2.03	7.99	1.33	2 44	1.42	4.98
	ORF SEQ ID NO:	28522	21088					27700	20138		22156	24425	26199	26683	28467	28796	28797	_	22208			21321	23694	23745			21967	23025	29033
	Exen SEQ ID NO:		_	l			旦	17480	10317	11136	12264	14638	19460	16496	18214	18897	18897	19389	12310	19501	15411	11464	13808	13969	18731	19250	12065	13223	18740
	Probe SEQ ID NO:	8394	1325	2260	2801	4096	4096	7629	361	1228	2384	4753	6909	6616	8337	9143	9143	9914	2433	9010	5492	1559	3868	4067	8923	9700	2178	3302	8932

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Table 4
Single Exon Probes Expressed

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to	as38h08.x1 Barsteadard HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to	wg65eu6.x1 Source, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369986 3' similar to	contains Alu repetitive element;	ES 133446 Emptyo, 12 week II Hamo sapiens cDNA 5' end	From Septents upstream binding transcription factor, RNA polymerase I (UBTF), mRNA	DKFZ0434I066 r1 444 (smoother: 14-2) 11	2730d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 6' similar to ch'hu44338 VITAAMIN K DEDENDEN EN SIMILAR DE SAPIEN CON CONTRAMIN K DEDENDEN EN SIMILAR SAPIEN CON CONTRAMIN K DEDENDEN EN SIMILAR SAPIEN CON CONTRAMIN K DEDENDEN EN SIMILAR SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN K DEDENDEN EN SAPIEN CONTRAMIN CONTRAMIN K DEDENDEN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN CONTRAMIN C	2030F10.r1 Strategene color (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374	2030f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374	ENGRADES EN INT. 1700 FFT.	Home series MI 1 AM 1.	OV2-PT0042-040406-4-2-5-PT22-2-1-3, and partial cds	QV2-PT0012-040400-124-605 PT0012 Home septens cDNA	nn37d05.s1 NCI_CGAP_GC5 Homo sepiens cDNA clone IMAGE:1086057 3' similar to conteins OFR #	Homo serviens characters 2	DKF7bfn61 171 c1 Fas (messes 1 La John)	M.muscallus mRNA for setzentia alegan 11. 11. Programme Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant C	Homo sapiens DNA for amyord measures and in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th	t089a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu	Indianated element contains element MER20 MER20 repetitive element;	Home capitals with Class 1 region	OVA LITORIO COMO 400 ACT INTERPRETATION DARGET COS	DKF7-22/14225	MR2-BN0114-240F50-030-007 BN044-4 U	Homo sapiens glyceraldeflyde-3-phosphate deflydrogenase (GADPH) mRNA, commiste color
gle Exon Pro	Top Hit Database Source	EST HIMAN	EST HIMAN	Per Linken	EST HUMAN	-1.	EST HIMANI	EST HUMAN	EST HUMAN	EST HUMAN	HOT LINAAN	EST HIMAN	L	EST HIMAN	EST HUMAN	TOT LIMAN	NA PLAN	EST HUMAN	M	TN.	111111111111111111111111111111111111111	T		T HI IMAN	7	EST HUMAN	77
S. I	Top Hit Acession No.	5.0E-26 AI708235.1	5.0E-26 AI708235.1	5 DE-26 A1761420 1	4.0E-26 AA329548 1	7857670 NT	3E266187 1	AL045855.2	3.0E-26 AA115895.1	VA152464.1	2	-	T				2.0E-26 AL163282.2	1	Γ		-	-				-	
	Most Similar (Top) Hit BLAST E Value	5.0E-26	5.0E-26	5 OF-26	4.0E-26	4.0E-26	4.0E-26/BE26618	3.0E-26 AL04585	3.0E-26/	3.0E-26 AA15246	3.0E-26 AA152464	3.0E-26	3.0E-26	3.0E-26	3.0E-26 A	3 0F-26	2.0E-26 A	2.0E-26 A	2.0E-26 X86694.1	2.0E-26 D87675.1	2.0E-26 A 801412	20E-26 AF055066	2.0E-26 AB037859	1.0E-26 BE170371	1.0E-26 AI 039363	1.0E-26 BE814995.	1.0E-26 AF261085
	Expression Signal	3.33	3.33	1.71	1.52	3.77	3.74	1.5	2.41	1.19	1.19	4.35	2.18	1.99	1.99	10.55	5.61	3.36	4.26	2.88	4.55	1.82	2.19	2.36	1.39	0.84	16.79
	ORF SEQ ID NO:	20918	20919				28194	21740		23408	23409	26114		28951	28952	28984	20418		22924		28690			19927	21786	22282	+
	Exon SEQ ID NO:	11073	11073	19435		17283	17944	11853	11880	13625	13625	15978	17998	18665	18665	18691	10600	11722	13118	18023	18420	18537	18962	10106	11894	12390	12521
	Probe SEQ ID NO:	1160	1160	9976	1525	7416	8053	1958	1987	3712	3712	6131	8108	8853	8853	8879	999	1825	<u>88</u>	8135	8549	8720	9252	132	2001	2516	7024

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Table 4
Single Exon Probes Fyngssed in 1

Most Similar   Top Hit Acession   Top Hit (Top) Hit (Top) Hit Top Hit Acession   Database   Value   1.0E-26   BE165980.1   EST_HUMAN   1.0E-26   H55083.1   EST_HUMAN   1.0E-26   H55083.1   EST_HUMAN   1.0E-26   H55083.1   EST_HUMAN   1.0E-26   H55083.1   EST_HUMAN   1.0E-27   Al831462.1   EST_HUMAN   1.0E-27   Al831462.1   EST_HUMAN   1.0E-27   Al831462.1   EST_HUMAN   1.0E-27   Al831462.1   EST_HUMAN   1.0E-27   Al89176.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1   EST_HUMAN   1.0E-27   Al9970.1			_	_	_																						
Exon         ORF SEQ         Expression (Top) Hit Acession No.         Most Similar Value Signal         Most Similar (Top) Hit Acession No.         Top Hit Acession Signal Value	bes Expressed in Heart	Top Hit Descriptor	MB9_UTD/82_60000 448_048_1	https://www.nich.io/cou-113-901 H10487 Homo septens cDNA	ONTZ popo C2146_T1 506 (synanym: hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5	Homo septiens MAGE-B2 (MAGE-B2), MAGE-B3), MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1  MAGE-B4), and MAGE-B2 (MAGE-B3), MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)	naa03c07.xt NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.H OFR repetitive element	W49c04x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2405150 3' similar to contains THR.b2	Homo sapiens chromosome 24 sources Howocore	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (Hi IMAN):	au87h08 x1 Schneider fetal brein 2000 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558	PAZOSNOGA 22030 002 -02 SNOGA 1	ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE	Homo senjene WDN WDN) See 11	MR4-BT0398-2508n0-204-dns BTn308-B-manian-	1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to	CM4.CT0345-09-200 DBS 402 CT0345 !!	CM1. CT0315-0315-03-007-01-03-13 Homo Sapiens CDNA	Human endonemers retracted classes U.S.	hi51h12.X1 Sorger Sorger defined to the septens cDNA done IMAGE:2975879 3' stmilar to TR:O76040	Home savient Vancardent	AV72328E HTB London Control of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of the London of	Urman and other Charles Converged to the HIBAHE02 5	Figure Inchesial protein (BZ3) mKNA, complete cds		Mus musculus spem fall associated protein (Stap), mRNA
Exon No:         ORF SEQ Expression Signal In Top Hit Aces Signal SEQ ID NO:         Most Similar Value No:         Top Hit Aces No:         No: Value No:         No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: Value No: V	gle Exon Pro		EST HIMAN	FOT LILEANN	EST HIMAN	L L	SWISSPROT	EST HUMAN	EST HIMAN	NT	EST HUMAN	EST HIMAN	EST HIMAN	SWISSPROT	LN LN	EST HUMAN	EST HIMAN	EST HIMAN	EST HUMAN		ST HIMAN	5	ST HIMAN		ST HIMAN	ST HUMAN	<u> </u>
Exon No:         ORF SEQ Expression In No:         Expression In No:         Most SEQ ID ID NO:         ORF SEQ Expression In No:         Most Seq ID In No:         ORF SEQ Expression In In In In In In In In In In In In In	us		BE165980 1	41 038487 4	H55083.1	U93163.1	P54296	BF445556.1				AW162737.1	Τ		1.	15.		9.1	9.1						\		910569
Exon ORF SEQ Express SEQ ID NO: Signs NO: 16034   18146   19737   17342   1812   1986   19787   11300   21159   16 112009   21159   15 12009   21809   15 12009   15 12009   17 180   21 18 10 10 10 10 10 10 10 10 10 10 10 10 10		Most Similar (Top) Hit BLAST E Value	1.0E-26	1 0F-26	1.0E-26	9.0E-27	9.0E-27	9.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	8.0E-27	7.0E-27	7.0E-27	7.0E-27	7.0E-27	6.0E-27	5.0E-27	5.0E-27	4.0E-27
Exon OR SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	2.75	3.17	1.84	3.11	3.48	3.97	3.09	4.13	18.87	18.87	0.98	3.31	0.91	3.12	4	1.68	1.68	1.22	2.09	4.22	2.07	6.21	2.92	2:32	1.54
												21159	21809	22874	23035		26088	27386	27387					28246	27970	27971	26080
Probe SEQ ID NO: NO: 6089 9483 9483 9483 9483 1395 1395 1395 6165 668 8132 9631 8132 9631 8132 9631 8132 9631 8109		Exon SEQ ID NO:		L									12009		13230	15122	15956	17186	17186	10602	14896	18020	19204	17999	17727	17727	15949
		SEQ ID NO:	6089	8266	9493	7364	8027	9013	10	545	1395	1395	2121	3148	3309	6165	6196	7310	7310	899	5023	8132	9631	8109	7877	7877	6046

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Table 4
Single Exon Probes Exoneral

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Table 4

	1	4		100	1~		$\top \top$		Т	Т	Т	T	T		Г	_	15				_	T -				
Single Exon Probes Expressed in Heart	Top Hit Descriptor	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE.3183188 3' sImilar to TR:Q07314 Q07314	AU128280 NT2RP1 Homo saniens china - Lata Manage 4.6 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	to12b09.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR	to 2009x1 NO_OGAP_U2 Homo saplens cDNA clone IMAGE:2178809 3' similar to contains OFR 11 OFR	Icheurve eternent;	aush08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to	1 N. Dougus U60302 KIAA0555 PROTEIN: contains element MER22 repetitive element;	ACTIVE TO LEAVE HOME SEPTING CONFINE CONFINE TO A 1000824 5'	Normo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	AV 20240 CB Homo saplens cDNA clane CBFAKA12 5	Homo sapiens mRNA for KIAA0866 protein, complete cds	as50e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:82534n 5' similar to contains Au	repetitive element contains element PTR5 repetitive element; worl8c07.x1 NCI_CGAP_Pen1_Home_continue_PNA_fit	THR repetitive element;	y89f10.r1 Scares placenta Nb2HP Homo sabiens cDNA clone IMACE: 46442 51	xr33c09.x1 NCI_CGAP_Kid11 Home sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95 HI MAAN	601300703F1 NIH MGC 21 Home saniens - PNA June 1846 Processes	q66610.x1 Soares, testis_NHT Home septems cDNA clone IMAGE:1755019.3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMO! OG CHI MAANY.	(Arthur 1)	Felix extra Capril 1974.	qf66f10xf Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 ensilm (ADAM22) mena	Complete cds	MK3-H10713-280500-013-f09 HT0713 Homo sapiens cDNA Homo sapiens MHC class 4	Class of the Class 1 region
gle Exon Pro	Top Hit Database Scurce	EST HUMAN	EST HUMAN	EST HUMAN	EST LINAM	EST HUMAN	EST LIMAN	EST HIMAN	-'	EST HIRAANI	N PANOL PAN	LV.		ESI_HUMAN		EST_HUMAN		EST_HUMAN				HUMAN		7	NT TOWAN	
Siú	Tap Hit Acesslön No.							T	7866	7.0E-28 AV735348 1	T	T		3	_		4.0E-28 AW195066.1		-	F029308 1 NT			,	- -		
	Most Similar (Top) Hit BLAST E Value	9.0E-28	9.0E-28	9.0E-28	9.0E-28	9.0E-28	8.0E-28	7.0E-28	7.0E-28	7.0E-28	6.0E-28	6.0E-28/AB020673	A OE 30	707-700	6.0E-28 AI921003.	5.0E-28 R79762.1	4.0E-28 A	4.0E-28 B	4.0E-28 AJ198941.	4.0E-28 AF029308	4.0E-28 AB038241	4.0E-28 AI198941.1	3.0F-28 AF455382	3.0E-28 BF354030	3.0E-28 U53588.1	
	Expression Signal	2.32	3.01	1.21	1.21	3.74	1,97	7.54	2.54	1.44	1.27	1.27	2.73		3.08	1.85	1.42	3.39	1.59	420	53.6	2.94	1.89	2.19	1.84	
	ORF SEQ ID NO:		20089	24760	24761			20922	28660		23670	23671			2000	01062	22347	22788	26359			26359		27193	28430	
	Exen SEQ ID NO:		10270	14986	_	18866	19592	11077	18395	18836	13894	13894	19232	1000	13836	0000	12455	12997	16199	18119	18248	16199	11169	17001	18183	
	Probe SEQ ID NO:	136	308	5118	5118	9093	9418	1164	8523	9053	3987	3987	9673	24	3927	+	2584	8 8 8	6336	8239	8371	8388	1262	1	8306	

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Table 4

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	-	_	Τ	Т	Т	Π.		TT	_	T	Т	TT.	7		7.7	- 1	_	_	Т	7	_	7	7	т т		-	<b>-</b>	<del></del>
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Himan 60 KD hart about a state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state	Home consists Diff.	OVA Broad 4 John Age 100 Proprietally diopterin synthase, complete cds	Human dene for Altracenter and 2 of 1000 Septens cDNA	xx17703.x1 Scares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2813405 3' similar to contains Ali	Home sariene chames we'll see it in the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of 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WESTORY Source, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains	wizigotixi Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains	element WEX6 repetitive element;	Hours expens chromosome 21 segment HS21C048	Home capitals chromosome 21 segment HS21C048	Homo saplens chromosome 21 segment HS2/C048	OVA-OTOMAS ABOARD 4 FE LAY OTAMAS 1	Home canisas chromosome 2	RC1-HN0003-220300-021-04 Unloads U.	nz20c07.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1288332 3' similar to contains National Land	WENT repetitive element;	Fromo Sapiens zincliron regulated transporter-like (ZIRTL), mRNA	no C31 U51 normalized Infant brain cDNA Homo saplens cDNA clone c-23f05	ESTS/17/1 Inymus I Homo sapiens cDNA 5' end similar to EST containing Q family repeat PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
gle Exon Pro	Top Hit Database Source	LN	Į.	EST HIMAN		EQT LIBRARY	TN TN	EST UTBAAN	TN TN	LN.	L'N	EST HUMAN	TOT IN MAN	TA TOWN	EST LIMAN	LOS LOS	EN TOWN	- L	Ę	LN	EST HIMAN		EST HUMAN		NAMOL	7 23 11 24 11	Т	HUMAN
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	Expression Signal	4.71	1.45	1.31	2.07	9,1	1.64	2.22	1.61	1.43	1.43	6.12	6.12	2.03	1.43	1.43	2.95	2.95	3.39	3.39	1.96	1.73	5.41	308	1.5	8.84	3.37	3.53
	ORF SEQ ID NO:		23997		27138	27429		28728		20240	20241	21278	21279	23855	25765	25765	27539	27540	27973	27974			27174	25995			26880	27105
	Exon SEQ ID NO:		_ !	_1	16947	17229	17362			10427	10427	11421	11421	14082	15658	15658	17334	17334	17729	17729	18618	18807	16982	15871	18889	15721	16691	16916
	Probe SEQ ID NO:	7079	4317	4626	7070	7362	7492	8591	9248	484	484	1516	1516	4182	5750	6461	7474	7474	7879	7879	8804	9004	7105	5966	9132	5815	6812	7039

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Table 4 ·
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA	Human lambda-immunoqlobulin constant region complex (germline)	Human mRNA for integrin alpha subunit, complete cds	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	Human lambda-Immunoglobulin constant region complex (germline)	tg92g03.xf NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element	Human aconitate hydratase (ACO2) gene, exon 7	Homo sapiens chromosome 21 segment HS21C078	Homo saplens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA	qq83c05x1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone iMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element	Homo sabiens telomerase reverse transcriptase (TERT) gene expre 1.8	TRANSCRIPTION FACTOR AP-2	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23fn5	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA	IL2-NT0101-280700-116-E04 NT0101 Homo saplens cDNA	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds	UI-H-BI1-afo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo saplens cDNA clone IMAGE:2722558 31	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5	601119860F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3029438 51	C18939 Human placenta cDNA (TFujlware) Homo saplens cDNA clone GEN-570C01 5'	7e37c12.x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:3284662.3' similar to SW:DHSA_HUMAN P310c101ATE DEHYDROGENASE RIDIOI INVONET ELANOR CONTINUE DELAYING CONTINUE DE ANORDOGENASE RIDIOI INVONET ELANOR CONTINUE DELAYING CONTINUE DE ANORDOGENASE RIDIOI INVONET ELANOR CONTINUE DE ANORDOGENASE RIDIOI INVONET ELA ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGENA CONTINUE DE ANORDOGEN	7e37c12x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:3284662 3' similar to SW:DHSA_HUMAN	P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
ie Exon Probes	Top Hit Database Source	EST HUMAN PM			T HUMAN	T	tg92	Т				EST HUMAN QV	EST HUMAN QV	Π	948 EST HUMAN conf	Т	ISSPROT	EST HUMAN CM	Т	Π	EST HUMAN 11.2-	NT TS	EST_HUMAN UI+	EST_HUMAN 601	EST HUMAN 601	Γ	7e3	1	EST_HUMAN P31
Sing	Top Hit Acession No.	7.0E-30 BE091133.1			6.0E-30 BE008026.1		5.0E-30 Al399992.1		8.2		2.0		4.1	38.1	3.0E-30 Al338551.1	3		15.1		7.1		2.0E-30 AF114156.1		2.0E-30 BE298945.1	2.0E-30 BE298945.1		7.1		=
	Most Similar (Top) Hit BLAST E Value	7.0E-30	6.0E-30 X51755.1	6.0E-30 D25303.	6.0E-30	6.0E-30	5.0E-30	5.0E-30 U87931.1	5.0E-30	5.0E-30	5.0E-30	4.0E-30	4.0E-30	4.0E-30	3.0E-30	3.0E-30	3.0E-30 P34056	2.0E-30 AW8573	2.0E-30 F08688.1	2.0E-30 BE17587	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30 C18939.1	2.0E-30 BE67061	L	Z.UE-30 BE6/061
	Expression Signal	1.16	0.95	1.26	2.41	3.15	31.23	7.35	3.55	6.68	6.68	1.64	1.64	1.49	1.7.1	0.91	2.38	1.18	2:32	5.91	10.97	6.38	. 2.11	1.72	1.72	3.46	1.55	4 1	
	ORF SEQ ID NO:			21505	22878		23620			28632	28633	21880	21881	27231		23395	28675	20411		21234	22438	22609	23419	24346	24347	27036	27085	27086	2/000
Ī	Exan SEQ ID NO:	11403	11454	11637	13078	11454	13840	19522	18141	18368	18368	11985	11985	17039	11048	13611	18410	10593	10984	11369	12548	12816	13633	14554	14554	16844	16896	80	06001
	Probe SEQ ID NO:	1499	1549	1736	3153	9915	3931	5205	8261	8495	8495	2096	2096	7162	1134	3697	8538	629	1068	1464	2683	2889	3721	4668	4668	9969	7019	7010	2 2

Page 195 of 413 Table 4 Single Exon Probes Expressed in Heart

Prob. EDM         Box 187 (Top) HI         Top HIA         Processed III T Teat T         Top HIA Denotifier         Top HIA Denotifier           702.0         18.0         D NO.         Signal         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0							γ		_						,	_			_									_		_		
Exon         ORF SEQ         Expression Signal         Most Similar Top Hit Acession (Top) Hit Acession         Top Hit Acession Database         Top Hit Acession (Top) Hit Acession         Top Hit Acession Database         Top Hit Acession (Top) Hit Acession         Top Hit Acession Database         Top Hit Acession (Top) Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top 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Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, alternatively	Homo emigra NUC -1	A 110005 HEMBA U.	RCS-BT0377-091-990-031-04-9 BT0377-0	801433087F1 NIH MGC 72 Home continue appears CUNA	Homo sapiens the I DNA tensional sapiens of the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens the Indiana sapiens sapiens the Indiana sa	Homo sepiers time I DNA transformers of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of the Indianate of	TWO SEPONDS APPLICATION OF THE PROPERTY OF THE PROPERTY OF SIMILAR TO TRICA 13537 Q 13537	Similar 10 POGO ELEMENT, contains L1.t1 L1 repetitive element;	Homo sapiens Xq pseudoautosomal region; segment 1/2	POLYPEPTIDE N-ACETYLGALACTOSAMINY, TRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-	Homo seniens chromosomo 24 com 11 (1922)	Torris separas circultosome z i segment HSZTC080
Exon No:-         CARF SEQ Puression No:-         Expression Signal         (Top) Hit Top Hit Acess No:-         Top Hit Acess No:-           17652         2789         4.47         2.0E-30 AW470791.1           10249         20281         1.6         1.0E-30 AW468897.1           10682         20281         1.6         1.0E-30 AW468897.1           10683         20457         2.92         1.0E-30 AW468897.1           10683         20457         2.92         1.0E-30 AW468897.1           12290         22699         1.03         1.0E-30 AW468897.1           12240         22736         0.83         1.0E-30 BF34728.1           12640         22736         0.83         1.0E-30 BF34728.1           12640         22786         0.83         1.0E-30 BF34728.1           12640         22786         0.83         1.0E-30 BF34728.1           16801         22786         0.83         1.0E-30 BF34728.1           16802         2232         1.0E-30 BF18283.1         1.0E-30 BF18283.1           16803         2278         0.0E-31 AA37263.1         1.0E-31 AA37263.1           16608         25202         1.7         7.0E-31 AA37263.1           16618         25251         7.0E-31 AA37263.1         1.0E	פופי באטוו דיוט		EST HIMAN	EST HUMAN	EST HIMAN	TN	EST-HUMAN	EST HUMAN	LN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN		LZ LZ	FST HIMAN	EST HIMAN	EST HIMAN	NT	H	Į.	FST HIMAN		Τ		L	1.0	ESI HUMAN	╗		Т	7
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Exon No:         ORF SEQ Expression Signal No:         Corporation Signal Signal No:         Corporation Signal Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Signal No:         Corporation Sign		Most Similar (Top) Hit BLAST E Value	2.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	9.0E-31	8.0E-31	8.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31	6.0E.34	6.0E-31	6.0E-31	6.0E-31/	6.0E-31	5.0E-31	5.0E-31	A 25.24	4 05 94 /	4.05-31	4.0E-31	4.0E-31	
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		ORF SEQ ID NO:				20457	21953	22187	22699	22736	26582			20820			22392	22393	25272			28255	25351		19973	19974		-		21357		
Probe SEQ ID NO: 7802 2843 2843 3015 6545 6545 6739 8120 9191 9319 185 185 185 185 1775		SEQ ID NO:		Ш		L	L		12900	12943	16403	19615	16890	10977	12242	10627	12500	12500	19168	13539	16618	18008	18926	19541	10157	10157	16793	10519		11498	11674	  - 
		Probe SEQ ID NO:	7802	284	527	669	2165	2413	2973	3015	6545	9733	7013	1060	2362	694	2633	2633	9583	3625	6739	8120	9191	9319	185	185	6915	581		1694	1775	

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Table 4
Single Exon Probes Expressed in Heart

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3 55 T	Exon OR SEQ ID IC NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2759	12621		1.38	4.0E-31	5730038 NT	LN T	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA
_ {	19186		1.52	4.0E-31	11430273 NT	IN	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
9718	19259		1.38	4.0E-31	4.0E-31 AB008681.1	TN	Homo sapiens gene for activin receptor type IIB, complete cds
2550	12423	22314	1.42	3.0E-31	6005871 NT	TN	Homo sepiens SEC83, endoplasmic reticulum translocon component (S. cerevisias) like (SEC62) いっしい
6341	16204	26366	9.03	3.0E-31	4826B53 NT	· TN	Homo sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens NADH dehudroranges (rikinimana) a beta in the sanjens (rikinimana) a beta in the sanjens (rikinimana) a beta in the sanjens (rikinimana) a beta in the sanjens (rikinimana) a beta in the sanjens (rikinimana) a beta in the sanjens (rikinimana) a beta in
6425 1	16286	26448	1.38	3.0E-31	11420329 NT	L	Homo sabiens hynothetical protein El 140842 (El 140842) - ENTA
6745 1	16624		1.95	3.0E-31	3.0E-31 AL163206.2	LN	Homo saplens chromosome 21 segment Hoor Character
	17376	27585	2.86	3.0E-31	3.0E-31 D14523.1	N L	Horse mRNA for ferritin I chain complete de
	17920	28167	2.01	3.0E-31	3.0E-31 P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
	18366		6.36	3.0E-31	3.0E-31 BF035327.1	EST HUMAN	601458531E1 NIH MGC 66 Home canions CDM Alone IMA CE 2863386 E1
	11771	21647	1.83	2.0E-31	1-	EST HUMAN	QV2-LT0051-260300-111-103 LT0051 Homo sanlens chiNA
	12054	21955	1.31	2.0E-31	2.0E-31 Al393388.1	EST HUMAN	tg44g05x1 Soares NFL T GBC St Homo sapiens CONA clare MACE: 3444572 91
2292	12174	22074	2.18	2.0E-31	2.0E-31 AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513_r3
2391	12269	22164	4.4	20E-31	2.0E-31 AA458824.1	EST HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element
5502	15421	25483	3.6	2.0E-31	2.0E-31 BE350127.1	EST HUMAN	ht09g01.x1 NC_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 renetitive element
7246 1	17123		1.8	20E-31	20E-31 AA877764.1	EST HUMAN	INDBF04.81 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSARI E El EMENT COMP. ETE CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSENSIS O CONSE
	17185	27385	3.99	20E-31	7661535 NT	L'A	Homo sapiens B9 protein (B9) mRNA
	17550	27774	1.27	2.0E-31	2.0E-31 AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAAI B07 5
┙	17660	27775	1.27	2.0E-31	2.0E-31 AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAAI 807 5
	17847	27883	2.17	2.0E-31	2.0E-31 BE408611.1	EST_HUMAN	601304125F1 NIH MGC 21 Hamo sapiens cDNA clone IMAGE:3638340 F
	17847	27884	2.17	2.0E-31	1	EST_HUMAN	601304125F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE-3638310 5
$\perp$	18993	7	2	2.0E-31	١,		Homo sapiens hexokinase II gene, promoter region
9431	19759	†	1.81	2.0E-31	2.0E-31 Al114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
16	10002	19794	8.34	1.0E-31	1.05-31 (193163 1	F	Homo saplens MAGE-82 (MAGE-82), MAGE-83 (MAGE-83), MAGE-84 (MAGE-84), and MAGE-81
	11544	21403	2	1.0E-31 095371		ISSPROT	OLFACTORY RECEDENCE
	1544	21404	2	1.0E-31 095371		Т	OLFACTORY RECEPTOR 2C1
	11544	21405	2	1.0E-31 095371		1	OLFACTORY RECEPTOR 2C1
4535 1,	14428	24209	1.01	1.0E-31	1.0E-31 AL134376.1	Γ	DKFZp547B235_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZn547B235_gr
							0 007011047 110 01010 1011

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Single Exon Probes Expressed In Heart	s cDNA clone IMAGE:3529159 5'	
Most Similar	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5* H.sapiens mRNA for myosin	H.saplens mKNA for myosin H.saplens mRNA for myosin
Most Similar (Top) Hit Top Hit Acess BLAST E No. Value  1.0E-31 AL134376.1 1.0E-31 AL134376.1 1.0E-31 AL134377.1 1.0E-31 AL134377.1 1.0E-31 AL134377.1 1.0E-31 AL134377.1 1.0E-31 AL134377.1 1.0E-32 AV7733976.1 1.0E-32 AL1627.1 1.0E-32 AL1627.1 1.0E-32 AL1632.1 1.0E-32 AL1632.1 1.0E-32 AV758634.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1 1.0E-32 AV776834.1	T_HUMAN	
	13.1	
	2.0E-32 BE29661 2.0E-32 Z38133.	2.0E-32 Z38133.
Expression Signal 3.15 1.87 1.87 1.87 2.34 2.82 2.82 2.82 2.82 2.82 2.82 2.82 2.8	19.04	19.01
24210 24272 24927 25738 24426 22456 20779 20779 20213 20213 21210 27478 24882 24883	25929	25930
	15806 15806	15806
Probe SEQ (D NO: 4535 5728 8235 6000 2032 2032 2032 2032 2032 4754 448 448 448 448 448 448 7404 7404 7404	5900	5900

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Table 4
Single Exon Probes Expressed in Heart

Т		Т	_		_	т-	T	_	Т		·	1		_		T ~	<del></del>	Т	T	1	1	1			۳-	<b>, , , , , , , , , , , , , , , , , , , </b>
	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens ubiquitin profein ligase E3A (human papilloma virus E6-associated profein, Angelman	syndrane) (UBE3A), mRNA	Homo sapiens chromosome 21 segment HS21C007	Homo saplens RAB1, member RAS oncogene family (RAB1) mRNA	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element contains MER28.b2 MER28 repetitive element:	Homo sapiens chromosome 21 segment HS21C010	UI-H-Bi2-ahl-c-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'	271a08.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12871_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	Homo sapiens killer cell immunoglobulin-like receptor, three domains, Iong cytoplasmic tail, 1 (KIR3DL1), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similær to contains MER29.b3 MER29 repetitive element;	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'	qb67g03.xf Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204.3' similar to contains OFR.t1 OFR repetitive element;	MR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA	ab51g11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA	ql96d01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'	ozz1d03.xt Soares, fetal liver, spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	wo88c06.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2462410 3'
	Top Hit Database Source	LN		NT	NT	TN	EST HUMAN	IN	EST HUMAN	EST_HUMAN	LNT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	NT	EST_HUMAN	EST_HUMAN		뉟	EST_HUMAN	NT	EST_HUMAN
	Top Hit Acession No.	5.0E-33 AL163285.2		11433063 NT	4L163207.2	4758987 NT	4.0E-33 AA626621.1	AL163210.2	4.0E-33 AW 293349.1	4.0E-33 AA053053.1	11425635 NT	3.0E-33 BE350127.1	3.0E-33 BE350127.1	3.0E-33 AV647851.1	2.0E-33 AI160189.1	2.0E-33 BE159039.1	2.0E-33 AA626683.1	11421332 NT	11421332 NT	2.0E-33 AI277492.1	2.0E-33 Al052256.1		9.1	18.1		1.0E-33 Al927191.1
	Most Similar (Top) Hit BLAST E Value	5.0E-33		5.0E-33	4.0E-33 AL16320	4.0E-33	4.0E-33	4.0E-33 AL16321	4.0E-33	4.0E-33	4.0E-33	3.0E-33	3.0E-33	3.0E-33	2.0E-33	2.0E-33	2.0E-33	2.0E-33	2.0E-33	2.0E-33	2.0E-33		1.0E-33	1.0E-33	1.0E-33	1.0E-33
	Expression Signal	1.3		1.62	3.28	1.77	7.39	3.77	1.83	20.94	1.72	4.46	3.4	1.48	2.33	427	5.1	1.73	1.73	1.61	1.8		4	2.02	5.33	1.92
	ORF SEQ ID NO:					21861		22265	24057	25043	29102						24565	24668	24669	25894					29024	
	Exan SEQ ID NO:	12111	<u> </u>	18858	11027	11968	12250		14278	15239	18810	10989	10989	12721	10003	14219	14790	14899	14899	15775	17138		╝	_		19151
	Probe SEQ ID NO:	2226		9082	1112	2078	2370	2498	4382	5318	2006	1073	1074	2400	66	4322	4911	5026	5026	5869	7261		8	8637	8921	9553

Page 200 of 413 Table 4

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sepiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat pregions	AV727809 HTC Homo saniens CDNA clane HTCCNC42 E	Homo saplens Xa pseudoauthermal radion: segment 4/9	Vd15605.r1 Soates fetal liver spiece 1NF S Home canions CINA class 144.0F-100000 2	W14c10.r1 Scares placents Nh2HD Home emission against class (NMACE:108220 5)	Human G2 protein mRNA, partial cds	Human G2 protein mRNA nartial cde	Mus musculus DAB/2.1 hair-sna-file (harl 4) xxxx	Homo sapiens New38-binding protein New 87 (1) gene	Human splicing factor SRn554 (SRn 55) work and the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of	Raffus nonepictus putative four report in secure — PNA	Homo sagiens mRNA for KIAA1435 profein representations	Homo sapiens chromosome 21 segment HS2100no	1994c08 x NCI CGAP Pr28 Home seniors CDNA class (MACE consists of	Homo saniens hynothetical protein El (10080 /El (10080) - PATA	601458531F1 NIH MGC 66 Home sealers ONIA Alexa 1140 Common 21	ADP,ATP CARRIER PROTEIN, LIVER ISOCRAM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSI OCATICA 3 (ADENINE	Homo sapiens X-Inked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	Homo saniens WNT3 pressures (MNIT9) - DNIA	Homo saplens WNT3 maximus (MNT2) - DNA	RC2-BT0506-240400-016-h08 BT0508 Home conjunction DNA	MR0-CT0068-280999-002-d11 CT0068 Home seniors cDNA	601484430F1 NIH MGC 69 Home senions of DNA class MAC Concessor 21	601484430F1 NIH MGC 69 Home sanians chivia Adam MA CE consession	CM4-HT0193-061099-022-006 HT0193 Homo caniens child	DKFZp564A1563 r1 564 (synonym: hfhr2) Home canions cDN Acre DV F7 - F644 F56 F1	Homo sepiens chromosome 21 seminant HS24Cons opposite construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromatome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromatome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromatome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construction of the London Sepiens chromosome 21 seminant HS24Construc	hh77b06 vf NCI CGAP GITH Home senions of DNA of the NA OF the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comment of the Comm	Homo sapiens prohibitin (PHB) mRNA	naa33a08x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912 075912 DIACYLGLYCEROL KINASE IOTA.
igle Exon Pro	Top Hit Database Source	IN	EST HUMAN	"	EST HUMAN	EST HUMAN		Į.	N.	Z	N	I-Z	Z L	NT	EST HUMAN	·I.	EST HUMAN	SWISSPROT	I-N	LNT.	L	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN LN	EST HUMAN	LN	T HUMAN
is	Top Hit Acession No.	1.0E-33 AF003528.1	1.0E-33 AV727809.1	9.0E-34 AJ271735.1	7.0E-34 T70845.1	7.0E-34 H12866.1	Ú10991.1	U10991.1	U03686.1	5.0E-34 7706500 NT	5.0E-34 U30883.1	AF078779.1	AB037856.1	5.0E-34 AL163209.2	AI804567.1	4.0E-34 8922807 NT	BF035327.1	212236	1.0E-34 AF003528 1	Τ		1.0E-34 BE071414.1	4W845706.1	1.0E-34 BE874052.1	Π	51.1		0.2	9.0E-35 AW663302.1	<del>2</del> 8	8.0E-35 BF589937.1
	Most Similar (Top) Hit BLAST E Value	1.0E-33	1.0E-33	9.0E-34	7.0E-34	7.05-34	6.0E-34 U10991	6.0E-34 U10991	6.0E-34	5.0E-34	5.0E-34	5.0E-34 AF0787	5.0E-34	5.0E-34	4.0E-34	4.0E-34	3.0E-34 BF0353	1.0E-34 P12236	1.05-34	1.0E-34 AY0093	1.0E-34/	1.0E-34	1.0E-34 AW8457	1.0E-34	1.0E-34	1.0E-34	1.0E-34 AL03663	1.0E-34 AL16321	9.0E-35/	8.0E-35	8.0E-35
	Expression Signal	3.04	1.34	2.09	1.98	3.08	1.46	1.48	1.4	2.23	4	1.18	2.12	2.01	2.11	0.98	4.81	8.56	1.46	0.78	0.78	4.02	0.86	1.99	1.99	3.87	8.89	2.92	1.26	24.25	3.3
	ORF SEQ ID NO:		25229		21198				25340		24631		28186					. 21254	23320	23661	23662			25743	25744	27226	27658		23296		21475
	Exon SEQ ID NO:	9994	19278	19399	11332	19020	10406	10406	18903	11734	14868	17021	17937	18446	11848	12552	18365	11393	13535	13886	13886	14277	14799	15639	15639	17032	17442	19307	13508	10189	11604
	Probe SEQ ID NO:	9723	9754	9927	1427	8340	463	463	9153	1837	4993	7144	8046	8278	1953	2687	8492	1488	3621	3979	3979	4381	4920	933	5731	7155	7594	9746	3294	249	1703

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	nea33e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similer to TR:O75912 075912 DIACYLGLYCEROL KINASE IOTA :	1 MGC 18 Homo saniens cDNA clone IMAGE: 4040324 FT	1 MGC 44 Homo sapiens cDNA clone IMAGE RARRETS ST	1 MGC 42 Homo sepiens cDNA clone IMAGE 4300660 31	osphatidylinositol givean class L (PIGL) mRNA	se_testis NHT Homo sapiens cDNA clone 1308397 3'	c finger protein 208 (ZNF208) mRNA	ile functional domain (PTPRF interaction) (TRIO) mRNA	3NA for KIAA1365 protein, partial cds	oglobulin kappa light chain variable region L14	Homo sapiens clk2 kinase (CLK2), propint, cotet, glucocerebrosidase (GBA), and metaxin genes, complete ods: metaxin pseudocene and clucocerebrosidase pseudocene and through the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contrac	gene, partial and an annual partial and an online sponding ( 1 mbss) gene, partial	1 MGC 72 Homo saplens cDNA clone IMAGE:3917229 5	se festis_NHT Homo sepiens cDNA clone IMAGE:1837448 3' similar to N Q92539 HYPOTHETICAL PROTEIN KIAA0249	is_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to	i fetal liver spleen 1NFI S S1 Homo conjunc 2010 also liver speed in	- MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5	yu98a07.r1 Soares fetal liver spleen 1NFLS Home sapiens cDNA clone IMAGE:241236 5' similar to contains	ement	ement;  MGC_21 Homo sapiens cDNA clone IMAGE:3635401 57	PTR5 repetitive element;  601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5' ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3  MER29 renetitive element:	MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'   MGC_21 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3   element;	MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'  MGC_21 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 element;  1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'  MGC_8 Homo sapiens cDNA clone IMAGE:334662 6'	MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'  MGC_21 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 element;  1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'  I MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'  Sabholibid scramblass 1 neme complete close.	Iment;  I_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'  SAP_Kd413 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 element;  1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'  I_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'  Sepholipid scramblase 1 gene, complete cds  900-010-e01 TN0045 Homo sapiens cDNA	MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5' :3AP_Kd413 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 element; 1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5' IMGC_8 Homo sapiens cDNA clone IMAGE:3345063 5' spholipid scramblase 1 gene, complete cds 900-010-e01 TN0045 Homo sapiens cDNA CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 PROTEIN FBL2.
Tabe 33a08 st NCI CCAP Kidda Home comisses of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the Alexander age of the A	7.1 EST HUMAN	5.1 EST HUMAN	0.1 EST HUMAN	2.1 EST HUMAN	5417 NT	EST_HUMAN	Π	6005921 NT Homo saplens triple functional domain (PTPRF Interacting) (TRIO) mRNA	N	NT	Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and meta cotes in the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction	LN	1992.1 EST_HUMAN   601431984F1 NIH MGC 72 Homo sapiens cDNA clone IMAGE :3817229 5:	1 EST_HUMAN	HEST HIMAN	1 EST HUMAN	.1 EST_HUMAN		EST HUMAN	EST_HUMAN EST_HUMAN	EST_HUMAN EST_HUMAN EST_HUMAN	EST_HUMAN EST_HUMAN EST_HUMAN	EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN	EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT	EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN	EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN
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(Top) Hit Top Hit Acession BLAST E No.	8.0E-35 BF58993	8.0E-35 BF18319	8.0E-35 BE37848	8.0E-35 BF56928;	7.0E-35	6.0E-35 AA757115.1	6.0E-35	6.0E-35	6.0E-35 AB037786.1	5.0E-35 X63392.1		5.0E-35 AF023268.1	5.0E-35 BE890992.1	5.0E-35 AI208765.	5.0E-35 Al20876	5.0E-35 AA001786	4.0E-35 BE257907.1	4.0E-35 H91193.1		4.0E-35 BE409102.1	4.0E-35 BE40910	4.0E-35 BE409102 4.0E-35 BE350127 4.0E-35 AL046598	4.0E-35 BE409102.1 4.0E-35 BE350127.1 4.0E-35 AL046596.1 3.0E-35 BE208182.1	4.0E-35 BE499102.1 4.0E-35 AL046599.1 3.0E-35 AF224492.1 3.0E-35 AF224492.1	4.0E-35 BE409102 4.0E-35 AL046590 3.0E-35 BE268182 3.0E-35 BF224492 3.0E-35 BF376402	4.0E-35 BE409102 4.0E-35 AL046590 3.0E-35 BE268182 3.0E-35 BF224492 3.0E-35 BF376402 3.0E-35 BF433100
Expression (Top) Hit Signal BLAST E Value	3.3	3.09	3	3.49	1.52	1.28	1.78	3.6	2.7	2.29		2.2	3.14	2.18	2.18	3.42	14.91	5.1	7	87.	1.82	1.82	1.82	1.82	1.06 1.06	1.05 1.06 1.06
ORF SEQ ID NO:	21476	24435	28217							21454		23992		26848	26849		21186	21552					27030			
Exon SEQ ID NO:	11604	14646		18969	15811	11296	11820	16490	17648	11583		14208	16640	16658	16658	18389	11321	11675	14914		16144	16144	16144 16835 11466	16144 16835 11466 12167	16144 16835 11466 12167 14678	16144 16635 11466 12167 14678
Probe SEQ ID NO:	1703	4761	8075	9205	5905	1391	1925	9610	7698	199		4311	6/61	6779	6779	8517	1415	1776	5042		6280	6280	6280 6957 1561	6280 6957 1561 2283	6280 6957 1561 4793	6280 6957 1561 2283 4793 5275

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Table 4
Single Exon Probes Expressed in

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	K6932F Human fetal heart, Lambda ZAP Express Homo saplens cDNA clone K6932 5' similar to REPETITIVE ELEMENT	A971F Heart Homo sepiens cDNA clone A971	Homo sapiens mRNA for Gab2, complete orls	Homo sapiens Grb2-associated binder 2 (KIAA0571) mRNA	Homo saplens Grb2-esseciated hinder 2 (KI A 0 574)	Homo sapiens mRNA for KIAA0895 profession partial cds	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens	Various of Samus Estal Black and AMP Set 1	OV0-BT0701-210400-109-bit BT0701 Home capiens cDNA done IMAGE:274079 5	H. sapiens PROS-27 mRNA	Como saplens GH2-associated hindor 2/2/4406741 == DNA	Homo sapiens Grb-associated binder 2 (KIAA0574) - DNA	601496774F1 NIH MGC 70 Home sanlars contact that CE contact is	601496774F1 NIH MGC 70 Home saliens contactions in the little in the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of the contaction of t	Homo sapiens chromosome 21 segment HS21C010	K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5 similar to	finite16 Regional genomic DNA snecific cDNA library Home	Imfe16 Regional genomic DNA specific characters and promise septents control can be CK12-1	II.2.ST0162-131099-006-412 ST0162 Home senions ADNA	IL2-ST0162-131099-006-012 ST0162 Homo saniens cDNA	yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens CDNA done IMAGE:115752 5' similar to	Homo sapiens hypothetical protein (I OCS1233) mBNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
gie Exon Pro	Top Hit Database Source	FN	EST HUMAN	EST HUMAN	N	NT	L	NT	EST HUMAN	EST HIMAN	EST HIMAN	EST HUMAN	N	N.	NT	EST HUMAN	EST HUMAN	NT	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	FST HIMAN	7705994 NT	EST_HUMAN	EST_HUMAN
alio I	Top Hit Acession No.	3.0E-35 AF223391.1	2.0E-35 N88965.1	2.0E-35 T11909.1	2.0E-35 AB018413.1	6912459 NT	6912459 NT	AB02070	2.0E-35 BE247575.1	2.0E-35 BF247575 1	2.0E-35 H49239 1	2.0E-35 BF332417.1	X59417.1	6912459INT		2.0E-35 BE904978.1			N88965.1	19.1		Γ	1.0E-35 AW389473.1		7705994	1.0E-35 BE350127.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35 X59417	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35 N88965	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1,0E-35	1.0E-35	1.0E-35
	Expression Signal	1.81	1.74	1.25	5.2	26.0	76.0	0.88	1.09	1.09	2.55	1.66	3.72	1.36	1.36	1.51	1.51	3.97	4.17	4.38	4.38	44.43	44.43	1.16	2.31	1.11	1.11
	ORF SEQ ID NO:		19902			22991			23539	23540		25401		22991		25354	26355		19902	19828	19829	20500	20501		22262	22496	22497
	Exen SEQ ID NO:	17325	12659	11083	_	- 1	13193	13427	13747	13747	14462	15347	18063	13193	13193	18936	18936	19264	12659	10028	10028	10667	10667	10817	12369	12602	12602
	Probe SEQ ID NO:	7465	103	1171	2171	3272	3272	3511	3835	3835	4570	5426	8175	9028	9028	9205	9206	9725	9832	<del>\$</del>	\$	735	735	894	2495	2740	2740
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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sabiens transcription elongation factor B (SIII) and marked at 1900 (1700 But)	AV650422 GLC Home saniens cDNA clone CI CCEERS 3	AV650422 GLC Homo sapiens cDNA clone GL CCEEns 3'	Mus musculus activin recentor interacting motion 1 (Arist pending) DNIA	Mus musculus activin receptor interacting protein 1 Ario1-pending), mRNA	Homo sapiens chromatin assembly factor 1 summit R (AD) (CHA E-12) - DAIA	AU158595 PLACE3 Homo sepiens cDNA clone PI ACEROGRAPO 2'	AU158595 PLACE3 Homo saniens cDNA clone PLACE30000323	promma-7.D01.r bytumor Homo sapiens cDNA 5'	Homo sapiens hypothetical protein (1 OC51233) mBNA	Homo sabiens casein kinase 1 ensilon (CSNK1F) mRNA	601584883F1 NIH MGC 7 Home centions of DAA close MACE consens of the	CM1-CT0315-091299-063-407 CT0345 Home sentens CNNA	Homo saplens C-terminal binding protein 2 (CTBD2) with A	Human carcinoembronic antigen gene family member 13 (CCM42)	Human carcinoambronic antigen gene family member 12 (CONTZ) gene, exons L and L/N	Homo sabiens of ratificine transferese A4 near 2000 A	Homo sapiens ninitirin 2 (NIN 12) mRNa	Homo sahiens TO 8 done even 42	UI-H-BW1-anv-c-12-0-UI-st NCI CGAP Sub7 Homo saniens cDNA clans IMA CE-2022 E.A.	th93b06.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:226196.3' similar to gb:M1949 PANCREATIC SECRETORY TRYPS:NI IMPLIBITION DEFICIES OF A 11 100.000.	ho06h02.x1 NCI_CGAP_Co14 Homo sepiens cDNA done IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN AI PHA.2 SI IRI INIT :	Homo sapiens syncytin precursor, mRNA, complete cds	#95c09.x1 NCI_CGAP_CLL1 Homo sepiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2	601305064F1 NIH MGC 30 Home sanions albita aleas 144.00 consesses.	Homo saniens Xa nee infoering regions against 2.00	601285567F4 NIH MPC A4 Home continue Chila III III Chila Continue Chila III III Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chila Chil	Homo saplens chromosome 21 comment HS21/000	Homo sapiens APISJika 1 (APISI 1) mPNA	Homo sapiens API5-like 1 (API5L1), mRNA	Homo sapiens Xq pseudoautosomal region; segment 1/2
gie Exon Pro	Top Hit Database Source	IN.	EST HUMAN	EST HUMAN		NT	LN PN	EST HUMAN	EST HUMAN	EST HUMAN	LN L	IN	EST HUMAN	EST HUMAN	NT	NT	LN	L L	Z	Į.	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST HIMAN	EST HUMAN	L	EST HIMAN	LN		NT.	
	Top Hit Acession No.	E006030 NT		AV650422.1	7656905 NT	7656905 NT	11526236 NT	AU158595.1	AU158595.1	AI525119.1	7705994 NT	11418110 NT	1.0E-35 BE792832.1	AW857579.1	4557498 NT		J06672.1	1.1	6622	6.0E-36 AB035346.1	6.0E-36 BF515101.1	6.0E-36 Al435169.1	6.0E-36 AW 780143.1		6.0E-36 Al380499 1				27	5729729	5729729 NT	5.0E-36 AJ271735.1
	Most Similar (Top) Hit BLAST E Value	1.0E-35	1.0E-35 AV65042	1.0E-35 AV65042	1.0E-35	1.0E-35	1.0E-35	1.0E-35 AU15850	1.0E-35 AU15859	1.0E-35 AI525118	1.0E-35	1.0E-35	1.0E-35	7.0E-36 AW8575	7.0E-36	7.0E-36 U06672.	7.0E-36 U06672	7.0E-36/	6.0E-36	6.0E-36/	6.0E-36	6.0E-36	6.0E-36	6.0E-36	6.0E-36	6.0E-36	5.0E-36/	5.0E-36 BE38843	5.0E-36 AL163209	5.0E-36	5.0E-36	5.0E-36
	Expression Signal	1.07	2.2	2.2	4.7	4.7	1.43	2	2	4.16	1.69	1.37	2.26	0.94	4.03	6.04	6.04	5.23	1.88	6.17	0.91	19.79	3.34	2.21	2.74	1.69	6.69	7.71	1.96	1.42	1.42	2.64
	ORF SEQ ID NO:	22826	22848	22849	24003	24004	25154	27578	27579		22262			22622		26548	26549	25279	21741		23290	24965	26237	27096	28931	25071	19928	22478	23264	24358	24359	19928
	Exon SEQ ID NO:	13030	13051	13051	14222	14222	15301	19469	19469	18782	12369	18971	19198	12827	13007	16371	16371	19071	11854	12247	13501	15190	16087	16904	18646	19580	10107	12584	13475	14564	14564	10107
	Probe SEQ ID NO:	3104	3126	3126	4325	4325	5382	7501	7501	8977	9186	9267	9620	2900	3080	6512	6512	9423	1959	2367	3587	5268	6221	7027	8833	9821	133	2722	3561	4678	4678	9026

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens calcineurib hinding madain 4 1/2/8 8 00000	PMS-BN0176-100400-001-004 BN0176 Home	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONI IN EACH.	ENDONOCE ENDE	2820020 Shifme NIH MGC 7 Home control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in 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gie Exon Proi	Top Hit Database Source	Ę	EST HUMAN	TOGGSWINS	EST HIMAN	EST HIMAN	EST HUMAN	EST HUMAN	L	Į	NT.	Z	EST HIMAN		HIMAN		Į		T HUMAN	Т	HIMAN	Т	EST HUMAN	Т	П	Т	7	EST_HUMAN	-					EST_HUMAN C
iio	Top Hit Acession No.	11417862 NT		510266	3E382574.1	AW247772.1	4.0E-36 BE389299.1	4.0E-36 BE389299.1	11497041 NT	4.0E-36 M33320.1			4.0E-36 AA400370.1	11420516 NT	4.0E-36 AV753629.1	Γ	7662401	TO181139 NT	27.1	37.1	76.1	7.1		_	10.1	3.1	3.1	1.0E-36 BF673761.1				1		1.0E-36 BF364169.1
	Most Similar (Top) Hit BLAST E Value	5.0E-36	4.0E-36 BE0100	4.0E-36 P10266	4.0E-36 BE382	4.0E-36 AW247	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36 D87675.1	4.0E-36 D87675.1	4.0E-36/	4.0E-36	4.0E-36/	3.0E-36 AF0998	3.0E-36	3.0E-36	3.0E-36 BF0353	2.0E-36 BE2592	2.0E-36	2.0E-36 AF26774	2.0E-36 T08756.	2.0E-36 T69629.	1.0E-36 BE4093	1.0E-36 BE1465	1.0E-36 BE14652	1.0E-36B	100	1.0E-36 AI86//1	1.0E-36 A	1.0E-36/A	1.0E-36 A	1.0E-36 B
	Expression Signal	2.36	1.43	1.54	1.58	1.63	3.21	3.21	221	1.74	1.41	1.41	2.19	1.31	285	2.73	0.89	5.15	1.78	2.7	4.62	2.16	3.99	11.82	1.9	0.86	0.86	1.31	,	5.00 5.00 5.00 5.00 5.00 5.00 5.00 5.00	203	2.03	2.84	4.06
	ORF SEQ ID NO:		20961	21196			23036	23037	25704	26547			28481			20437	22033	24081	28584	22857	24534	25127	25556	25989	20643	21884	21885	21942		77777	20/11	20172	787,7	71817
	Exon SEQ ID NO:	19010	11115	11329	11530	12062	13231	13231	15602	16370	16856	16856	18233	19015	19545	10614	. 12136	14297	18325	13057	14757	15291	15483	15867	10793	11987	11987	12043	15660	4650	10020	17007	1,037	1,0/4
	Probe SEQ ID NO:	9318	1205	1424	1626	2175	3310	3310	5693	6511	6979	6979	8356	9334	9380	681	2252	4402	8452	3132	4877	5371	2267	5962	867	2098	2098	2155	5752	BRAO.	OF OF	7220	7002	1024
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Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	S	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
8317			3.43	1.0E-36	1.0E-36 AW897636.1	EST_HUMAN	CM3-NN0081-140400-147-h12 NN0061 Homo sapiens cDNA
8686		28857	3.91	1.0E-36	1.0E-36 AW 504143.1	EST HUMAN	UI-HF-BNO-ale-c-03-0-UI-1 NIH MGC 50 Homo seniens chay alone (MAOE 2007/077 FI
9203	_ [		3.74	1.0E-36	11418177 NT	N L	Homo saplens Ran GTPasa activating property Applicatory world
9374	_	25305	1.29	1.0E-36	11418121 NT	N F	Homo saplens chromosome 22 onen reading frame 2 (C2000Ex)
9647			3.07	1.0E-36	1.0E-36 AL163213.2	N.	Homo sapiens chromosome 21 segment HQ21 CA12
9890			2.89	1.0E-36	1.0E-36 AF202723.1	Z	Homo sapiens Sad1 uno-84 domain protein 2 (S1N2) mBN/A matrix 2
8388			1.96	9.0E-37	9.0E-37 AW009277.1	EST HUMAN	ws80b07x1 NCI CGAP Cos Home saniens c INA Alma IMA CE SEA ATA E
9368	16231	26391	1.96	9.0E-37	9.0E-37 AW009277.1	EST HUMAN	WS80b07.XT NCI CGAP Co3 Home saniens chiva clone living consequence
9462	19093		2.79	9.0E-37	9.0E-37 W22618.1	EST HUMAN	73D4 Human refina cDNA Tsn5nol changed sublificant Locations (2014)
5143	15010	24781	1.38	8.0E-37	8.0E-37 AB020684.1	L L	Homo saplens mRNA for KIAADA77 mater working all processes conva not directional
5213	15136		1.7	8.0E-37	8.0E-37 BE698077.1	EST HUMAN	CM0-UT0003-050800-503-d09 LT0003 Home sanians CNA
5559	15475	25547	7.7	20 00	8 OE 37 DE250107 4		ht09g01.x1 NCI_CGAP_Kld13 Homo sapiens cDNA.clone IMAGE:3146256 3' similar to contains MER29.b3
			7	0.0E-3/	BE35012/.1	ESI_HUMAN	MER29 repetitive element;
5559	15475		4.1	8.0E-37		EST HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
5584	15499	25576	5.63	8.0E-37	8.0E-37 AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09 1 CN0008 Homo sanians CDNA
6602	16482	26670	6.25	8.0E-37 X87344.1			H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 ones.
1263	11170		2.51	7.0E-37	1	T HI MAN	DX F7n444F0472
8140	18028	28274	6.77	7.05-37			WG5b17x1 NOL CGAP Bm25 Homo sepiens cDNA clone DKFZp434E0422 5' WG5b17x1 NOL CGAP Bm25 Homo sepiens cDNA clone IMAGE:2413341 3' similar to contains PTR5:2'
						NUMBER OF THE	tm87g03.x1 NCI CGAP Bm26 Homo saplens cDNA clone IMA CE 2266340 21 21 21 21 21 21 21 21 21 21 21 21 21
	18148	28388	4.16	7.0E-37,		T_HUMAN	repetitive element;
2/12	19292		2.48	6.0E-37			Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA martial cris
)QC	15615	25716	3.37	5.0E-37 /	.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo saniens CDNA 57 and
2/0/9	15615	25717	3.37	5.0E-37	5.0E-37 AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo saniens CDNA 57 and
8282	18171		4.17	5.0E-37	7657117 NT		Homo saplens dixine C-acetyltransferase (2-amin-2) control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the
9198	18931		3.57	5.0E-37	5.0E-37 AF149773.1	LN LN	Homo sapiens NOD1 protein (NOD1) gene expres 1.2 and 3
2374	12254	22145	2.23	4.0E-37	4.1	EST HUMAN	zi90b04.s1 Soares feta liver soleen 1NFIS S1 Homo contono of NA Liver Spices
2460	15027		1.11	4.0E-37 N62051.1		Т	EST52010 WATM1 Homo septems cDNA clare 5240 clarifier to Care Care Care Care Care Care Care Care
1970	11863	21755	2.85	3.0E-37	3.0E-37 AL048956.1	EST HUMAN	DKFZp43412418 r1 434 (sunnum Hess) Home seriens con Alexandra Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control
1970	11863	21756	2.85	3.0E-37 ∤		_	DKFZp434L2418 r1 434 (synonym: htes3) Home sapiens cDNA clone DKFZp434L2418
2465	12341		1.7	3.0E-37	3.0E-37 AW961150.1	EST HUMAN	EST373222 MAGE resequences: MAGE Homo senione Child
2836	12863		3.02	3.0E-37 A		EST_HUMAN	EST373222 MAGE resequences, MAGF Homp semiens china
							WAIGH CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF

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Single CAULTIONES EXPRESSED IN REAL	Top Hit Descriptor	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 51	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous Xanthomatosis), polymentide 1 (CYP27414) mRNA	EST52931 Fetal heart III Homo saniens cDNA 57 end	601869157F1 NIH MGC 17 Home sapiens cDNA clone IMAGE-44114/08 F1	Homo sapiens J domain containing profess 1 softom h ( IDPA) mRNA complete 2.3	Homo saplens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES3) mBNA	Homo sapiens chromosome 21 segment HS21C081	Homo sapiens ribonuclease III (RN3) mRNA, complete crts	601448619F1 NIH MGC 65 Homo sanians CDNA Home IMAGE 128526E2 51	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA	क21602.r1 Stratagene neuroepithellum (#937231) Homo sapiens cDNA done IMAGE:610059 5' similar to	Himen comoffic adouble actually	Charles Solitate Cytochiums C (no.1) processed pseudogene, complete cds	Rathis notificing multidametria management 1.	Homo sapiens Grb2-associated binder 2 (VIAA0574) — BNA	602018401F1 NCI CGAP Bring Homo semiens Child Alone MACE: 14 52000 El	Homo sapiens Grb2-associated hinder 2 (KIAA0571) mRNA	EST384920 MAGE reseguences, MAGI, Homo sepiens cDNA	601455722F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3859348 F.	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo sapiens chromosome 12 open reading frame 3 (C12ORE3) mRNA	Homo sapiens DNA for Human P2XM, complete cds	EST383908 MAGE resequences. MAGI Homo saniens conta	Homo sapiens RIBIIR gene (partia), exon 8	801450148F1 NIH MGC 65 Homo sabiens cDNA clane IMAGE-3854074 El	B.taurus mitochondrial aspartate aminotransferase mRNA complete CDS	B. faurus mitochondrial aspartate aminotransferase mRNA complete CDC	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
Bie Exoli Pio	Top Hit Database Source	EST HUMAN	EST HUMAN	TN.	Į.	EST HUMAN	EST HUMAN	LN	NT	FN	NT	EST HUMAN	EST_HUMAN	EST HIMAN	TN	EST HIMAN	-1	LN	EST HUMAN	Z L	EST HUMAN	EST HUMAN	LN FN	F	F	NT	EST HUMAN	NT	EST HUMAN	TN	N	TN	TN
	Top Hit Acession No.	AU131202.1	ĺ	7.2	3210	2.0E-37 AA346720.1	BF204032.1	AF176013.1	2.0E-37 11417972 NT	1.0E-37 AL163281.2	AF189011.1	1.0E-37 BE872365.1	1.0E-37 BF371719.1	1 0F-37 AA171406 1	M22878 1	4.1	8482	11436955 NT	-	1436955	5.1	<u>~</u>	11425114 NT	11425114 NT	11435947 NT	AB002059.1	9.1	5.0E-38 AJ237740.1	7.			11435947 NT	
	Most Similar (Top) Hit BLAST E Value	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37 BF20403	2.0E-37	2.0E-37	1.0E-37	1.0E-37 AF18901	1.0E-37	1.0E-37	1 0F-37	1 0F-37 M22878	1.0F-37	9.0E-38	8.0E-38	8.0E-38 BF34622	8.0E-38	7.0E-38 AW97282	6.0E-38 BF03303	6.0E-38	6.0E-38	6.0E-38	6.0E-38 AB00205g	5.0E-38 AW97181	5.0E-38	5.0E-38 BE871610	4.0E-38 Z25466.1	4.0E-38 Z25466.1	3.0E-38	3.0E-38 AF003530
	Expression Signal	1.94	1.94	1.47	5.05	3.36	3.23	16.4	3.15	3.61	22.51	96.0	2.13	2.85	20.59	2.46	3.05	1.95	1.44	1.36	1.38	1.76	1.69	1,69	4.46	6.66	1.15	1.79	2.42	2.56	2.56	0.82	4.39
	ORF SEQ ID NO:	20824	20825	21695	23519			28945		21828	23577	23753	24517	27141	28222		25514	20959	22225	20959	21920	22726	25407	25408		25286	20468	22178	26225	19909	19910	20897	
	Exon SEQ ID NO:	10980	10980	11816	13730	15912	16565	18657	19403	11932	13789	13974	14737	16949	17973	19122	15447	11113	12326	11113	12023	12933	15352	15352	18842	19143	10642	12281	16076	10092	10092	11055	11943
	Probe SEQ ID NO:	1064	1064	1921	3818	2009	9899	8845	9933	2041	3878	4072	4857	7072	8082	9208	2230	1203	2449	9568	2135	3002	5432	5432	0906	9542	710	2404	99	113	113	<u>+</u>	2053

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA	SSU72 PROTEIN	SSU72 PROTEIN	601157633F1 NIH_MGC_21 Hamo sapiens cDNA clane IMAGE:3504272 5	Homo sapiens chromosome 21 segment HS21C100	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA	yw88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775.5	y488b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	zw30d01.r1 Soares ovary fumor NbHOT Homo saptens cDNA clone IMAGE:770785 5' similar to SW:MA12 RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1.2-MANNOSIDASE	zw30d01.r1 Soares ovary fumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12 RABIT P45701 MANNOSYI -OI IGOSACCHARIDF AI PHA-1 2-MANNOSYI -OI -OI -OI -OI -OI -OI -OI -OI -OI -O	MR3-HT0487-150200-113-g01 HT0487 Homo septens cDNA	hu09g02.xt NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:002710 002710 GAG POLYPROTEIN.	Homo sapiens mRNA for KIAA0145 protein, partial cds	QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA	Homo saplens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA martial cris	Homo sapiens leucine-rich repeat-containing G protein-counled recentur 8 // GRS/ mBNA merial and	AV726988 HTC Homo saplens cDNA clone HTCAXH075	Homo sapiens gene for kinesin-like protein, complete cds	CHR220580 Chromosome 22 exon Homo septens cDNA clone C22 788 5'	E1 beta=pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]		3E:742539 5' similar to contains element	leotide binding protein-like 1 (GNI 1) mRNA		Homo sapiens cyclin K (CCNIK) gene, exon 7
OL LINGUIST OUT	Top Hit Database Source	LN LN	SWISSPROT	SWISSPROT	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	N.	IN	LN LN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	N	EST_HUMAN	TN	Ę	EST HUMAN	IN	EST HUMAN	NT	LN L	EST HUMAN	4	LN	TN
5	Top Hit Acession No.	7549807 NT			3.0E-38 BE279301.1	3.0E-38 AL163300.2	3.0E-38 BF373664.1	3.0E-38 H85494.1	3.0E-38 H85494.1			5902097 NT	2.0E-38 AA437353.1			6.1		0.1	2.0E-38 AF190501.1	2.0E-38 AF190501.1	8.1	2.0E-38 AB012723.1			11418248 NT	0.1	4885288	7661969 NT	1.0E-38 AF270831.1
	Most Similar (Top) Hit BLAST E Value	3.0E-38	3.0E-38 P53538	3.0E-38 P53538	3.0E-38	3.0E-38	3.0E-38	3.0E-38	3.0E-38	3.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38 H55641.1	2.0E-38 S74908.1	2.0E-38	1.0E-38 AA40157	1.0E-38	1.0E-38	1.0E-38
	Expression Signal	1.11	1.65	1.65	0.85	7.17	7.64	1.78	1.78	1.58	1.41	2.6	1.66	1.68	4.7	1.47	1.66	5.24	3.69	3.69	4.05	2	3.86	2.28	2.56	2.29	0.94	1	1.58
	ORF SEQ ID NO:			23481		26083	26504	27094	27095		19836	21120	21390	21391			28063	28885	29008	29009			25313	,			21736	21758	22221
	Exan SEQ ID NO:	13552	13693	13693		19429	16337	16902	16902		10032	11264	11531	11531	16819		17820	18596	18715	18715	18876	18878		19099	19396	10993	11849	11866	12322
	Probe SEQ ID NO:	3638	3781	3781	4513	6050	6478	7025	7025	7727	44	1358	1627	1627	· 6941	7316	7970	8781	8907	8907	9112	9115	9412	9472	9924	1077	1954	1973	2445

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Table 4
Single Exon Probes Expressed in Heart

					6)		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4063	13965	23743	1.41	1.0E-38	1.0E-38 AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4223	14121	23896	0.83	1.0E-38	4505016 NT	NT	Homo saplens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4229	L			1.0E-38	~	NT	Homo sapiens chromosome 21 segment HS21C003
4229				1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21 C003
4493	<u> </u>		1.21	1.0E-38		NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5673	15582	25682		1.0E-38	7305360 NT	NT	Mus musculus otogelin (Otog), mRNA
5673	15582	25683	3.61	1.0E-38	7305360	L	Mus musculus otogelin (Otog), mRNA
6378	16240	26400			1.0E-38 AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
					7.000000	1444	ht09g01.x1 NCI_CGAP_Kld13 Home saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
7414		2/489				ESI_HUMAN	WIENZS Jebeunye dennan,
9264	19481		2.33		AL163284.2	NT	Homo saplens chramosome 21 segment HS21C084
48	10036	19842	5.14		*	ŅŢ	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1372	11278	21134	1.51	8.0E-39	4758229 NT	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
							wh53f10.x1 NCI_CGAP_Kld11 Homo saplens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
1788	11686	-	1.06		8.0E-39 AI823404.1	EST_HUMAN	POL PROTEIN;
2047	11938	3 21832	5.54		2	IN	Homo sapiens chromosome 21 segment HS21C027
8184	18070	28319	2,12		6.0E-39 BF331829.1	EST_HUMAN	QV1-BT0631-040900-357-f02 BT0631 Homo sepiens cDNA
							7e34c03.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3284356 3' similar to WP:R151.6
9838	19337		2.23	İ	6.0E-39 BE670394.1	EST_HUMAN	CE00828;
ğ	40042	20757	13		5 0E.30 AE003528 1	IN	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat recions
3				L			
		_					at36b04x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
2957	12884	4 22682	5.13	3	AI750154.1	EST_HUMAN	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.t1 LTR7 repetitive element ;
9556	19154				11420289 NT	NT	Homo sapiens hypothetical protein FL:110803 (FLJ10803), mRNA
538	10479				4.0E-39 AB015610.1	TN	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3525	13441	1 23238	96.0		4.0E-39 AL163210.2	NT	Homo saplens chromosome 21 segment HS21C010
							ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
6707	16587	7 26775	1.49		4.0E-39 AA6B2949.1	EST HUMAN	OFR.b1 OFR repetitive element;
9575		+	3.08		11418177 NT	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9687	19240				4.0E-39 BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
41					3.0E-39 AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo saptens cDNA clone CR12-1
41	10029	19831	11.27		3.0E-39 AA631949.1	EST_HUMAN	finfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1

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Examely District Signal No: SEQ ID No: Sequestion No: SEQ ID DIA No: Signal No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequestion No: Sequesti			_	Τ.	т. —	-	_	_	_	_	Т.	_		7-	т-	Τ-	Τ.	_	Ť	T	~	<del>''</del>	Т"	<b>"-</b> "		т-	<del>7"</del>		_	·		<del></del>
Exant No: Signal         Most Similar Top Hit Aces Signal         Most Similar Top Hit Aces No: No: No: No: No: No: No: No: No: No:	oes Expressed in Heart	Top Hit Descriptor	finfc16 Regional genomic DNA specific cDNA library Homo saplens cDNA clone CR12-1	ox63a10.s1 Soures_NH-IMPu_S1 Homo saplens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE:	ox63a10.s1 Soures_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5. SMAIL! INTESTINE	yp51c06.s1 Soares retina NZb4HR Homo saciens cDNA clone IMAGE-190954.3	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'	promme-7.D01.r bytumor Homo saplens cDNA 5'	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds	PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA	nw21g02.s1 NCI_CGAP_GCB0 Homo saplens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element:	Homo sapiens chromosome 21 segment HS21C048	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA	ng86f03.s1 NCI_CGAP_Pr6 Homo saplens cDNA clone IMAGE:941693	zn06f02.r1 Strategene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'	Human mRNA for KIAA0209 gene, partial cds	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA	Homo sapiens KVLQT1 gene	Homo sapiens KVLQT1 gene	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	EST364065 MAGE resequences, MAGB Homo sapiens cDNA	EST364065 MAGE resequences, MAGB Homo sapiens cDNA	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	yd26g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains	Alu repetitive element contains LTR1 repetitive element;	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)	Homo saplens tubby like protein 3 (TULP3), mRNA	Homo saplens mRNA for ras-related GTP-binding protein, complete cds	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA	Homo sapiens AE-binding protein 1 (AEBP1) mRNA	Homo saplens AE-binding protein 1 (AEBP1) mRNA
Exant No: Signal         Most Similar Top Hit Aces Signal         Most Similar Top Hit Aces No: No: No: No: No: No: No: No: No: No:	JIO EXON Pro	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	LN TN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	Z.	N	N L	N	Z	EST_HUMAN	EST_HUMAN	NT		EST_HUMAN	LN	보	LN LN	NT	F	NT	LN T
Exart SEQ ID         ORF SEQ Expression of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mossion of Factors         Mo	SIN		AA631949.1				BE409203.1	AI525119.1		4W372318.1	4A720574.1	Π					11425464	5.1	5.1	7657020	4W951995.1	4W951995.1	7657020							5803210	4755145 NT	4755145 NT
Exan ORF SEQ Express NO: Signs NO: 10029 19832 1 18871 28781 18871 28782 19890 10820 10833 11418 12458 22349 14201 23985 15295 14453 24240 14453 24240 14453 25451 16028 16530 25382 10484 20294 11539 25254 16520 25382 10484 20294 1173 20071 1413		Most Similar (Top) Hit BLAST E Value	3.0E-39	3.0E-39	3.0E-39	3.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	1.0E-39	1.0E-39 /	1.0E-39	1.0E-39 /	1.0E-39	1.0E-39	l	1.05-39	1.0E-39/	1.0E-39 /	1.0E-39	1.0E-39 I	9.0E-40	9.0E-40	9.0E-40
Exan SEQ ID DR NO: 10029 10029 10029 10029 10029 10020 10033 11445 11445 11445 11445 115295 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 15395 1539			11.27	5.51	5.51	4.42	4.03	17.44	3.61	10.15	10.03	1.75	1.36	3.4	2.17	2.33	2.31	1.78	1.78	4.95	5.49	5.49	8.58	i	8	4.36	4.36	1.66	1.75	1.67	10.19	10.19
		ORF SEQ ID NO:	19832	28781	28782						21707	22349	23985	25142	26384	28874		21261	21262	21275	24239	24240	24279	0	25439	26460	25461		26382	20294	20971	20972
Probe EQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Exan SEQ ID NO:	10029	18871	18871	18900	10805	10820	10933	11418	11825	12458	14201	15295	16223	18587	19394	11401	11401	11419	14453	14453	14492	02020	8/8	CSSOL	15395	16028	16220	10484	11123	11123
		Probe SEQ ID NO:	41	9104	9104	9147	879	894	1015	1513	1930	2587	4303	5375	6360	8731	9922	1497	1497	1514	4561	4561	4604	6750	200	04/5	5475	8083	6357	543	1215	1216

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	Top Hit Acession Database No. Source	3.0E-39 AA631949.1 EST_HUMAN   fmfc16 Regional genomic DNA specific cDNA library Homo saplens cDNA clone CR12-1	a.0E-39 AI084557.1 EST_HUMAN P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;	3.0E-39 A1084557.1 EST HUMAN P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE:	EST_HUMAN	3.1 EST_HUMAN	2.0E-39 A1525119.1   EST_HUMAN   promma-7.001.r bytumor Homo sapiens cDNA 5'	2.0E-39 AF000573.1 NT Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds	2.0E-39 AW372318,1   EST_HUMAN   PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA	2.0E-39 AA720574.1 EST HUMAN THK repeative element;	A FOT LII MAANI	2.0E-38 BF3/0207.1 EST LITIMAN INCRETED CONTROL TO THE HOME SAPERIS CONTROL TO THE TITLING TO THE TITLING TO THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE TITLING THE T	1 EST HIMAN	MT	11425464 NT	AJ006345.1 NT	-N	7657020 NT	1.0E-39 AW951995.1   EST_HUMAN   EST364065 MAGE resequences, MAGB Homo sapiens cDNA	T_HUMAN	7657020 NT	•	EST_HUMAN		AJ278170.1 NT	11436736 NT	4.0E-39 D78132.1 NT Homo saplens mRNA for ras-related GTP-binding protein, complete cds	40 5803210 NT Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA	4755145 NT	,
VI OBIID		-	-			.1	1 EST	.1		-,	,,				425464	-	-	7657020 NT	5.1	5.1 EST	7657020 NT			1	.1	11436736 NT		5803210 NT	4755145 NT	4755145 NT
-	Most Similar (Top) Hit BLAST E Value	3.0E-39	3.0E-39/	3.0E-39	3.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-391	Z.OE-29.	2.0E-39	2.05-39	2000	2.0E-39			1.0E-39	1.0E-39,		1.0E-39							9.0E-40		9.0E-40
	Expression Signal	11.27	5.51	5.51	4.42	4.03	17.44	3.61	10.15	10.03	6.6	9.	3.4	2000	231	1.78	1.78	4.95	5.49	5.49	8.58		1.54	4.36	4.36	1.66	1.75	1.67		10.19
	ORF SÉQ ID NO:	19832	28781	28782							25048		75797			21261	21262		24239	24240	24279	_					26382	20294		2002
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	Probe SEQ ID NO:	4	9104	9104	9147	879	894	1015	1513	1930	/907	4303	53/5	0200	9922	1497	1497	1514	4561	4561	4604		6459	5475	5475	6083	6357	543	1215	1215

Page 210 of 413 Table 4 Single Exon Probes Expressed in Heart

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| Top Hit Descriptor                            | Homo sapiens tissue inhibitor of metalloproteinese 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA                                                            | Homo sapiens mRNA for KIAA1244 protein, partial cds                                                                                                                                                                                                       | Homo sapiens ubiquitin specific protease 13 (Isopantidase T-3) (ISP13) mRNA                                                                                                                                                                                                                                                                                                                                                         | Homo sapiens ubiquitin specific protease 13 (Isopentidase T-3) (USP13) mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Human DNA polymerase gamma mRNA, nuclear gene encoding milochondrial protein complete cels                                         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            | EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger prodein familio                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | EST70527 T-cell hmphoma Homo senione cDNA 5' and similar to aimite to aim at a similar to aim at a similar to aim at a similar to aim at a similar to aim at a similar to aim at a similar 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1 (FADS1) mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                            | AV653028 GLC Hamo sapiens cDNA clone GLCDGF043'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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                         | 1891601.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:073505 073505 POL PROTEIN.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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                                                                | RC1-CN0017-120200-012-004 CN0017 Homo seniens CNNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE: つまねらちゅう                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| Top Hit<br>Database<br>Source                 | LN                                                                                                                                                                         | NT                                                                                                                                                                                                                                                        | N                                                                                                                                                                                                                                                                                                                                                                                                                                   | N                                                                                                       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|                                               | Exon     ORF SEQ     Expression ID NO:     Signal NO:     Signal No:     Most Similar (Top) Hit Acession No:     Top Hit Acession No:     Top Hit Acession Database Source | Exon ORF SEQ Expression (Top) Hit Acession No. Signal Value 11338 21205 6.04 9.0E-40 4507512 NT Pap Hit Acession Scarce Scarce Scarce Scarce Scarce Scarce Scarce Scarce Scarce Scarce Scarce Scarce Homo saplens tissue inhibitor of metalloprotein mRNA | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>Value         (Top) Hit<br>Signal<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT           15069         23586         3.58         9.0E-40 AB033070.1         NT | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>ID NO:         Expression<br>Signal<br>Value         (Top) Hit<br>PLAST E<br>Value         Top Hit Acession<br>No:         Top Hit | Exon<br>NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>No:         (Top) Hit<br>BLASTE<br>Value         Top Hit Acession<br>No.         r>NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>NO:         (Top) Hit<br>BLASTE<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT           14149         23923         0.82         9.0E-40         4507848 NT           14332         22726         9.0E-40         4507848 NT           12932         22726         9.0E-40         4507848 NT | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>PLAST E<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT           14149         23923         0.82         9.0E-40         4507848 NT           14149         23923         1.12         9.0E-40         4507848 NT           12932         22725         0.95         8.0E-40         4507848 NT           13768         2.2725         0.95         8.0E-40         AA078165.1         EST_HUMAN           13768         2.41         8.0E-40         BE396541.1         EST_HUMAN | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal         Expression<br>FLAST E<br>Value         (Top) Hit<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source         Top Hit Acession<br>No.         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT         NT           15069         23586         3.58         9.0E-40         4507848 NT         NT           14149         23923         1.12         9.0E-40         4507848 NT         NT           12932         22725         0.95         8.0E-40         4507848 NT         EST HUMAN           15768         2.241         8.0E-40         BE396541.1         EST HUMAN           16399         25578         7.0E-40         NOT         NT | Exon<br>NO:         ORF SEQ<br>Signal         Expression<br>Fluid         Moet Similar<br>Top Hit<br>Na         Top Hit Acession<br>No.         Top Hit Acession<br>Packed         Top Hit Acession<br>No.         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT         NT           14149         23923         0.82         9.0E-40         4507848 NT         NT           12932         22725         0.95         8.0E-40         4507848 NT         NT           16399         26578         1.56         7.0E-40 U60325.1         NT         NT           16399         26579         1.56         7.0E-40 U60325.1         NT         NT | Exon<br>NO:         ORF SEQ<br>Signal         Expression<br>Fluid         (Top) Hit<br>Fluid         Top Hit Acession<br>No:         Top Hit Acession<br>Pathbase         Top Hit Acession<br>No:         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT         Source           14149         23923         0.82         9.0E-40         4507848 NT         NT           142932         22725         0.95         8.0E-40         4507848 NT         NT           16392         26578         1.66         0.95         8.0E-40         HG0325.1         NT           16399         26579         1.56         7.0E-40         UG0325.1         NT         NT           18150         28391         2.83         7.0E-40         HG0325.2         NT         NT | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>Top) Hit<br>PLAST E<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512 NT         NT           15069         23586         3.58         9.0E-40         4507848 NT         NT           14149         23923         1.12         9.0E-40         4507848 NT         NT           12932         22725         0.95         8.0E-40         4507848 NT         NT           143768         2.41         8.0E-40         AA078165.1         EST HUMAN           16399         26578         1.56         7.0E-40         U60325.1         NT           18150         28391         2.83         7.0E-40         AL163246.2         NT           12560         22449         3.88         6.0E-40         AA361275.1         EST HUMAN                                                                                                                                                                                                                                                                                                       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Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit | Exon<br>NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>Signal<br>NO:         Most Similar<br>Signal<br>NO:         (Top) Hit<br>Signal<br>No:         Top Hit Accession<br>No:         Top Hit Accession<br>No:         Top Hit Accession<br>Source           11538         21205         5.04         9.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14149         23923         0.12         9.0E-40         4507848         NT           12592         22725         0.95         8.0E-40         AA078165.1         EST HUMAN           13768         26578         1.56         7.0E-40         U60325.1         NT           16399         26579         1.56         7.0E-40         U60325.1         NT           18150         22449         3.88         6.0E-40         AA361275.1         EST HUMAN           15580         22450         3.88         6.0E-40         AA361275.1         EST HUMAN           1588         26124         3.08         6.0E-40         AA361275.1         EST HUMAN           1588         26126         3.08         6.0E-40         AA361275.1         EST HUMAN           1588         26126         3.08         6.0E-40 <td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>NO:         Expression<br/>Signal<br/>Signal<br/>NO:         Most Similar<br/>Signal<br/>NO:         (Top) Hit<br/>Pub.         Top Hit Accession<br/>No:         Top Hit Accession<br/>Source         Top Hit Accession<br/>No:         Top Hit Accession<br/>Source         Top Hit Accession<br/>Accorded         Top Hit Accorded         Top Hit Accorded         Top Hit Accorded         Top Hit Accorded<!--</td--><td>Excm         ORF SEQ         Expression Signal         Most Similar Plus         Most Similar Plus         Top Hit Acession Patabase Plus Plus         Top Hit Acession Signal Plus         Most Simal Plus Plus         Most Simal Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         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Acession<br/>No.         Top Hit Acession<br/>Particle         Top Hit Acession<br/>No.         Top Hit Acession<br/>Source           11338         21205         5.04         9.0E-40         4507512         NT           14149         23923         1.12         9.0E-40         4507848         NT           12932         22725         0.95         8.0E-40         A607848         NT           14368         28023         1.12         9.0E-40         4507848         NT           12932         22725         0.95         8.0E-40         A607848         NT           16399         26578         1.66         7.0E-40         U60325.1         NT           16399         26578         1.66         7.0E-40         U60325.1         NT           12560         22449         3.88         6.0E-40         AA361275.1         EST HUMAN           15683         26124         3.88         6.0E-40         AA361275.1         EST HUMAN           15689         26125         3.08         6.0E-40         AA361275.1         EST HUMAN           15689         26125         3.08         6.0E-40         AA362328.1</td><td>Exom<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Moet Similar<br/>(Top) Hit<br/>Palue         Top Hit Acession<br/>No.         Top Hit Acession<br/>Palue         Top Hi</td><td>Exon<br/>NO:-<br/>1336         ORF SEQ<br/>21205         Expression<br/>Signal         Top Hit Acession<br/>Top) Hit<br/>BLAST E         Top Hit Acession<br/>Active         Top Hit Acession<br/>Polity         Top Hit Acession<br/>Database           11336         21205         5.04         8.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14368         22725         1.15         9.0E-40         4507848         NT           14390         226578         1.56         7.0E-40         MG0325.1         NT           16399         26579         1.56         7.0E-40         MG0325.1         NT           1650         22450         3.88         6.0E-40         AA361275.1         EST HUMAN           16531         27450         3.88         6.0E-40         AA361275.1         EST HUMAN           1589         26140         A663266.1         EST HUMAN           17581</td><td>Exon<br/>NO:-         ORF SEQ<br/>Signal<br/>NO:-         Expression<br/>Signal<br/>Signal<br/>NO:-         Moet Similar<br/>Signal<br/>No:-         (Top) Hit<br/>Signal<br/>No:-         Top Hit Acession<br/>Value         Top Hit Acession<br/>No:-         Top Hit Acession<br/>Source           11338         21205         5.04         8.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14349         23923         0.12         9.0E-40         4507848         NT           14349         23923         0.12         9.0E-40         4507848         NT           14349         23923         0.12         8.0E-40         4507848         NT           14349         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    Top Hit Acession<br/>Particle         Top Hit Acession<br/>No.         Top Hit Acession<br/>Source           11338         21205         5.04         9.0E-40         4507512         NT           14149         23923         1.12         9.0E-40         4507848         NT           12932         22725         0.95         8.0E-40         A607848         NT           14368         28023         1.12         9.0E-40         4507848         NT           12932         22725         0.95         8.0E-40         A607848         NT           16399         26578         1.66         7.0E-40         U60325.1         NT           16399         26578         1.66         7.0E-40         U60325.1         NT           12560         22449         3.88         6.0E-40         AA361275.1         EST HUMAN           15683         26124         3.88         6.0E-40         AA361275.1         EST HUMAN           15689         26125         3.08         6.0E-40         AA361275.1         EST HUMAN           15689         26125         3.08         6.0E-40         AA362328.1</td> <td>Exom<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Moet Similar<br/>(Top) Hit<br/>Palue         Top Hit Acession<br/>No.         Top Hit Acession<br/>Palue         Top Hi</td> <td>Exon<br/>NO:-<br/>1336         ORF SEQ<br/>21205         Expression<br/>Signal         Top Hit Acession<br/>Top) Hit<br/>BLAST E         Top Hit Acession<br/>Active         Top Hit Acession<br/>Polity         Top Hit Acession<br/>Database           11336         21205         5.04         8.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14368         22725         1.15         9.0E-40         4507848         NT           14390         226578         1.56         7.0E-40         MG0325.1         NT           16399         26579         1.56         7.0E-40         MG0325.1         NT           1650         22450         3.88         6.0E-40         AA361275.1         EST HUMAN           16531         27450         3.88         6.0E-40         AA361275.1         EST HUMAN           1589         26140         A663266.1         EST HUMAN           17581</td> <td>Exon<br/>NO:-         ORF SEQ<br/>Signal<br/>NO:-         Expression<br/>Signal<br/>Signal<br/>NO:-         Moet Similar<br/>Signal<br/>No:-         (Top) Hit<br/>Signal<br/>No:-         Top Hit Acession<br/>Value         Top Hit Acession<br/>No:-         Top Hit Acession<br/>Source           11338         21205         5.04         8.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14349         23923         0.12         9.0E-40         4507848         NT           14349         23923         0.12         9.0E-40         4507848         NT           14349         23923         0.12         8.0E-40         4507848         NT           14349         23923         1.12         8.0E-40         Ad078165.1         EST_HUMAN           16399         26578         1.56         7.0E-40         U60325.1         NT           16399         26579         1.56         7.0E-40         U60325.1         NT           1650         22450         3.88         6.0E-40         AA.163246.2         NT           16540         26740         A.0E-40         AG03225.1         RT         HUMAN           16541         27804         6.0E-40         AG053028.1         EST_H</td> <td>Ekon<br/>NO:<br/>11338         ORF SEQ<br/>21205         Expression<br/>Signal         (Top) Hit<br/>Value         Top Hit Acession<br/>Acade         Top Hit Accession<br/>Acade         Top Hit Accession<br/>Acade         Top Hit Accession<br/>Acade         Top Hit 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Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acession Plus         Top Hit Acess | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>ILASTE<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>Particle         Top Hit Acession<br>No.         Top Hit Acession<br>Source           11338         21205         5.04         9.0E-40         4507512         NT           14149         23923         1.12         9.0E-40         4507848         NT           12932         22725         0.95         8.0E-40         A607848         NT           14368         28023         1.12         9.0E-40         4507848         NT           12932         22725         0.95         8.0E-40         A607848         NT           16399         26578         1.66         7.0E-40         U60325.1         NT           16399         26578         1.66         7.0E-40         U60325.1         NT           12560         22449         3.88         6.0E-40         AA361275.1         EST HUMAN           15683         26124         3.88         6.0E-40         AA361275.1         EST HUMAN           15689         26125         3.08         6.0E-40         AA361275.1         EST HUMAN           15689         26125         3.08         6.0E-40         AA362328.1 | Exom<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Moet Similar<br>(Top) Hit<br>Palue         Top Hit Acession<br>No.         Top Hit Acession<br>Palue         Top Hi | Exon<br>NO:-<br>1336         ORF SEQ<br>21205         Expression<br>Signal         Top Hit Acession<br>Top) Hit<br>BLAST E         Top Hit Acession<br>Active         Top Hit Acession<br>Polity         Top Hit Acession<br>Database           11336         21205         5.04         8.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14368         22725         1.15         9.0E-40         4507848         NT           14390         226578         1.56         7.0E-40         MG0325.1         NT           16399         26579         1.56         7.0E-40         MG0325.1         NT           1650         22450         3.88         6.0E-40         AA361275.1         EST HUMAN           16531         27450         3.88         6.0E-40         AA361275.1         EST HUMAN           1589         26140         A663266.1         EST HUMAN           17581 | Exon<br>NO:-         ORF SEQ<br>Signal<br>NO:-         Expression<br>Signal<br>Signal<br>NO:-         Moet Similar<br>Signal<br>No:-         (Top) Hit<br>Signal<br>No:-         Top Hit Acession<br>Value         Top Hit Acession<br>No:-         Top Hit Acession<br>Source           11338         21205         5.04         8.0E-40         4507512         NT           14149         23923         0.82         9.0E-40         4507848         NT           14349         23923         0.12         9.0E-40         4507848         NT           14349         23923         0.12         9.0E-40         4507848         NT           14349         23923         0.12         8.0E-40         4507848         NT           14349         23923         1.12         8.0E-40         Ad078165.1         EST_HUMAN           16399         26578         1.56         7.0E-40         U60325.1         NT           16399         26579         1.56         7.0E-40         U60325.1         NT           1650         22450         3.88         6.0E-40         AA.163246.2         NT           16540         26740         A.0E-40         AG03225.1         RT         HUMAN           16541         27804         6.0E-40         AG053028.1         EST_H | Ekon<br>NO:<br>11338         ORF SEQ<br>21205         Expression<br>Signal         (Top) Hit<br>Value         Top Hit Acession<br>Acade         Top Hit Accession<br>Acade         Top Hit Accession<br>Acade         Top Hit Accession<br>Acade         Top Hit Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>A | Expn<br>SEQ ID<br>NO:<br>ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID NO:<br>ID SEQ ID 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Similar<br>Pulse         (Top) Hit<br>Pulse         Top Hit<br>No:<br>Signal         Top Hit<br>Pulse         Top Hit | Expn<br>NO:         ORF SEQ ID<br>SIGNAI<br>IN:         Expression<br>Signal<br>PLASTE         Moet Similar<br>No:         Top Hit Accession<br>PLASTE         Top Hit Accession<br>No:         Top Hit Accession<br>PLASTE         Top Hit Accession<br>No:         Top Hit Accession<br>PLASTE         "></t<> |

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Single Exult riobes Expressed in Heart	Top Hit Descriptor	Homo sapiens HBV associated factor (XAP4) mRNA	Raffus norvegicus putative four repeat ion channel mRNA complete cola	Rettus norvegious putative four repeat ion channel mRNA, complete cds	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element :	Homo sapiens serine threonine protein kinase (NDR), mRNA	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:015804 [015804 SIMII AR TO ENV OF TYPE A AND TYPE B DETECTION INC.	1952/108.X1 Scares testis NHT Homo saniens cDNA clone IMAGE 483647 2	XZ4e10.X1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE_P97461 40S RIBOSOMAL PROTEIN S5	AV731601 HTF Homo sapiens cDNA clone HTFAZF05.5'	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products	Homo sapiens profeasome (prosome, macropain) subunit, aipha type, 7 (PSMA7) mRNA, and translated products	wt90a11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTFIN	Homo sapiens adenvik cyclase-associated protein 2 (CAP2) mPNA	Homo sapiens partial TIN gene for titin	601121567F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE-3345784 F	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C080	nc09a09.s1 NCI_CGAP_PrI_Homo sapiens cDNA clane IMAGE-1007808	601460375F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3863803 5	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17	602068604F1 NIH MGC 58 Home sanians 27NA Alma 144.0E: 4057770 F1	602068604F1 NIH MGC 58 Homo seniens CDNA clone IMAGE-1067726 F1	Homo sapiens sorting nextra 3 (SNX3) mRNA	Homo saplens zinc finger protein 200 (ZNE200) mRNA and translated	Homo saplens CGI-65 protein (LOC51103), mRNA
JIE EXUII FIU	Top Hit Database Source	NT	N	N	EST HUMAN	N.	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	TN	FZ	EST HUMAN	LN LN	NT	EST_HUMAN	Į.	TN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	4	<u> </u>	17
	Top Hit Acession No.	5454167 NT	3.0E-40 AF078779.1	3.0E-40 AF078779.1	BE350127.1	6005813 NT	3.0E-40 AW118799.1	2.0E-40 AI223036.1	2.0E-40 AW303868.1	=	4506188 NT	4506188 NT	-	5453592	2.0E-40 AJ277892.1		5453592 NT			1.1	۴.	1.0E-40 BE018348.1			37142	4508012 NT	7705778 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-40	3.0E-40	3.0E-40	3.0E-40	3.0E-40	3.0E-40	2.0E-40	2.0E-40	2.0E-40 AV73160	2.0E-40	2.0E-40	2.0E-40 AI968562	2.0E-40	2.0E-40/	2.0E-40 BE275932	2.0E-40	2.0E-40 AL163280	2.0E-40 /	1.0E-40 /	1.0E-40 BF036881	1.0E-40 E	1.0E-40 E	1.0E-40 E	1.0E-40	1.0E-40	1.0E-40
	Expression Signal	4.28	1.49	1.52	1.93	11.23	1.96	12.69	2.72	1.4	2.19	2.19	1.08	2.61	2.35	1.08	3.59	1.49	1.49	1.65	1.91	1.92	0.92	0.92	1.81	6.28	0.88
	ORF SEQ ID NO:		27253	27389		28725	28954				21664	21665	21807	21910	22112		22806	24478	24479		22343	<u> —</u>	22460	22461		24184	24550
	Exon SEQ ID NO:		17063	17188	18264	18456	18667	10283	10707	11681	11787	11787	11917	12011	12214	12525	13014	14691	14691	10791	12451	12520	12570	12570	13181	14398	14772
	Probe SEQ ID NO:	6882	7186	7312	8387	8588	8855	322	##	1783	1892	1892	2026	2123	2333	2858	3087	4807	4807	<u>S</u>	7288	2653	2707	2707	3258	4505	4892

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	nj42704.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'	AU149345 NT2RM4 Homo saplens cDNA clone NT2RM4002122 3'	qh31h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846339 3'	MR2-CT0222-211099-002-e10 CT0222 Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C003	wp04h04x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'	wp04h04 x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2463895 3'	Homo saplens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1) mRNA	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	601340485F1 NIH MGC 53 Homo sapiens cDNA clone IMAGE:3682677 5:	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE-79626 31	Homo saplens target of myb1 (chicken) homolog (TOM1), mRNA	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794.3' similar to TR:000597 000597 CYTOCHROMF CALIKE POI VPEPTIDE *contains   TEALEM   TEALEM	ow45e06.s1 Soares parathyroid tumor NbHPA Homo saniens cDNA class IMAGE 4640704 at allegations	TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element	Homo sapiens gene for activin receptor type IIB, complete cds	tm98c04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element :	Homo saplens 959 kb cantig between AMI.1 and CBR1 on chromosome 21n22: seament 1/3	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21o22: segment 1/3	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'	601888096F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:4122119 5'	AV710480 Cu Homo sapiens cDNA clone CuAACC07 5'	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT.	L	NT	NT	EST HUMAN	EST HUMAN	1	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	NT	EST HUMAN	NT	TN	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	1.0E-40 AA573201.1	1.0E-40 AA573201.1	1.0E-40 AU149345.1	1.0E-40 AI239572.1	1.0E-40 BF334112.1	8.0E-41 AL163203.2	7.0E-41 AI934364.1	7.0E-41 A1934364.1	11419208 NT	11417972 NT	AB037163.1	7657042 NT	6.0E-41 BE567816.1	T62628.1	4885636 NT	5.0E-41 BE067042.1	4.0E-41 BE156318.1	4.0E-41 AU119344.1	A1027117.1		4.0E-41 Al027117.1	4.0E-41 AB008681.1	4.0E-41 Al500406.1				4.0E-41 AV758295.1	4.0E-41 BF304683.1	1V710480.1	AV708431.1
	Most Similar (Top) Hit BLAST E Value	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	8.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41		6.0E-41	6.0E-41	5.0E-41	5.0E-41	5.0E-41	4.0E-41	4.0E-41	4.0E-41 Al027117		4.0E-41	4.0E-41	4.0E-41	4.0E-41 AJ229041	4.0E-41	4.0E-41 X92685.1	4.0E-41	4.0E-41	4.0E-41 AV710480	4.0E-41 AV70843
	Expression Signal	2.03	2.03	5.72	53.3	3.93	1.73	2.36	2.36	3.27	4.82	1.72	2.19	0.94	1.31	0.98	2.55	1.91	1.28	9.42		9.42	2.12	8.5	3.03	3.03	1.89	1.39	6.01	7.62	2.31
-	ORF SEQ ID NO:	26230	26231		28480		26689			25663		20064	21851		21532				20839	21149		21150	21170	21380	22578	22579	23730		27657		
	Exon SEQ ID NO:	16081	16081	18168	18232	19622	16501	12678	12678	15567	19618	10244	11954	14260	11660	13922	15850	10332	10998	11293		11293	11309	11522	12787	12787	13954	15825	17441	18733	19510
	Probe SEQ ID NO:	6215	6215	8289	8355	9521	6621	811	811	5655	9931	279	2064	4364	1761	4018	5945	385	1082	1388		1388	- 404 404	1618	2859	2859	4052	5920	7590	8925	6696

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The same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same and a same a same a same a same a same a same a same a same a same a same a same a same a same a same	Top Hit Descriptor	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens mRNA for KIAA1327 protein, partial cds	H.sapiens mRNA for putative p64 CLCP protein	Homo sapiens mRNA for KIAA1387 protein, partial cds	Human ribosomal protein L23a mRNA, complete cds	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end	Human mRNA for KIAA0207 gene, complete cds	G.gorilla DNA for ZNF80 gene hamolog	Human ribosomal protein L23a mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	Human B-cell specific transcription factor (BSAP) mRNA complete cds	Human B-cell specific transcription factor (BSAP) mRNA complete cds	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end	ZINC FINGER PROTEIN 135	EST84555 Colon adenocarcinoma IV Homo saplens cDNA 5' end	Mus musculus tubulin alpha 6 (Tuba6), mRNA	q75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3/	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA	Homo saplans hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens hypothetical CZH2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	nh07c02.s1 NCI_CGAP_Thy1 Homo sepiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304	30/BF EXPRESSED SEQUENCE I AG MRNA;	Homo sapiens chromosome 21 segment HS21 C085	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
SIC TYOU LOW	Top Hit Database Source	NT		LZ.	ΝΤ	ΝΤ	N	¥	EST_HUMAN	N	¥	Į,	LN LN	Į.	F	LN	LN.	EST HUMAN	SWISSPROT	EST_HUMAN	NT	EST_HUMAN	1528291 NT	1.1 EST_HUMAN	IN	NT	NT	NT	TOTAL TOTAL	ES L'HUMAN	NT L	NT	NT
5	Top Hit Acession No.	3.0E-41 AB030176.1		3.0E-41 AB026898.1	3.0E-41 AB037748.1	3.0E-41 X87689,1	3.0E-41 AB037808.1	2.0E-41 U43701.1	2.0E-41 AA331940.1	2.0E-41 D86962.1	2.0E-41 X89631.1	2.0E-41 U43701.1		2.0E-41 AL163267.2	AF038404.1	2.0E-41 M96944.1	2.0E-41 M96944.1	2.0E-41 AA328265.1	1	4A372637.1	6678468 NT	Al217868.1	11528291	9.0E-42 BE179191.1	11560151	11560151 NT	8.0E-42 AF003530.1	8.0E-42 AB026898.1	VA 400000 4	0.UE-42 A4493090.1	2	ļ	6.0E-42 AF012872.1
	Most Similar (Top) Hit BLAST E Value	3.0E-41	100	3.0E-41	3.0E-41	3.0E-41	3.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41 P52742	2.0E-41 AA37263	1.0E-41		1.0E-41	9.0E-42	9.0E-42	9.0E-42	8.0E-42	8.0E-42	27 10 0	0.0E-42 /	7.0E-42/	6.0E-42	6.0E-42/
	Expression Signal	1.64	000	30.5	0.85	7.36	1.49	7.3	2.3	1.03	4.07	5.31	1.06	1.06	6:29	1.33	1.33	1.39	1.7	3.46	4.64	1.8	2.63	1.33	2.63	2.63	5.37	1.32	9.00	35.0	8	3.25	3.25
	ORF SEQ ID NO:	20704		23914		25143	25873	21305	21688	21962	22010	21305	24199	24200		26772	26773	26786	27255	28882	24149	27494			27367	27368	20216	21849		1		21586	21587
	Exan SEQ ID NO:	10857	7 1100	14139	14919	15296	16755	11445	11810	12059	12106	11445	14414	14414	16381	16582	16582	16596	17065	18594	14359	17287	18930	16836	17168	17168	10399	11952	10825	2000	10840	11709	11709
	Probe SEQ ID NO:	932	7070	4240	5047	5376	6849	1782	1915	2172	2221	2798	4521	4521	6522	6702	6702	6716	7188	8777	4465	7420	9197	6958	7292	7292	455	2062	9238	070	916	1812	1812

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Single Exon Probes Expressed in Heart

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onigie Exult Flobes Expressed in near	Top Hit Descriptor	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA done IMAGE:2741799 3' similar to contains L1.t1 L1 repetitive element;	qu24h09x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element,	Homo sapiens mRNA for KIAA 1067 protein, partial cds	Homo sapiens mRNA for KIAA1067 protein, partial cds	Homo sapiens Xq pseudoautosomal region; segment 1/2	hv31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo saplens ublquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo saplens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo saplens myotubularin related protein 3 (MTMR3), mRNA	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II deltaz isoform mRNA, complete cds	Homo sapiens mRNA for KIAA1294 protein, partial cds	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA	Homo sapiens MHC class 1 region	Homo sapiens MHC class 1 region	Homo sapiens ribonuclease III (RN3) mRNA, complete cds	H.saplens PROS-27 mRNA	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	Homo sapiens zinc finger protein 177 (ZNF177) mRNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains	THR.2 THR repetitive element;	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA	RC3-NN0070-270400-011-h10 NN0070 Hamo sapiens cDNA	2819293.3prime NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2819293 3'	EST367438 MAGE resequences, MAGC Homo sapiens cDNA
JIE EXUIT FIO	Top Hit Database Source	EST_HUMAN	EST_HUMAN	Z	F	N _T	EST_HUMAN	LZ.	Z	IN	Į.	TN	Į.	N.	占	Z	IN	TN	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	6.0E-42 AW238656.1	AI284770.1	6.0E-42 AB028990.1	6.0E-42 AB028990.1	5.0E-42 AJ271735.1	3.1	5730038 NT	5730038 NT	11433063 NT	11433063 NT	11417957 NT	5.0E-42 AF071569.1	15.1	8923162 NT	4.0E-42 AF055066.1		1.1		4506496 NT	8008	4.0E-42 AW818630.1				5.1			59.1	58.1
-	Most Similar (Top) Hit BLAST E Value	6.0E-42	6.0E-42 AI28477	6.0E-42	6.0E-42	5.0E-42	5.0E-42 BE21791	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42 AB0377	5.0E-42	4.0E-42	4.0E-42	4.0E-42/	4.0E-42 X59417.1	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	l	3.0E-42/	2.0E-42 BF37683	2.0E-42	2.0E-42	2.0E-42 AW9553
	Expression Signal	3.51	1.04	1.81	1.72	5.44	1.17	2.94	1.27	1.76	1.76	2.75	1.57	2.76	2.15	8.83	8.89	2.67	1.61	4.52	10.26	2.07	2.07	3.22	,	0.78	3.63	3.86	215	10.2
	ORF SEQ ID NO:				25105		20197			26050	26051	26203	26294	27168	28494	20502	20503	20809	23779	23830	24162			28815			21239	ı	22146	25500
	Exan SEQ ID NO:	12128	14814	16275	15275	10105	10376	10422	10423	15920	15920	16055	16138	16975	18243	10668	10668	10987	14000	14056	14374	17932	17932	18531	10001	1008	11372	12241	12255	15437
	Probe SEQ ID NO:	2244	4936	5355	5504	131	431	478	479	6016	6016	6072	6274	7098	8366	736	736	1050	4100	4156	4488	8041	8041	8714		88	1467	2361	2375	5519

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Single Exon Probes Expressed in Heart

		_	_	_	_	_	_					_			_		_		·R	flu			-111		u.	•,	uett_e-	an.		Approx.	*****
Onigio Ladii Flobes Eaphessed III fleati	Top Hit Descriptor	EST367438 MAGE reseguences. MAGC Homo saniens CONA	601061284F1 NIH MGC 10 Homo sapiens cDNA clune IMAGE-3447820 5	Human endogenous retrovirus pHE.1 (ERV9)	Ul-H-BI1-afth-e-04-0-Ul.s1 NCI CGAP Sub3 Home saniens cDNA clone IMA CE: 2724 974 91	Homo sapiens partial C9 gene for complement component C9 expn 1	Homo sapiens partial C9 gene for complement component C9 expn 1	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds	Homo saplens NADH-ublquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene	Home seniors rec (1 OC51201) with the	Home satisfact gas away 1, 11 at 1, 11	Homo sapiens mater histocompatibility compley class II DM abba (UI & DMA). DMA	Homo sepiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated	products	nomo sapiens NAAU255 gene product (KIAA0255), mRNA	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C080	RC3-ST0197-161099-012-a03 ST0197 Homo saplens cDNA	Homo sapiens proteasome inhibitor (PI31), mRNA	Homo sapiens proteasome inhibitor (PI31), mRNA	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Home carians a distribution of MARIZES protein, partial cds	Homo saniens a disintegrin and metallogroteinase domain 23 (ADAM23) mRNA	Homo satistic chromodomali moteti V Atomocoma (11.700)	279807.s1 Soares testis NHT Homo canians PNA Alaca MACE: Jacobs of	AV736824 CB Hamo sapiens cDNA clone CBI AKHAR F.	AV736824 CB Homo saniens cDNA clone CBL AKHOR 87	Homo sapiens hypothetical protein FI (20097 (FI (20097) mDNA	Homo sapiens hypothetical protein FL 120297 (FL 120297), mRNA	Homo saplens hypothetical protein FL/20297 (FL/20297) mRNA	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5
	Top Hit Database Source	EST HUMAN	EST HUMAN	N	EST HUMAN	N	N L	Į.	TN.	LN L	NT	NT.	<u> </u>	IN PARTIES	12	I N	N.	EST HUMAN	Z !	LN !	2 12		TN	L L	EST HUMAN	EST HUMAN	EST HUMAN		5	ト	HUMAN
	Top Hit Acession No.	2.0E-42 AW955368.1		X57147.1	1.0E-42 AW 295809.1	1.0E-42 AJ251818.1	1.0E-42 AJ251818.1	1.0E-42 AF067166.1		3219	1.0E-42 AF110296 1	4458	VENERAL	TIM 7500092	1002021	7.5	7	7.1	5803122 N	5803122 NT	4506758 N I	4501012	4501912 NT	47579B9 NT	9.0E-43 AA435719.1			8923276	8923276 NT	8923276	2.1
	Most Similar (Top) Hit BLAST E Value	2.0E-42	2.0E-42 BE5389	1.0E-42 X57147	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1 05 42	1 OF 42	4 05 42	1.0E-42 AL10320	1.0E-42	1.0E-42 AW8136	1.05-42	1.0E-42	1.0E-42	1 0F 42	1.0E-42	9.0E-43	9.0E-43	8.0E-43	8.0E-43 AV73682	8.0E-43	8.0E-43	8.0E-43	7.0E-43 AW 2464
	Expression Signal	10.2	1.27	1.06	96.0	1.11	11.11	12.78	12.78	1.46	0.91	- 28	80	2 15	2 5	202	2/:-	0.80	2.00	2.85	5	86.0	0.98	3.80	2.84	12.13	12.13	4.33	4.33	4.33	6.05
	ORF SEQ ID NO:	25501	27739		20789		20843	20983	20984		21772		CBBCC		23552	23827	24170	24110	24247	11 5457	24442	24693	24694	27893	28525	20386	20387	20441	20442	20443	23292
	Exan SEQ ID NO:	15437	17513	10648	10944	11001	11001	12688	12688	11575	11879	12372	12862	13561	13760	14053	14383	14528	14520	14555	14654	14920	14920	17655	18273	10573	10573	10618	10618	10618	13503
	Probe SEQ ID NO:	5519	7663	717	1026	1085	1085	1222	1222	1673	1986	2497	2935	3647	3840	4153	4480	4640	4840	4660	4769	. 5048	5048	7805	8397	929	636	685	685	982	3589

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	Top Hit Descriptor	wp69b01.x1 NCI_CGAP_Brn25 Homo sepiens cDNA clone IMAGE::2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN :contains LTR7.b1 LTR7 renetitive element	ne72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S RIBOSOMAL PROTEIN 1.30 (Ht IMAN):	4 clone ADCACC10 5	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA	hd30b04,x1 Scares_NF_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element:	mo saplens cDNA clone IMAGE:665410 5' similar to TR:G529641	DKEZD7611.772 rt 764 (samonum: hamano) Home seniore Challe des Districtions	namyzy romo sapiens corva done okrzpych 1772 5	INA 5' end	Cone HTFANCAS S'	o sapiens cDNA clone IMAGE-815055 5'	0052c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591	DKF78470110 11 434 (suranm: hbr2) H-m-c-(n-1)	107 Home sanians CONA clone UNFZP434D0119	rimed sublibrary Homo saniens cDNA		Homo sapiens X-linked anhidrolite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat rections	SCDHB6) mRNA	qj76e02.x1 NC]_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354.3' similar to contains MER10.t3 MER10 repetitive element :	ตุ76ฮ02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10 เส MER10 repetitive element	yd72h10.r1 Soares fetal liver spleen 1NFLS Homo saniens cDNA clane IMAGE:442627 51	vg06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 is repetitive element:	
Chigae Laures Laplesseu III neall				Т				Τ	Т	T	Т	Г		Т	Т	1	Г	Homo sapiens X-linked anhidrolitic ectodermal or regions	Homo saplens protocadherin beta 6 (PCDHB6) mRNA			Γ		Т
IBIO LAGII	Top Hit Database Source	EST_HUMAN	EST HUMAN	EST_HUMAN	N E	EST_HUMAN	EST HUMAN	EST HUMAN	N	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	FST HIMAN	EST HUMAN		NT	Į.	IN S	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	
5	Top Hit Acession No.	7.0E-43 AI936748.1	6.0E-43 AA491890.1	6.0E-43 AV708201.1	8955973 NT	6.0E-43 AW468897.1	6.0E-43 AA195154.1	6.0E-43 AL119158.1	5.0E-43 AL163213.2	5.0E-43 AA382780.1	5.0E-43 AV732578.1	5.0E-43 AA465288.1	5.0E-43 AI733244.1		5.0E-43 AW863007.1	5.0E-43 W29011.1	5.0E-43 X15804.1	4.0E-43 AF003528.1	11416793 NT	4.0E-43 AI244341.1	4.0E-43 AI244341.1	4.0E-43 T77380.1	4.0E-43 R20950.1	
	Most Similar (Top) Hit BLAST E Value	7.0E-43	6.0E-43	6.0E-43	6.0E-43	6.0E-43	6.0E-43	6.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	4.0E-43	4.0E-43	4.0E-43	4.0E-43	4.0E-43	4.0E-43	
	Expression Signal	1.76	10.17	4.15	2.02	2.02	1.83	6.54	1.98	3.01	1.36	4.47	22	1.41	5.46	2.67	2.6	4.85	1.72	4.49	4.49	1.8	1.89	-
	ORF SEQ ID NO:				25829	26111	27745			20249	22539	27514	28035	28055	28280	28468	28146	20728		26824	26825	28761		
	Exon SEQ ID NO:	16969	11227	12421	15716	15975		18322		10437		17308	17795	17814	ı	ļ	17902	12643	16097	16636	16636	18489	18915	
	Probe SEQ ID NO:	7092	1320	2547	5811	6128	7668	8449	137	494	2816	7390	7945	7964	8145	8338	8753	957	6231	6757	6757	8624	9174	

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Top Hit Descriptor	Homo sapiens mRNA for thymidine kinase, partial	Homo saplens myosin mRNA, partial cds	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA		Γ	Homo sapiens minisatellite ms32 repeat region	Homo sapiens minisatellite ms32 repeat region	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Г	Г	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	1	┰	Т	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA complete cds	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6). mRNA	Г		Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA	Homo sapiens transmembrane trafficking protein (TMP21), mRNA	Homo sapiens transmembrane trafficking protein (TMP21), mRNA	Homo sapiens RAB36 (RAB36) mRNA, complete cds		Т	Human mRNA for integrin alpha subunit, complete cds
Top Hit Database Source	NT	NT LN	ΤN	N L	F	Į.	EST_HUMAN	1	NT	LΝ	Ę	ΤN	Į.	EST HUMAN	EST_HUMAN	۲N	F	MAN LI HAAN	EST HIMAN	NI	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	N I	N	N	EST HIMAN	N	Ν
Top Hit Acession No.		L29139.1	11527389 NT	11418086 NT	11418099 NT	11418086 NT	7.0E-44 R06035.1	5031886 NT	7.0E-44 AF048729.1	7.0E-44 AF048729.1	7.0E-44 AL163284.2	7.0E-44 AF231919.1	7.0E-44 AF231919.1	7.0E-44 AU159839.1	6.0E-44 AW954050.1	5.0E-44 AJ289880.1	5.0E-44 AJ289880.1	5 DE 44 AISBB523 4	-   -	32	4.0E-44 U90878.1	6912477 NT	3.0E-44 BE880626.1	3.0E-44 AA169851.1	4826685 NT	4826685 NT	5803200 NT	5803200 NT	2.0E-44 AF133588.1	2.0E-44 BE465325.1		2.0E-44 D25303.1
Most Similar (Top) Hit BLAST E Value	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	6.0E-44	5.0E-44	5.0E-44	5 0E-44	5.0E-44	4.0E-44	4.0E-44	3.0E-44	3.0E-44	3.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44
Expression Signal	3.39	5.06	2.59	1.89	1.75	1.84	0.85	1.2	2.2	2.2	2.28	1.17	1.17	2.05	2.51	2.52	2.04	3 70	2.59	2.9	13.3	1.07	1.54	5.08	2.75	2.75	4.63	4.63	2.79	\$	2.03	1.1
ORF SEQ ID NO:			25304		25059	25191		21978	22663	22664	23485	23821	23822	26828	29080			26672		23086	28702		22254	22777	20793	20794	20945	20946	21052	21108	21894	22294
Exon SEQ ID NO:	Ш		19031		19532	19369	10580	12074	12864	12864	13698	14048	14048	16641	18791	10264	10288	18485	17317	13287	18433	11646	12360	12986	10951	10951	11099	11099	11197	11252	11994	12403
Probe SEQ ID NO:	8504	8935	9359	9400	9742	9885	643	2187	2937	2937	3786	4148	4148	6762	9868	300	329	6605	7399	3368	8564	1746	2485	3029	1033	1033	1189	1189	1290	1346	2105	2529

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4) mRNA	Homo sapiens DNA for amyoid precursor protein, complete cds	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA	Homo sapiens general transcription factor 2.1 (GTE2)) mRNA elternativety seifficed academia	Homo sapiens glutamate receptor, metabotronic 3 (GRM3) mRNA	Homo sapiens glutamate receptor, metabotronic 3 (GRM3) mRNA	601286914F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:361358R F	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795	Human mRNA for KIAA0376 gene, partial cds	Homo sapiens cat eve syndrome chromosome region candidate 1 (CECR1) mDNA	Homo saplens Misshapen/NIK-related kinase (MINK) mRNA	Homo saplens Misshapen/NIK-related kinase (MiNK) mRNA	RC1-CT0249-030300-026-h12 CT0249 Homo saniens cONA	RC1-BN0039-110300-012-b01 BN0039 Homo sepiens CDNA	Homo saplens chromosome 21 segment HS21C103	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:773763 5' similar to contains THR.t3 THR repetitive element:	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:773763 5' similar to	2888911.11 Soares, testis NHT Homo sapiens cDNA clone IMAGE 729476 5'	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein T54 protein	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptonysin genes	complete cds; and L-type calcium channel a>	ae01c09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'	Homo sapiens alpha satellite DNA, M1 monomer type	Homo sapiens alpha satellite DNA, M1 monomer type	AV714608 DCB Homo saplens cDNA clone DCBBYE03 5'	Homo saplens Sushi domain (SCR repeat) containing (BK65A6.2) mRNA	RC1-CT0198-150999-011-C08 CT0198 Home sapiens cDNA	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
Top Hit Database Source	NT.	N.	EST_HUMAN	i i	Ā	IN	F	EST HUMAN	EST HUMAN	N	F	F	N-	EST HUMAN	EST HUMAN	N	EST HUMAN	EST HIMAN	EST HUMAN			노	EST_HUMAN	NT	NT	EST_HUMAN	Ä	EST HUMAN	EST_HUMAN	ΤN
Top Hit Acession No.	5901933 NT	2.0E-44 D87675.1	AW864379.1	11449901 NT	AF038968.1	11419226 NT	11419226 NT	2.0E-44 BE389058.1	2.0E-44 BE244902.1	AB002374.1	11526293 NT	7657334 NT	7657334 NT	4W853132.1	803.1	33.2	1.0E-44 AA434554.1	AA434554 1	4A398099.1				1.0E-44 AA455869.1		5.1	18.1	10092664 NT	П	1.0E-44 AW846967.1	8922391 NT
Most Similar (Top) Hit BLAST E Value	2.0E-44	2.0E-44	2.0E-44 AW864	2.0È-44	2.0E-44 AF0389	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44 AB0023	2.0E-44	1.0E-44	1.0E-44	1.0E-44 AW853	1.0E-44 AW9948	1.0E-44 AL1633	1.0E-44	1.0E-44 AA4345	1.0E-44 AA3980			1.0E-44 AF1967.	1.0E 44 /	1.0E-44 /	1.0E-44/	1.0E-44 AV71460	1.0E-44	1.0E-44 /	1.0E-44	9.0E-45
Expression Signal	3.32	1.36	1.76	1.39	1.46	3.86	3.86	1.88	222	2.72	1.38	3.64	3.64	1.85	1.52	5.54	3.53	3.53	1.05			1.39	5.08	-0.81	0.81	10.75	4.18	3.43	3.43	1.74
ORF SEQ ID NO:		i	24152	25719	24870	26406	26407	27078		24910		19839	19840	20312			21965	21966	22024			22489		24/02	24703		28918	28970	28971	24169
Exon SEQ ID NO:				15617	15107	16245	16245	16886	18816	19735	19383	10034	10034	10505	11090	11460	12064	12064	12716			12594	135/8	14931	14931	18255	18629	18681	18681	14370
Probe SEQ ID NO:	2567	3425	4468	5709	6097	6383	6383	7009	9022	9710	9066	46	46	566	1179	1555	2177	2177	2237		000	2/32	3004	Land	5061	8378	8816	8869	8869	4476

Page 220 of 413 Table 4 Single Exon Probes Expressed in Heart

Profest   Extra   Circ   174   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ   Circ		_	_				_						_							#1mxP	_31			******		-						
Exon No.         CRF SEQ Expression No.         Most Similar Agine         Most Similar Agine         Most Similar Agine         Most Similar Agine         Top Hit Acession No.	Top Hit Descriptor	Homo sablens hypothetical protein El 100320 (El 100370)	Homo sapiens TRK-fitsed game (NIOTE:	Homo sapiens TRK-fused gane (NOTF: non-standard symbol and name) (TFG) mRNA	au83h07.x1 Schneider fetal brain 00004 Home sepiens CDNA clone IMAGE:2782909 3' similar to	Home series ADB Home 1 Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control	Homo saniens chromosome 21 commet US24 Society (ARFGAP1), mRNA	CM4-CN0044-180200-515-601 CN0044 Homo seniers, CNNA	tg94f07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX1	21/2d03.s1 Soares_festis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element	Homo saniene programmed and doubt E (DDODE)	Homo sapiens onlyin like protein (CLD) - DNA	Histories ART4 dens	60119440F1 NIH MGC 7 Hams company obbits discussions	802084052F1 NIH MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M MGC 83 Home contact of 11 M M MGC 83 Home contact of 11 M M MGC 83 Home contact of 11 M M M M M M M M M M M M M M M M M M	vd35f07 r1 Soares fetal liver selection 11 c. 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Exon ORF SEQ Express NO: NO: NO: Signa 14370 24160 12363 22245 14889 24656 19718 13098 22304 13098 22304 13098 22027 14870 22027 14870 22027 1530 12310 12324 22057 15834 22657 15834 22657 15834 22657 16347 226315 2718 18608 28899 28652 18608 28899 28652 18608 28899 28652 18608 28899 28652 18608 28899 28652 18608 28899 28652 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28899 28852 18608 28852 18608 28852 18608 28852 18608 28852 18608 28852 18608 28852 18608 28852 18608 28852 18608 28852 1860	Most Similar (Top) Hit BLAST E Value	9.0E-45	8.0E-45	8.0E-45	6.0E-45	6.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	4.0E-45	4.0E-45	4.0E-45	3.0E-45	3.0E-45 /	3.0E-45	3.0E-45/	3.0E-45	3.0E-45	2.0E-45 /	2.0E-45 /	200	2 05 45 6	2 05 45 5	Z.UE-#3	2.0E-45	2.0E-45 A	2.0E-45	2.0E-45	
Even SEQ ID ORU NO: 14370 ID 100 ID 14370 ID 14889 ID 14889 ID 19718 ID 14889 ID 14889 ID 14889 ID 14889 ID 14889 ID 14889 ID 14889 ID 14889 ID 14889 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 14898 ID 148	Expression Signal	1.74	3.9	7.49	5.25	1.46	1.11	5.01	201	8.8	1.67	2.67	8.96	1.98	1.62	1.17	1.51	3.44	8.37	8.37	1.33	2.17	0.93	4	175	27.64	5:17	3.96	2.13	2.13	2.76	
								21739	22904	25155	27292	29043	20883	22027				27173	27996	27997			22718	25957	26516	28315		28652	28898	28899		
Probe SEQ ID NO: NO: NO: NO: 14476 5015 9707 874 1957 1127 1127 1127 1127 1127 1127 1127 11			12353	$L_{\scriptscriptstyle{-}}I$		L	10800	11852	13098	15303	17103	18748	11041	12130	19192	13210	16798	16981	17757	17757	19660	12331	12924	15834	16347	19471		18388	18608	18608	19346	
<del>``````````</del>	Probe SEQ ID NO:	4476	2477	5015	3896	9707	874	1957	3173	5384	7226	8940	1127	2246	9613	3997	6920	7104	7907	7907	9814	2454	2996	5929	6489	8179		8516	8794	8794	9853	

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Table 4
Single Exon Probes Expressed in Heart

	escriptor	OWACE SERVED	INTO E. SOUGLOS S	V(BAB4A) TENA	NCEDIN) BMA	MOSENIA), IIIKINA	ie, compiete cas	AVINITA), IIINIA	12 X X X X X X X X X X X X X X X X X X X	0 200 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10 SOLOS DO 10	140 CE:00000000000000000000000000000000000	CIVE CE. 391 2030 0	774	KKCABP), mKNA	4), mKNA	AP1), mRNA	ia 11 subunit (CACNA11), mRNA	\$NA		ne IMAGE:2822449 5'	MAGE:2132199 3' similar to gb:J00314_ma2	MAGE:2132199 3' similar to gb:J00314_ma2		ANOTO TO TO TO TO TO TO TO TO TO TO TO TO	NA ANTAGE, SO 18119 5		J, InKWA	IWAGE:4042736 5	MAGE:24375753' similar to contains MER19.t2	MAGE:2437575 3' similar to contains MER19.12	MAGE:2232835 3' similar to TR:060363 060363
and Lypicased III riedil	Top Hit Descriptor	601284360F1 NIH MGC 44 Homo sanians a NA Alexa 1140 E 2505450 E	601284360F1 NIH MGC 44 Homo seniens CDNA close 1140 OF 1000 1100	Homo saplens RAP1A, member of RAS oncodene family (RAD1A) with the saplent RAS oncodene family (RAD1A) with the saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple saple sa	Homo sabiens Landerhans cell specific c-has lectin // ANCEDIM) DAY	Human pro-a2 chain of colladen type XI (COI 1142) general de de	Homo sapiens chromosome 21 onen reading frame 1 (2312-61) - ENIA	Homo sapiens mRNA for KIAA1501 profein partial cac	601289116F1 NIH MGC 8 Homo saniens CNA class 114ACE 25210802 F1	Homo sapiens niban protein (NIRAN) mPNA	601511226F1 NIH MGC 71 Homo canions cDNA close 1446 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE 2000 CE	Human mRNA for KIAA0299 gene partial cde	Homo saniene profein kinasa C. alaha kinaling anglis (mpikokana)	Homo saniene handhelted and in 1997 (1917)	Homo capiene Ben GTDang ordinal	Homo capiens cale in change activating protein 1 (KANGAP1), mRNA	Misseries Carbuill Chairle, Voltage-dependent, alpha 11 subunit (CACNA11), mRNA	Imas milesculus keraun complex 2, gene 6g (Krtz-6g), mRNA	normo suprems conformation of the segment HS21C009	Z8ZZ449.3ptime NIH_MGC_7 Homo sapiens cDNA clone IMAGE;2822449 5	132108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);	ti32f08.x1 NCI_CGAP_Gas4 Home saplens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2	RC5-HT0506-280200-042-C42 UT0506 US	601277292F1 NIH MGC 20 Homo senions of NIA ALL MA OF SOCIETY	RC4-BT0310-110300-015-f10 BT0310 Homo saplems CDNA	Homo sabiens hypothetical protein El 140847 /El 140847	601822835F1 NIH MGC 77 Home series COMA - 1 144 OF 1012000	Homo sapiens chromosome 21 segment HS21C046	wm31f08x1 NCI_CGAP_Ut4 Homo sepiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element:	wm31f08.x1 NCI_CGAP_Ut4 Homo saplens cDNA done IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element:	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:060363 060363 SA GENE.
all all all all all all all all all all	Top Hit Database Source	EST HUMAN	EST HUMAN	NT	FN	۲	LN L	NT	EST HUMAN	IN	EST HUMAN	NT	NT	LN	Į.	Į.	FIN	I N	14) TOT 111 BANK	ESI HOMAN	EST_HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	Į.	EST HUMAN	NT	EST_HUMAN	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	1.0E-45 BE389855.1	1.0E-45 BE389855.1	4506412 NT		U32169.1	TN 8659558	1.0E-45 AB046811.1		11545796 NT	1.0E-45 BE887843.1	1.0E-45 AB002297.1	11418099					Al 183200 2	7, 2		8.0E-46 AI433261.1	8.0E-46 Al433261.1			Γ	8922708 NT	7.0E-46 BF105845.1	5.2	6.0E-46 AI884381.1	+-	6.0E-46 Al635448.1
	Most Similar (Top) Hit BLAST E Value	L						1.0E-45	1.0E-45	1.0E-45	1.0E-45		1.0E-45	1.0E-45	1.0E-45	1.0E-45	9 OF 46	9 0F-48	O DE 48	3.00	8.0E-46	8.0E-46	8.0E-46	7.0E-46	7.0E-46	7.0E-46	7.0E-48	7.0E-46	6.0E-46	6.0E-46 AI884381	6.0E-46
	Expression Signal	2.22	2.7	1.5	1.7	6.76	1.04	0.81	4.08	1.05	5.22	1.25	4.3	5.38	2.56	3.17	2.28	6.71	7 80	2	8.79	8.79	3.97	6.54	1.01	4.01	1.35	1.35	5.53	5.53	8.85
	ORF SEQ ID NO:				20915			23239		24541	27347	27559	25358			25207	26861		28077		22165	22166				25693	25943		22483	22484	25737
	Exon SEQ ID NO:		10349	10407	11070	12992	13364	13442	14274	14765	17151	17355	18950	19067	19070	19324	16669	16895	17836		12270	12270	16572	14372	14587	15592	15818	19144	12588	12588	15634
	Probe SEQ ID NO:	118	403	464	1157	3065	3447	3526	4378	4884	7274	7485	9231	9415	9421	9820	6790	7018	7986		2392	2392	6692	4478	4701	2883	5912	9543	2726	2726	5727

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Single Exon Probes Expressed in Heart

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יילה כיספת ווו ופפון	Top Hit Descriptor	601478409F1 NIH MGC 68 Homo sanjens chwa clare IMAGE 3890005 Ei	Homo sablens chromosome 21 segment HS21C040	7d81g01.x1 Lubski dorsal root ganding Home saniens chivia cleus Man Ceresarians si	7481g01.x1 Lupski dorsal root gandlion Homo sanians cDNA clone IMA CE-3270408 2	nea38f07.x1 NCI_CGAP_Kid11 Homo sapiens GDNA clone IMAGE:3258757 3' similar to TR:O75202 O75202 HOMOLOG OF RAT KIDNEY SEPECIFIC	602021164F1 NCI CGAP Bm67 Home saciens cDNA clane MACE 1156870 F	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	hi86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAQE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element :	hl86c03.x1 NC!_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECIRSOR (HI MAN) romains element MED37	Human endocenous refrontus RTVI -H2	Homo sapiens mRNA for KIAA0620 motion mortiel cds	Homo sepiens mRNA for KIAA0622 protein partial cds	Human ig germine gamma 3 heavy-chain gene V region partial cuts	Human Ig germline gamma-3 heavy-chain gene V radion padial cds	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MADAKA) mbhia	H.sapiens (g lambda light chain variable region gene (7c.11.2) germline; (g-Light-Lambda: VI embde	H.saplens Ig lambda light chain variable region gene (7c 11.2) germline: Incl. High Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda Lambda La	WJ49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR,b2 THR repetitive element :	Human mRNA for KIAA0061 cene partial cds	ne08a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element:	227a11.s1 Soares feta liver splean 1NFI S S1 Homo saniens CONA clara MACE 222000 8	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
	Top Hit Database Source	EST HUMAN	NT L	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	Т			₽ L	TN	NT		NT	<u> </u>	EST HUMAN	Т	EST HUMAN	П	
	Top Hit Acession No.	6.0E-46 BE784971.1	5.0E-48 AL.163210.2	5.0E-46 BE677194.1	5.0E-46 BE677194.1	5.0E-46 BF590442.1	5.0E-46 BF347229.1	4.0E-46 AA601143.1	4.0E-46 AW770544.1	4.0E-46 AW 770544.1	4.0E-46 M18048.1	4.0E-46 AB014522.1	4.0E-49 AB014522.1	4.0E-46 M36852.1	4.0E-46 M36852.1	4.0E-46 AB002059.1	4506376 NT	3.0E-46 Z73660.1	3.0E-46 Z73660.1	3.0E-49 A[831462.1	3.0E-46 D31765.1	2.0E-46 AA468646.1	2.0E-46 AA678246.1	
	Most Similar (Top) Hit BLAST E Value	6.0E-46	5.0E-48	5.0E-46	5.0E-46	5.0E-46	5.0E-46	4.0E-46	4.0E-46	4.0E-48	4.0E-46	4.0E-46	4.0E-48	4.0E-46	4.0E-46	4.0E-46	3.0E-46	3.0E-46	3.0E-46	3.0E-46	3.0E-46	2.0E-46	2.0E-46	2.0E-46 U78027.1
	Expression Signal	3.03	6.41	1.12	1.12	1.79	3.52	1.51	3.57	3.57	3.55	1.07	1.07	1.84	1.84	1.91	8.0	1.13	1.13	8.3	2.63	5.91	1.32	2.43
	ORF SEQ ID NO:				23206		26155		21446	21447		23999				25237	23976	24343	24344	27151	28955	, 20594		21385
	Exan SEQ ID NO:			13400	13400	15942	16017	10562	11578	_ 1	12573	14217	14217	15258	15258	19221	14192	14552	14552	16958	18668	10747	11447	11527
	Probe SEQ ID NO:	8694	197	3484	3484	6033	6144	625	1676	1678	2710	4320	4320	5338	5338	9660	4294	4666	4666	7081	8856	819	1542	1623

Page 223 of 413 Table 4 Single Exon Probes Expressed in Heart

| )escriptor                                    | IMAGE:726650 5' similar to SW:RSP1_MOUSE                                                     |                                                                                                                                                                                                                                                                                | 0040007 5                                                                                                                                                                                                                                                                                                                                                                                                                                 | 04878/ 3                                                                                                                                                   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	Expression Signal	3.41	2.06	2.06	4.84	1.75	1.75	5.17	8.9	1.5	4.99	6.97	4.26	4.26	1.89	4.27	2.18	2.18	1.18	1.22	4.44	2.3	1.66	1.75	1.75	2.06	1.1	1.6	1.6	1.33	2.1	2.1	1.77	5.77
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Top Hit Descriptor	y/92e08.s1 Soares infant brein 1NIB Homo sepiens cDNA clone IMAGE:29966 3' similar to contains OFR	Homo sabiens chromosome 21 searment HS21 Choo	1099h03.x1 Soares fettel ling Nikili 102 Louis annions albus 11 It is a constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the constant and the	601155321F1 NIH MGC 21 Homo conjens cONA American 11/4 OF 222000 1	601155321F1 NIH MGC 21 Homo septems CONA denie IMAGE:3136883 5	RC3-ST0197-130400-017-h02 ST0197 Home caniene cDNA	at19e06.x1 Barstead aorta HPLRB6 Homo septems cDNA clone IMAGE:2355586 3' similar to gb:M22995 RAS.RFI ATED PROTTEIN DAD 4A (LIII MAAN).	Papio hamadryas alcohol dehydrocenase class I (ADH) dene E' region	Homo sapiens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	CM2-MT0100-310700, 290-605 MT0100 Home conference CN12	6013/0479F1 NIH MCC 44 Home emisse ablit all the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the pr	Homo sapiens aminoacidase 1 (ACV4) mRNA	Homo sapiens aminocodase 1 (ACV1), makin	hke1b03 xt NCI_CGAP_Lym12 Homo saplens CDNA clone IMAGE:3001133 3' similar to gb;X64707 BREAST BASIC CONSERVED PROTEIN 141111AAN.	hk61b03.x1 NCI_CGAP_Lym12 Homo sepiens cDNA clone IMAGE:3001133 3' similar to gb:X64707	Homo sanians mBNA for KIA A 4000 milein - 11-11-11	Homo sablens mRNA for KIAA1200 mentaln mentaln de	Homo sapiens tousied-like kinase 1 (TI K1) mDNA	Homo saplens SET domain and mariner transposes their and SETMARS	Homo saplens histidyl-tRNA synthetase (HARS) mRNA	Homo sapiens putative oncodene profein mRNA partial As	Homo sapiens hypothetical protein FLJ11006 (FLJ11006) mRNA	2945b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to	Omo saplens phesiocensory	14/2/2021 NCI COAD BOS Umas and the Commission of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of the Country of t	AV690964 GKC Home sanions which services and services in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr	Homo sapiens chromosome X open reading frame 6 (CXORES) BNA	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
Top Hit Database Source	EST HIMAN	NT	T HUMAN	Т	Т	Т	1	Т	۲	T HUMAN	Т			HUMAN		Т					E		EST HUMAN		T HUMAN			
Top Hit Acession No.	R42423.1	2.0E-47 AL163209.2	1.0E-47 Al333429.1	1.0E-47 BE280477.1	1.0E-47 BE280477.1	1.0E-47 AW813906.1	1.0E-47 AI880886.1		9.0E-48 AF223391.1	Г	3E393813.1	4501900 NT	4501900 NT		7.1	5.1		6912719	5730038 NT	11416831 NT	6.1	11427428 NT	0.1	4826891		1.1	4885170	4885170 NT
Most Similar (Top) Hit BLAST E Value	2.0E-47 R42423	2.0E-47	1.0E-47	1.0E-47	1.0E-47	1.0E-47	1.0È-47	1.0E-47 L30115.	9.0E-48	9.0E-48	9.0E-48 BE39381	8.0E-48	8.0E-48	8.0E-48 AW7684	8.0E-48 AW7684	7.0E-48	7.0E-48 AB03303	7.0E-48	7.0E-48	7.0E-48	6.0E-48 AF02681	6.0E-48	6.0E-48 AA18908	5.0E-48	4.0E-48 AI620420	3.0E-48 AV69096	3.0E-48	3.0E-48
Expression Signal	1.98	1.32	4.5	0.79	0.79	2.59	7.68	1.75	2.34	0.83	322	1.32	1.51	3.62	3.62	1.37	13.37	1.12	3.49	22.88	1.52	1.9	3.38	1.39	3.55	0.92	18.97	18.97
ORF SEQ ID NO:	24988		21142	23443	23444	24648		28017			28595			22818	22819			21250	21382	25975 .	27348	27577	27654	22989	28451	21124	21710	21711
Exan SEQ ID NO:	19658	19659		13662		14882	15954	17778	11499	13425	18333	11138	11138	13023	13023	10426	10426	11387	11524	15852	17152	17370	17438	15067	18202	11269	11828	11828
Probe SEQ ID NO:	9219	9257	1383	3749	3749	2008	6194	7928	1595	3509	8460	1230	1231	3096	3096	482	483	1482	1620	5947	7275	7500	7587	3269	8325	1363	1933	1933

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hi14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA done IMAGE.29722553' similar to SW:DCRB_HUMAN nv03f05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo Homo sapiens v-rel avian reticuloendothellosis viral oncogene homolog A (nuclear factor of kappa light JI-H-BW1-ani-e-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3 fmfc7 Regional genomic DNA specific cDNA library Homo saplens cDNA clone CR17-26 Homo saplens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA 2x80c03.r1 Soares ovary fumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5 no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA done IMAGE:1101072 3' no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072.3 601888086F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 6 601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA Human endogenous retroviral DNA (4-1), complete retroviral segment P66555 DOWN SYNDROME CRITICAL REGION PROTEIN B.; Homo saplens dopamine transporter (SLC6A3) gene, complete cds Homo sapiens dopamine transporter (SLC6A3) gene, complete cds Top Hit Descriptor polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDN Homo sapiens huntingtin (Huntington disease) (HD) mRNA AV743451 CB Homo sapiens cDNA clone CBCCGG10 5' Homo sapiens RNA binding motif protein 6 (RBM6) mRNA Homo sapiens mRNA for KIAA1501 protein, partial cds Homo sapiens mRNA for KIAA1501 protein, partial cds Homo sapiens mRNA for KIAA1245 protein, partial cds Homo saplens chromosome 21 segment HS21C102 Homo saplens chromosome 21 segment HS21C046 Homo sapiens B cell linker protein (SLP65), mRNA Homo sapiens B cell linker protein (SLP65), mRNA Mus musculus T-box 20 (Tbx20), mRNA sapiens cDNA clone TCBAP3842 Single Exon Probes Expressed in Heart PTR5 repetitive element EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN Top Hit Database EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN HUMAN **EST HUMAN** Source 11496238 NT 7706534 NT 4502166|NT z 5032032 NT Z z 눌 11429808|NT 10048417 NT Top Hit Acession 4755137 3.0E-48 AW 664531.1 3.0E-48 BE084571.1 3.0E-48|AA659930.1 3.0E-48 BF514170.1 2.0E-48 AA613171.1 2.0E-48 AB040934.1 2.0E-48 AB040934.1 2.0E-48 AV743451.1 2.0E-48|BE246065.1 AA465007.1 2.0E-48 BE737164.1 AB033071.1 2.0E-48 AA631940.1 2.0E-48 AA613171.1 1.0E-48 AL 163302.2 AL163246.2 ģ 1.0E-48 AF119117.1 1.0E-48 AF119117.1 1.0E-48 BF304683. 1.0E-48 M10976.1 1.0E-48 W 26785.1 2.0E-48 1.0E-48 1.0E-48 BLASTE 2.0E-48 1.0E-48 1.0E-48 Most Similar 1.0E-48 1.0E-48 1.0E-48 1.0E-48 (Top) Hit Value 0.88 7.08 1.18 1.35 72.29 4.29 239 2.35 2.86 72.29 2.45 1.63 3.26 0.85 44.65 1.23 5.06 4.29 1.1 2.21 4.48 1.56 5.06 Expression Signal 25582 ORF SEQ 23284 28376 24114 25540 19827 26464 26465 26473 26936 25070 21648 24828 21032 26325 Ω̈́ 19844 20632 23167 24728 27404 27586 28023 25702 13493 16768 SEQ ID 15507 18128 10027 14326 15469 15469 16308 16743 15082 19579 10782 16301 16301 10037 16167 17784 11772 14952 7377 17784 18802 17205 18802 19606 15601 ÿ SEQ ID 3579 5592 6889 8248 5553 6440 6440 9184 8 5553 6447 5082 443 6864 8 855 1876 6303 7934 9511 1274 3443 7337 7526 7934 8999 8999 9145 5692

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Table 4
Single Exon Probes Expressed in Heart

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igo Evol Lobes Expressed III near	Top Hit Descriptor	Mus musculus T-box 20 (Tbx20) mRNA	Human Inositol 14.5 trisphosphale recentor time 1 mBN martial and	Homo sabiens professome (presonal macrosia) 285 stricting ATESS 4 (25) 250	Homo sabiens professome (prosome mercmein) 265 c.rit-mit ATT	Homo saplens proteasome (prosome macronain) 288 c. inc., it ATD.	Homo saplens professione (procome macropin) 265 c.i.b.mit, ATD	Homo sapiens proteasome (prosome, macronain) 250 subunit, A1 rase, 4 (PSMC4) mKNA	Homo sabiens professome (prosome macropaln) 265 cultumit ATD	Homo sablens chrimnsome 31 segment IPCAC for a	HYPOTHETICAL PROTEIN DJ845024 3	WZ5h04.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:054923 O54923 RSFC15.	DKFZp762C033 s1 762 (synonym: hmel2) Homo serviens cDNA close DKEZ-7500000 g1	ba55g05.x1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:2900504 3' similar to ab:X17208 40S	RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (Mol ISE).	UI-H-Bisaloa-0504 II st NO COAP Site Views	EST77675 Parriese timer III Home casises DAM 61 and Called IMAGE:3068048 3	ESTITES Pancreas timor III Home capiens con a con	zi29c08.sf Spares fetal liver saleen 1/151 S. 21 Done and in 1/152 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S. 1000 S.	Homo sapiens chromosome 21 segment Designation	Homo sapiens chromosome 21 seament HS21C010	2p29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone iMAGE:610860 5' similar to	II. Cocoozzo Gzoozzo R I VL-H PRO I EIN.; contains LTR7.13 LTR7 repetitive element;	nomo sapiens putatve tumor suppressor ST13 (ST13) mRNA, complete cds	Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sanjane) (I. OCasasa)	X08b01.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B	29005 11 NCL CRAP GORT Home content of NA Content at MACON ACT.	Homo sapiens glutatrione S-transferase theta 2 (GSTT2) and glutatrione S-transferase theta 1 (GSTT1) enems. complete orts	H.sapiens mRNA for acetyl-CoA carboxylase
Bio Evoli 1 10r	Top Hit Database Source	N	NT	Į.	Į.	F	Ľ.	NT	LN L	IN	SWISSPROT	EST HUMAN	EST HUMAN		EST HUMAN	Τ	Г	Т	HUMAN				TIN LINE			EST HIMAN	Г		Į.
5	Top Hit Acession No.	10048417 NT	U23850.1	5729990 NT		5729990 NT	5729990 NT	5729990 NT	5729990 NT	7.0E-49 AL163284.2	060811	7.0E-49 AI807191.1			6.0E-49 AW731740.1	6.0E-49 AW 452218.1	6.0E-49 AA366556.1	6.0E-49 AA366556.1	6.0E-49 AA707567.1	AL163210.2	5.0E-49 AL163210.2	5 OF 40 AA472424 4	1477444	1	11436355 NT	4.0E-49 AW 189533 1	T		
	Most Similar (Top) Hit BLAST E Value	8.0E-49	8.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49 O60811	7.0E-49	7.0E-49		6.0E-49	6.0E-49	6.0E-49	6.0E-49	6.0E-49	5.0E-49	5.0E-49	5 OF 40	5 0F-40   147744	0.01	5.0E-49	4.0E-49/	4.0E-49	4.0E-49	3.0E-49 X68968.1
	Expression Signal	2.95	3.19	1.47	1.47	1.74	1.74	1.99	1.99	4.05	0.95	1.88	1.34		11.77	292	2.69	2.69	3.43	3.37	3.37	194	5 18	2	5.13	37.46	243	3.3	0.93
	ORF SEQ ID NO:	25703			20158		20158	20157	20158	20958	. 24227	25100	25107		19979	28738	29022	29023		20452	20453	21524	22477		22957	20266			20298
	_ 0	15601			10335		10335		10335	11112	14443	15271	16277		10162	18467	18728	18728	19498	10628	10628	11653	12583		13159	10456	19710	19090	10489
	Probe SEQ ID NO:	5692	6827	134	134	388	388	380	389	1202	4650	5351	2989		190	8600	8920	8920	9507	695	695	1753	2721		3235	514	9376	9459	548

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Table 4
Single Exon Probes Expressed in

		31.1	T			T	T	$\top$	₽ c	1	I	T	T	T	T	T		T	Ť	T	1	T	T	"	Ť	ή,	٦	T	T	T	T
Single Exon Probes Expressed in Heart	Top Hit Descriptor	ze31c05.rf Soares retina N2b4HR Homo septens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element:	Human type IV collagen (COL4A6) gene, exon 40	EST25e12 WATM1 Homo sapiens cDNA clone 25e12	EST42572 Endometrial fumor Homo sapiens cDNA 5' end	MR3-HT0487-150200-113-q01 HT0487 Homo saniens cDNA	Jy23d08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMACE: 252574 F	Homo sapiens RNA binding protein II (RBMII) gene, complete cds	oz88402.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);contains Alu repetitive element contains element MFR??	repetitive element;	UI-H-BI4-aps-d-02-0-UI.s1 NCI_CGAP_Sub8 Home sapiens cDNA clone IMAGF-3088438 3	AV717638 DCB Homo sapiens cDNA clone DCBALB01 5'	EST02558 Fetal brain, Stratagene (cat#936206) Homo seniens cDNA clune HEROVSO	Homo sapiens SNCA isoform (SNCA) gene complete rols, alternatively spilosed	601458531F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE-38520R8 F	601115769F1 NIH MGC 16 Homo sepiens cDNA clone IMAGE 2388272 F	601820053F1 NIH MGC 58 Homo septems cDNA clone IMAGE-A052062 F1	601290330F1 NIH MGC 8 Homo saniens cDNA done IMAGE 3F30863 F1	801290330F1 NIH MGC 8 Homo saciens cDNA clone IMAGE:3620863 5	W78g12.s1 Soares, placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258408 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN):	W78g12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258406.3' similar to ob.X65873 KINFSIN HFAVY CHAIN HI IMAAN.	Homo saplens succinate CoA ligase GDP-forming alpha subunit /SLD/ GAV DNA	Homo sapiens succinate CoA ligase GDP-forming alpha submit (COCCO), Illinity	601300992F1 NIH MGC 21 Homo seniens china clara MAACE sassasso et	DKFZp434D2423 r1 434 (synonym: htes3) Homo saniens cDNA clans DKFZA34D3433 E	Homo sapiens brefeldin A-inhibited quanina nucleotide-exchange profess 17813-1 mPM	MR0-HT0407-010200-006-f02 HT0407 Homo sepiens cDNA	Homo sapiens cadhein EGF LAG seven-bass G-type recentor 1 (CEI SR1) mRNA	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cris	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens mRNA for VIP receptor 2
gle Exon Pro	Top Hit Database Source	EST HUMAN	TN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	N-		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	N L	¥	EST HUMAN	EST HUMAN	1	EST_HUMAN	1	5	NT	TN
Sin	Top Hit Acession No.	AA016131.1	U46999.1	3.0E-49 H39479.1	AA337561.1	2.0E-49 BE165980.1	N26446.1	2.0E-49 AF026564.1		2.0E-49 Ai167357.1	2.0E-49 BF511846.1	2.0E-49 AV717938.1	2.0E-49 M86033.1	1	1.0E-49 BF035327.1	1.0E-49 BE255216.1		10.1	10.1	1.	<del>-</del> -	11321580 NT	11321580 NT	40.1	29.2	11427366 NT	43.1	11418322	75.1	02.2	2
	Most Similar (Top) Hit BLAST E Value	3.0E-49 AA0161	3.0E-49 U46999	3.0E-49	3.0E-49 AA3378	2.0E-49	2.0E-49 N26446	2.0E-49		2.0E-49	2.0E-49	2.0E-49	2.0E-49	2.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49 BE3981	1.0E-49 BE3981	1.0E-49 N25884	1.0E-49 N25884	1.0E-49	1.0E-49	1.0E-49 BE4093	1.0E-49 ALD431	1.0E-49	1.0E-49 BE1593	1.0E-49	9.0E-50 AF1014	8.0E-50 AL1632(	8.0E-50 X95097
	Expression Signal	2.01	2.08	9.6	2.3	2.66	1.4	0.93		1.12	125	1.47	1.97	1.53	3.95	2.58	4.97	2.93	2.93	2.17	2.17	1.29	1.29	1.22	1.21	3.88	1.73	2	1.06	2.59	1.89
	ORF SEQ ID NO:				28759		22914	23235		24373	24381	26075					25011	26307	26308	26346	26347	26777	26778	27262	27924	28769				19951	20460
	Exon SEQ ID NO:	12479	14788	16248	18487	10582	13110	13437	-	145/9	14590	15943	16597	19599	10807	11659	15210	16151	16151	16185	16185	16589	. 16589	17071	17680	18495	18813	19035	14802	10136	10635
	Probe SEQ ID NO:	2611	4909	6386	8621	645	3185	3521		4093	4/04	6040	6717	9467	88	1760	5289	6287	6287	6322	6322	6209	6209	7200	7830	8630	9018	8367	4923	<u>8</u>	702

Page 229 of 413 Table 4 Single Exon Probes Expressed in Heart

Oiligie Lyon Flobes Lypiessed III Nealt	Most Similar (Top) Hit Acession (Top) Hit Acession ID No: Signal BLAST E No. Source Source	35 20461 1.89 8.0E-50 X95097.2 NT Homo sapiens mRNA for VIP receptor 2	1.21	21497 2.51 8.0E-50 4501890 NT	. 22204 1.36 8.0E-50 7706394NT	22205 1.36 8.0E-50 7706394 NT	22421 1.69 8.0E-50 4826658 NT	28811 2.1 8.0E-50 AA633467.1 EST HUMAN	20349 0.96 7.0E-50 BE089591.1 EST HUMAN	28273 9.52 7.0E-50 AI872137.1 EST HUMAN	4.47 6.0E-50 BE044076.1 EST HUMAN	28326 3.17 6.0E-50 AA312079.1 EST HUMAN	28327 3.17 6.0E-50 AA312079.1 EST HUMAN	21522 0.85 5.0E-50 BF332938.1 EST HUMAN	21523 0.85 5.0E-50 BF332938.1 EST HUMAN	5.64 5.0E-50 AA557683.1 EST_HUMAN	29086 1.85 5.0E-50 AA403053.1 EST HUMAN G1335769 GAG-POL POLYPROTEIN.	1.29 4.0E-50 AA601143.1 EST HUMAN	2.45 3.0E-50 M18048.1 NT	22981 1.14 3.0E-50 AA746142.1 EST_HUMAN	23392 4.6 3.0E-50/AW755254.1 EST HUMAN	26180 1 55 2 0E 50	111111111111111111111111111111111111111	64 26540 4.01 3.0E-50 AF233436.2 NT cds complete	Homo saplens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds	27721 1.17 3.0E-50 AB046818.1	28153 5.94 3.0E-50 AJ245621.1 NT
	ORF SEQ ID NO:			21497	22204	22205	22421	28811	20349	28273		28326	28327	21522	21523		29086		-	22981	23392	26180	3	26540	26541	27721	28153
	Exen SEQ ID NO:	10635	10934	11628				18528	10539	18027	16660	18076	18076	11652	11652	17132	18795	10824	11791	13182	13606	16039	1	16364	16364		17909
	Probe SEQ ID NO:	702	1016	1727	2432	2432	2666	8711	603	8139	6781	8190	8190	1752	1752	7255	8991	899	1896	3259	3692	6056		6505	6505	7649	8760

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Single Exon Probes Expressed in Heart

							_													m.		1818. 541141			<u> </u>	4.				Altres -
Top Hit Descriptor	Homo sapiens MHC class 1 region	Homo saplens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo sapiens decorin D mRNA, complete cds. alternatively spliced	Human HALPHA44 gene for alpha-tubulin, exons 1-3	Human HALPHA44 gene for alpha-tubulin exons 1-3	Mus musculus keratin complex 2, dene 6a (Krt2-6n), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g) mRNA	PM3-BN0137-290300-002-q11 BN0137 Homo sepiens cDNA	PM3-BN0137-290300-002-011 BN0137 Homo saniens CNA	Homo sapiens chromosome 21 segment HS21Cnng	Homo sapiens Xa bseudoautosomal region segment 1/2	2451c09.r1 Soares pregnant uterus NbHPII Home saniens contact that CE-1963557 E	np98e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1152440 3' similar to gb:X12671_ma1 HETEROGENEOUS NITCLEAR RIBONI ICLEOPED A CLOUR A CLOUR AND AND A CONTROL OF CONTROL AND AND A CONTROL OF CONTROL AND AND A CONTROL OF CONTROL AND AND A CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF 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PROTEIN	DKF2b434B229g r1 434 (summyrr https://dx.com/marchines/	DKFZP434B2229 r1 434 (synonym: https://www.htms.aniens.chu/A.clone.htm27434B2229 5	UI-H-BW0-alp-b-05-0-UI-S1 NCI CGAP Sub6 Home saniens CONA class (NA GE-2720847 2)	Homo saplens KIAA0929 protein MsvZ interacting muclear terms (MINIT) boxanics (VIAA0929 protein MsvZ interacting muclear terms)	Homo sabiens KIAA0929 profein Mey Interacting professional to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 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Homo sapiens solute carrier family 2 (facilitated clucose transporter) member 6 (SLC2A9), mKNA	Human haptoglobin related (Hbr) gene exon 3	Homo sapiens mitoden-activated protein kinase kinase 1 (MKKA) nene avvn. 4	Homo sapiens mitogen-activated protein kinase kinase 1 (MKKA) nene	Homo sapiens cerebral cell adhesion molecule (1 OCS1148) mBNA	Homo sapiens B9 protein (B9), mRNA	Homo sapiens interleukin 17 receptor (IL17R), mRNA
Top Hit Database Source	NT	NT	NT	TN	LN L	TN	LN	EST HUMAN	EST HUMAN	N	IN	T HUMAN			T HUMAN	Т		Г	Т	Т					N	N I				
Top Hit Acession No.	2.0E-60 AF055066.1	4557752 NT	AF138303.1	X06956.1	X06956.1	TN 59310293 NT	9910293 NT	1.0E-50 BE007080.1	3E007080.1	1.0E-50 AL163209.2		9.0E-51 AA043738.1	AA610842.1	11439587 NT	AU138590.1	7.0E-51 AW889219.1	7.0E-51 AW 274720.1	7.0E-61 AL079628.1	7.0E-51 AL079628.1	1W 295603.1	7657266 NT	7657266 NT	9910553INT	9910553 NT		6.0E-51 AF070083.1		1429665	7661535 NT	11526289 NT
Most Similar (Top) Hit BLAST E Value	2.0E-60	2.0E-50	2.0E-50 AF1383	2.0E-50 X06956	2.0E-50 X06956	2.0E-50	2.0E-50	1.0E-50	1.0E-50 BE00708	1.0E-50	1.0E-50	9.0E-51	8.0E-51 AA61084	8.0E-51	8.0E-51 AU13859	7.0E-51	7.0E-51	7.0E-51	7.0E-51	7.0E-51 AW2956	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51 X01788.1	6.0E-51	6.0E-51 AF07008	6.0E-51	6.0E-51	6.0E-51
Expression Signal	4.91	4.6	18.02	6.27	6.27	1.53	1.63	1	1	2.1	8.98	1.22	4.89	2.34	1.28	1.36	0.83	1.26	1.26	2.38	5.3	12.92	0.78	0.78	2.26	6.68	6.68	2.16	2.26	1.72
ORF SEQ ID NO:			21197		26938		27762	20018		20215		27450	24151	26546	-	22967	23042	23757	23758	23927	21714	23150	23887	23888	25651	25656	25657	24859	27649	28716
Exon SEQ ID NO:	10691	10979	11330	16802	16802	17536	17536	10204	10204	10398	12195	17244	14361	16369	17257	13168	13238	13978	13978	14153	11831	13345	14110	14110	15558	15562	15562	15116	17434	18448
Probe SEQ ID NO:	761	1063	1425	6924	6924	7686	7686	235	235	454	2314	7375	4467	6510	7448	3245	3317	4076	4076	4254	1936	3428	4212	4212	5645	2650	5650	6158	7583	8580

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Single Exon Probes Expressed in Heart

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The control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co	Top Hit Descriptor	Homo sabiens chromosome 21 seament HS21Cnn3	Homo saplens T-cell lymphoma invasion and melastesis 4 /TIAM4)	Novel human gene manning to chomosome Y	Homo sabiens 265 professome essociated and themales (DOLM) - DAM	Homo sepiens mRNA for nucleonarin 155	Human Ku (o70/p80) subtuilt mRNA complete ods	Human Ku (b70/b80) subtunit mRNA complete cus	Homo sapiens mRNA for KIAA1411 profein nettial cals	Homo saplens RNA binding molif protein 3 (PBMA) monA	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' strailar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 HILIMANN	tr81c09.x1 NCI_CGAP_Pan1 Homo sepiens cDNA done IMAGE:2224720 3' similar to gb:M26326 KFRATIN TYPE I CYTOCKEL ETAL AGAILLIANS	Novel himso gone manning to champed and an arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged and arranged arranged and arranged arranged and arranged arranged arranged and arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arranged arra	rose namen gene mapping to cromosome 22	ya47c08.r1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4	Human hnRNP C2 protein mRNA	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sepiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (I IRE3A) mRNA	601285694F1 NIH MGC 44 Homn Saniens cDNA clara MACE 25502452 51	601285694F1 NIH MGC 44 Homo sepiens cDNA clone IMAGE: 3807463 5	# 20a05.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:0233226 G233226 RTM H PROTEIN CONTROL TEXT OF TEXT	## ## ## ## ## ## ## ## ## ## ## ## ##	UI-H-BIT-edi-d-02-0-11 st NCI CGAP Site Home continue PNA Line	601470446F1 NIH MGC 67 Homo seniens CDNA class (MA CE 2020 CE	601676787F1 NIH MGC 21 Homo seniers CDNA clare INA/CE:305325	601676787F1 NIH MGC 21 Homo sabiens cDNA clone IMAGE:3058613 5	1874407 x1 NCI_CGAP_GC6 Homo saplers CDNA done IMAGE:2236980 3' similar to SW:TRKC_HUMAN	WISS IN SOME HEACH ON RECEPTOR PRECURSOR;
201 111000 016	Top Hit Database Source	NT	IN IN	N	TN.	N	N.	N	NT.	LN LN	EST HUMAN		L	Т	EST HUMAN	Т	N.		T HUMAN	Г	EST HUMAN	Т	Т	EST HUMAN	Т	П		Т
,	Top Hit Acession No.	AL163203.2	4507500	AL133204.1	5031980	38.1	-		2.1	5803136 NT	3.0E-51 AI587348.1	1.0	12.1		<b>-</b>	-	3.0E-51 AF003528.1	4507798 NT		2.0E-51 BE391063.1		2.0E-51 Al492415.1		l		2.0E-51 BE901994.1 E		2 OF 54 BE485080 4
	Most Similar (Top) Hit BLAST E Value	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51 AJ0075	5.0E-51	5.0E-51	5.0E-51	5.0E-51	3.0E-51	3.0E-51 AI58734	3.0E-51 A		3.0E-51 R15914.	3.0E-51 M29063.	3.0E-51 A	2.0E-51	2.0E-51 B	2.0E-51 B	2.0E-51 A	2.0E-61 A	2.0E-51 A	2.0E-51 B	2.0E-51 B	2.0E-51 B	2.0E-51 A	205 54 10
	Expression Signal	10.92	1.47	1.37	0.84	11.48	1.08	1.08	2.34	3.72	0.92	4.16	2.13		1.73	5.87	1.58	1.81	1.08	1.08	2.24	2.21	1.02	2.96	1.61	1.61	1.68	5.25
	OR!	20543			21354	22311		23567	24643	28739	19926	20917	23906		26500			20139	20424	20425	21431	23373	24071	25670	27114	27115	27652	27600
	တ								14879	18468	10104	11072	14130			17008	19233	10318	10607	10607	11564	13586	14288	15573	16924	16924	17348	17390
	Probe SEQ ID NO:	774	786	975	1590	2548	3863	3863	5004	8601	130	1159	4232		6474	7131	9675	362	673	673	1662	3672	4392	5662	7047	7047	7478	7539

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Table 4
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5	0634f09.x5 NCJ_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE INMDAI RECEPTOR SUBLINIT EPSII ON 1 PRECI IRSON .	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAEC1325609 similar to SW:NME1_MOUSE P35438 GLUTAMATE INMDAI RECEPTOR SUBUNIT FPRII ON 1 PPET inscrep	Homo saplens myelold/lymphold or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA	Homo sabiens eukarvotic franslation initiation forter 4A inches 4 (Elizaka) - Extra	AV742248 CB Homo septiens cDNA close CRERCO12 2:	Homo sapiens small inducible cutofficials cutofficially A (2 - 2 - 3	Homo sapiens small inducible cutotine subfamily A (Oc. C.)	120568 Testis 1 Homo series Charles (1905) (1905) (1905) (1905) (1905) (1905) (1905)	AV760590 MDS Homo sablens cDNA clone MDSCRRPO 51	zi95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE-449500 3' similar to	contains THR t3 THR repetitive element;	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR t3 THR repetitive element	H.sapiens mRNA for laminin-5, alpha3h chain	Homo saplens hypothetical profein FLJ13556 similar to N.m.vr downetracts and a version of the same same and the same same and same same and same same and same same same same same same same same	Homo sapiens hypothetical profein F 113558 similar to N. m. commenced in Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control	domo saplens hymothetical protein El 1925s aimilia L. M.	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Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN			T HUMAN			T HIJMAN	Г	П	EST_HUMAN	EST HUMAN	Т						٦	EST_HUMAN C	TN q	EST_HUMAN F	1
Top Hit Acession No.	AV682474.1	AI732851.1	AI732851.1	11419159 NT	4503528 NT	AV742248.1		4759071 NT	17	1.0E-51 AV760590.1		9.0E-52 AA777621.1	8.0E-52 AA720574.1	X84900.1	11968028 NT	11968028 NT	11968028 NT	1106RD28 NT		W 554/1.1	BE072409.1	17.1	6.0E-52 BE048172.1	
Most Similar (Top) Hit BLAST E Value	2.0E-51 AV6824	2.0E-51 AI7328	2.0E-51 AI7328	2.0E-51	1.0E-51		1.0E-51	1.0E-51	1.0E-51 T18862	1.0E-51		9.0E-52	8.0E-52	8.0E-52 X84900.	8.0E-52	8.0E-52	8.0E-52	8.0E-52	L	7.0E-52 W 5647	6.0E-52 BE0724	6.0E-52 AF10990	6.0E-52	
Expression Signal	1.71	8.63	8.63	1.33	4.4	7.22	98.0	96.0	3.12	3.57		3.28	7.31	1.33	2.05	2.05	6.44	6.44	,	9	0.86	2.25	223	
ORF SEQ ID NO:	28054	25084	25085	25240	19905			08682	25036		<del></del>		,19939	21249	21397	21398	21397	21398	97.770	21210	+	21436	28678	
Exan SEQ ID NO:	17812	15259	15259			11383	14206		15231	19771	000	19080	10120	11386	11537	11537	11537	11537	47088	3 6	201	11570	18412	
Probe SEQ ID NO:	7962	8640	8640	8996	109	1478	4309	4309	5310	8989	0.454	40	146	1481	1633	1633	3913	3913	7241	1475	2	1668	8540	

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	Top Hit Descriptor	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA18H7	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds	Homo sapiens nucleoporin 155kD (NUP155) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	601440687F1 NIH MGC 72 Homo sapiens cDNA clone IMAGE 3915836 5	Hómo sapiens hydroxysterold (17-beta) dehydrogenase 4 (HSD1784) mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens hypothetical protein FLJ10675 (FLJ10675) mRNA	Human endogenous retroviral DNA (4-1), complete retroviral segment	Human endogenous retroviral DNA (4-1), complete retroviral segment	bb68b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zof-1 zinc finger protein (Mol.ISF).	602084710F1 NIH MGC 83 Homo seniens cDNA class MAAGE-4248904 gt	Novel human gene mapping to chromosome 20. similar to membrane transmeters	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA	Homo sapiens interleukin 21 receptor (II 21R) mRNA	Macaca mulatta beta-tubulin mRNA, complete cds	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUESS) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) BNA	Homo sapiens SET domain and mariner transposase fusion dene (SETMAR) mRNA	wi49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2 THR repetitive element :	wi49c04x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2	AV745277 DCB Long confere CNIA - Long All Societies 21	z449q12,r1 Sogres fetal heart NhHH19W Homo sanions cDNA clone INA CE:244222	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA	xn72e07.x1 NCI_CGAP_CMI.1 Homo saplens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element,contains element LTR2 repetitive element:	wf67d05x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE:	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
110000	Top Hit Database Source	닐	N.	N	NT.	EST HUMAN	Ί.	N	닐	LN	NT	N	EST HUMAN	EST HUMAN	NT	EST HUMAN	Ί.	N _T	ļ Į	LN	LN	EST HUMAN	ECT LIMANI	EST HIMAN	EST HUMAN	N FN	EST_HUMAN	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	Z78898.1	AF257318.1	4758843 NT	4507500 NT	BE622032.1	11417035 NT	11418177 NT	4.0E-52 AB002059.1	11437042 NT	M10976.1	M10976.1	BE207675.1	BF677892.1	2.0E-52 AL137188.3	2.0E-52 AW848041.1	11141868 NT	2.0E-52 AF147880.1	4758789 NT	5730038 NT	5730038 NT	2.0E-52 AI831462.1	A1831462 1	AV745377 4	N70260.1	11417990 NT	4W236297.1	2.0E-52 AI808985.1	1.0E-52 AA634445.1
	Most Similar (Top) Hit BLAST E Value	5.0E-52	4.0E-52 AF2573	4.0E-52	4.0E-52	4.0E-52 BE62203	4.0E-52	4.0E-52	4.0E-52	3.0E-52	2.0E-52 M10976.	2.0E-52 M10976.	2.0E-52 BE20767	2.0E-52	2.0E-52	2.0E-62	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2 NE-52 A1831465	2 0F-52 AV74537	2.0E-52 W70260.1	2.0E-52	2.0E-52 AW2362	2.0E-52 /	1.0E-52
	Expression Signal	2.07	0.93	8.58	0.82	1.24	7.25	4.25	5.09	86'6	1.39	1.39	1.75	20.53	2.74	2.74	1.49	8.39	1.98	4.53	4.53	5.33	533	3.09	2.08	3.22	8.86	4.28	1.37
	ORF SEQ ID NO:						27035				20299	20300	22226		24557	25479	25860			27918	27919	28671	28672	28689			24894		20276
$\cdot$	Exon SEQ ID NO:				13761			18992	19293	13908	10491	10491	12327	12569	14782	15416	15747	16905	17267	17675	,17675	18408	18408	18419	18548	18701	19755	19112	10464
	Probe SEQ ID NO:	4340	1639	1748	3850	6686	6965	9291	9778	4002	550	550	2450	2706	4902	5497	5841	7028	. 7458	7825	7825	8536	8536	8547	8659	8891	9101	9496	223

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Single Exon Probes Expressed in Rear	st Similar Top Hit Acession Database LASTE No. Source	1.0E-52 4504026 NT Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA	1.0E-52 4502238 NT Homo sapiens ary/sulfatase D (ARSD), transcript variant 1, mRNA	ŢN	FZ		INT	1.0E-52 AL163227.2 NT Homo sapiens chromosome 21 segment HS21C027	12.2 NT	U48296	11426321 NT	16064 NT		1713 NT	7.0E-53 BF238465.1 EST_HUMAN 601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5	7.0E-53 A421782.1 FST HTMAN THR repetitive element	58543 NT	AW813563.1 EST HUMAN	35.2 NT	4.0E-53 AL163285.2 NT Homo sapiens chromosome 21 segment HS21C085	4.0E-53 7705414 NT Homo sapiens hook1 protein (HOOK1), mRNA	01.1 EST_HUMAN	4.0E-53 BF128701.1   EST_HUMAIN   601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	COT CHANN	1	EST HIMAN	NT	5901953 NT	AA366556.1 EST_HUMAN	TN
	Most Similar (Top) Hit BLAST E Value	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52	9.0E-53	9.0E-53	9.0E-53	7.0E-53	7.0E-53	5.0E-53	5.0E-53	4.0E-53	4.0E-53	4.0E-53	4.0E-53	4.0E-53	· 200 83	3 05 53	3.0F-53	3.0E-53	3.0E-53	3.0E-53	2.0E-53	2.0E-53
	Expression Signal	8.25	1.2	1.41	3.59	2.11	3.19	1.64	1.61	1.84	2.04	1.03	1.01	0.93	2.06	2.98	2.2	1.72	1.92	1.92	1.09	3.33	3.33	. 0	200	1.18	0.85	9.88	8.59	4.25	2.98
	ORF SEQ ID NO:	21111		22741	24967		26417			28283			23975	24611			23690	_	19834	19835	24387	28685	28686	79267	23374	24167		26905	l		22060
	Exon SEQ ID NO:		12364	12949	15192	15757	16256			18035	18094	13635	14191	14841	19018	19632	13915	19048	10031	10031	14601	18417	18417	12403	13584	14380	14715	16712	17115	10394	12163
	Probe SEQ ID NO:	1349	2489	3021	5270	5851	6394	6932	8023	8147	8210	3723	4293	4966	9338	9752	4009	6386	43	43	4715	8545	8545	2625	3870	4486	4833	6833	7238	450	2279

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Table 4
Single Exon Probes Expressed in Heart

Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, at 9c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.t3 MER30 Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, w68d12.s1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:257399 3* Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA Homo sapiens dihydropyridine receptor apha 2 subunit (CACNA2D1) gene, exon 6 Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA Homo saplens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA 2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 57 601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814031 5 Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA Human Krueppel-related DNA-binding protein (TF34) gene, partial cds Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA Fop Hit Descriptor CM4-NN1029-150800-543-e02 NN1029 Homo saplens cDNA PM1-CT0396-170800-001-903 CT0396 Homo sapiens cDNA PM1-CT0396-170800-001-903 CT0396 Homo sapiens cDNA Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA Homo sapiens mRNA for monocyte chemotactic protein-2 Homo saplens Xq pseudoautosomal region; segment 2/2 similar to contains LTR7.b3 LTR7 repetitive element; Homo saplens chromosome 21 segment HS21C081 Homo sapiens chromosome 21 segment HS21C081 subunit E; V-ATPase, subunit E (ATP6E), mRNA H.sapiens mRNA for hnRNPcore protein A1 (CBFA2T1) mRNA (CBFA2T1) mRNA repetitive element; complete cds) EST_HUMAN EST_HUMAN NT EST_HUMAN Database HUMAN EST_HUMAN 上的上 **EST HUMAN** EST_HUMAN Source 4502316|NT EST 4757915|NT 4757915|NT 눋 눋 4506962 NT 눋 4507848 NT 4507848 NT 4507848 NT 4507848 NT 4507500 NT 눋 4507500 NT 6005700 NT Top Hit Acession 4506786 4504610 AW 245676.1 2.0E-53/AL163281.2 AL163281.2 BF334740.1 AF083822.1 1.0E-53 AJ271736.1 1.0E-53 AB026898.1 BF334740.1 7.0E-54 AA812537.1 7.0E-54 Y16645.1 ġ BF364201.1 M61873.1 7.0E-54 N27177.1 X79536. 2.0E-53 2.0E-53 1.0E-53) 2.0E-53 2.0E-53 2.0E-53 2.0E-53 2.0E-53 1.0E-53 8.0E-54 **Most Similar** (Top) Hit BLAST E 2.0E-53 9.0E-54 9.0E-54 8.0E-54 8.0E-54 8.0E-54 9.0E-54 8.0E-54 8.0E-54 Value 10.54 1.12 6.93 1.18 2.06 1.07 1.12 3.11 5.6 0.9 3.09 1.42 0.8 4.71 1.25 1.26 0.8 1.33 1.08 1.08 20.81 1.54 Expression 4.61 Signal 22446 23653 24735 ORF SEQ 25056 24068 24736 21200 24939 25057 24788 9988 21568 20186 24787 24307 24308 24307 21563 21945 24308 ÖNO 12365 12559 12559 SEO ID 13131 14286 17280 15925 15019 15019 10363 14961 14961 11334 17129 12045 15251 15251 19439 11692 15529 10172 ö 1387 14517 14517 14517 11687 14517 SEQ ID 2490 2694 2694 3207 4390 5331 7413 5152 5152 5244 5091 5091 1429 3364 5331 1794 4629 5030 2158 3970 7252 8 4629 5030 379 1789 ÿ

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Top Hit Descriptor	Homo sepiens similar to nuclear factor related to kappa B binding protein (H. saniens) (LOCR3182) mRNA	db67g03.xt Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204.3' similar to contains OFR.tt OFR repositive element:	Homo sapiens DNA for MICB, exon 4, 5 and partial cds	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	Homo sapiens chloride channel 6 (CLCN6) mRNA	AV754746 TP Homo saplens cDNA clone TPGAAC10 5'	H.sapiens shc pseudogene, p66 Isoform	H.sapiens she pseudogene, p66 isoform	RC3-ST0197-151099-011-f08 ST0197 Homo saniems cDNA	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)	Tupaia belangeri beta-actin mRNA, partial cds	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate	denydrogenase	Human mRNA for KIAA0077 gene, partial cds	Human mRNA for KIAA0077 gene, partial cds	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' stmilar to TR:O02711 PRO-POL-DUTPASE POLYPROTEIN :	EST185371 Colon carcinoma (HCC) cell line Homo seniens cDNA 5' end	DKFZp434E0731_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434E0731 5'	IL-BT189-190399-007 BT189 Homo sapiens cDNA	Homo sapiens BWX non-receptor tyrosine kinase (BWX) mRNA	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo saplens cDNA clone IMAGE:1388270.31	ai92co8.s1 Soares_parafflyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE-1388770.3'	602019408F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4155121 5	270f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315	GISTSTD ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;	EST366629 MAGE resequences, MAGC Homo sapiens cDNA	RC1-BT0313-131199-011-b09 BT0313 Homo saplens cDNA	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
Top Hit Database Source	F	EST HUMAN	LN.	NT	N	IN	Ą	EST_HUMAN	N	N7	EST HUMAN	SWISSPROT	IN		ESI_HUMAN	LN.	TN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	100	EST HOMAIN	EST_HUMAN	EST_HUMAN	TN	N
Top Hit Acession No.	11417222 NT	7.0E-54 A160189.1	8.1	4505052 NT	4505052 NT	8922148 NT	4502872 NT	6.0E-54 AV754746.1	Y09846.1	r'09846.1	6.0E-54 AW813567.1		03.1	, , , , ,	4.1			4.0E-54 Al935086.1	7.1	3.0E-54 AL110383.1		4502434	1	1	3F345600.1			9.1	5.1	5031900 NT	4507164 NT
Most Similar (Top) Hit BLAST E Value	7.0E-54	7.0E-54	6.0E-54 AB00361	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54 Y09846.1	6.0E-54 Y09846.1	6.0E-54	5.0E-54 P51523	4.0E-54	70 10 7	4.0E-54	4.0E-54 D38521.1	4.0E-54 D38521.1	4.0E-54	3.0E-54 AA31348	3.0E-54	3.0E-54 AI908757	3.0E-54	3.0E-54 AA844061	3.0E-54 AA844061.	3.0E-54	1000	3.05-34	3.0E-54 AW95455	3.0E-54 AW 74896	2.0E-54	2.0E-54
Expression Signal	2.23	6.24	1.64	0.87	0.87	0.84	2.4	1.24	1.71	1.3	1.77	2.25	106.86	70 77	45.F4	3.24	3.24	1.17	5.11	0.92	0.88	1.48	1.68	1.68	4.17	0	#C'0	2.86		6.29	1.94
ORF SEQ ID NO:	27925		19802	21605	21606	22968	23612	24040				21893		00740	20/12	21536	21537		19888	22287		25590	26394	26395	28565	2000	72020	20303	+	20374	21105
Exon SEQ ID NO:	17681	18478	10009	11730	11730		13832	14255	14658	14658	17899	11993	10147	1000	2000	11663	11683	13083	10072	12396	12454	15512	16235	16235	18309	18663	2000	18932	19714	10563	11248
Probe SEQ ID NO:	7831	8611	22	1833	1833	3246	3923	4359	4774	4930	8750	2104	176	5	3 1	1/84	1764	3168	88	2522	2583	2238	6373	8373	8435	8675	2 2	881.6	9242	979	1342

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Table 4
Single Exon Probes Expressed in Heart

			T	T	و	T	Т	П	٦	Т	$\neg$		$\neg$	$\neg$	T	$\top$	"	Thank	٦	Ť	7	T	ij	177		1	-132	11
onigie Ekul riobes Expressed in Heart	Top Hit Descriptor	nt78a09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element :	aug2g03.y/ Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1 HUMAN 013646 CULLIN HOMOLOG 4	Homo sapiens chromosome 21 segment HS210010	W60b12x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA done IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NFIGHRORING.	nj45g09.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN 23 (HI IMAN):	Homo sapiens chaperonin containing T-complex subunit 6 (CCTs) DNA	Homo sabiens chromosome 21 segment HS24CMM	Homo sapiens nenfidylarginine delminase time III (1 0054302) — Bhi A	Homo sabjens dihydronyridine recentr sinhe 2 submit (CACNIASIA)	Homo sabiens small inducible codyline entrement (CACIVAZDI) gene, exon /	1243c11.v1 NCI CGAP Bin52 Homo sanians chNA close 144 CECYA14) mRNA	Homo sablens KIAA0100 dene broding (KIAA0100) - DNA	Homo sepiens mRNA for KIAA1501 modeln modeln add	Homo sapiens mRNA for KIAA15501 protein partial rute	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA	Homo sapiens mBNA for brain pranceline recombar complete and	Homo saniens, Janus Khase 2 (a profein two-first Khase 2 (a profein two-first Khase 2)	Homo sapiens pescadillo (zebrafish) homolog 1 containing BDCT domain (DESA)	Homo sapiens period (Drosophile) homolog 3 (PER3) mRNA	601899230F1 NIH MGC 19 Homo sapiens cDNA clone IMAGF-4128535 F	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zrv6C880 similar to 5'-end region of Human	Homo sapiens RFB30 gene for RING finance model.	Homo sabiens RFB30 dene for RING finder motorin	fh02a02.x1 NIH MGC 17 Home saniers CNN a charallance consens zi	V/28c04.rf Soares fetal liver spleen 1NFCs Homo sapiens cDNA clone IMAGE:127998 5' similar to SP-C561 ROVIN Prosez CYTOCLEDAME.	ak28a11.s1 Soares fastis NHT Homo seniers CONA closs (MACE 4 167202 p.)	Company of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
JIE EXOII PIOL	Top Hit Database Source	EST_HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN		NT	LZ L	L		T HUMAN	T								EST_HUMAN			Т	EST HUMAN	HIMAN	T	
JIIIO	Top Hit Acession No.	08.1	175.1	0.2	24.1	25.1	4502642	1.2	7706446	33.1	4759069	1.4	1426657	1.1	1.1	11426544 NT	2.0E-54 AB001025.1	9127	7657454 NT	8567387 NT	8.1	4.4			1.4			
	Most Similar (Top) Hit BLAST E Value	2.0E-54 AA6550	2.0E-54 AW163	2.0E-54 AL16321	2.0E-54 AW0575	2.0E-54 AA5329	2.0E-54	2.0E-54 AL16320	2.0E-54	2.0E-54 AF0838;	2.0E-54	2.0E-54 BE0478	2.0E-54	2.0E-54 AB04681	2.0E-54 AB0468	2.0E-54	2.0E-54 A	2.0E-54	2.0E-54	2.0E-54	1.0E-54 BF31541	1.0E-54 AU07734	8.0E-55 Y07829.2	8.0E-55 Y07829.2	8.0E-55 AW 4097	7.0E-55 R09346.7	7.0E-55 A	
	Expression Signal	1.6	1.3	1.82	1.65	4.06	2.03	1.13	1.45	0.84	3.75	1.34	3.59	18.19	18.19	8.14	3.62	1.26	2.57	1.46	1.07	2.26	14.56	2.32	2.76	1.19	1.26	
	ORF SEQ ID NO: '	21290	22261	22321	22587				24450	24790	25116	25417	25503	25564	25565	26243	27617	27821		25216						20826	27373	
	Exan SEQ ID NO:	11434	12367	12428	12793	13418	14010	14240	14664	15023	15283	15360	15439	15488	15488	16093	17403	17599	18770	19244	14259	19345	11201	11204	18402	10981	17173	
	Probe SEQ ID NO:	1529	2493	2556	2865	3501	4110	4343	4780	5156	5363	5440	5521	6673	5573	6227	7552	7749	8983	9693	4363	9852	1294	1297	8530	1065	7297	

Page 238 of 413 Table 4 Single Exon Probes Expressed in Heart

		T	Т	T	T	Т	T	T	Т	T	Ţ	T	Τ	T	Т	Т	T	T	T	Ì	٦	"	Ť	Τ	T	T	Τ	1	T	Τ	Τ,	Ť	7	"
Single Exon Flobes Expressed in Heart	Top Hit Descriptor	ta29f09.x1 NCI CGAP Utf Homo sapiens cDNA clone IMAGE-2210246.3	tq29f09.x1 NCI CGAP Utf Hamo sapiens cDNA clone IMAGE-2240243	ym57q07.r1 Soares infant brain 1NiB Homo saniens cDNA clone MAGE:52444 Fr	Homo sapiens mRNA for KIAA1501 protein, partial cds	295b09.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens clone IMA CE GREAT 21	295b09.s1 Soares fetal liver splean 1NFLS S1 Homo sapiens chinA crome 1MA CE: 467647 3	Homo sapiens anysulfatase E (chondrodysplasia punctata 1) (ARSE) mRNA	Homo sapiens anisulfatase E (chondrodysplasia punctata 1) (ARSF) mRNA	Homo saplens protein tyrosine phosphatase, receptor type, alpha polymentide (PTPRA) mRNA	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens nel (chicken Like 2 (NELL2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1 containing BRCT domain (PES4) mBNA	EST370064 MAGE resequences, MAGE Homo sabiens cDNA	Homo sapiens RNA binding motif protein. Y chromosome, family 1 member A1 (RBMV1 A1) mRNA	Homo sapiens predicted osteoblast protein (GS3786), mRNA	Homo sapiens predicted osteoblast protein (GS3786), mRNA	7j52b10x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3390043 3' similar to	Contains L1.13 L1 repetitive element;	Homo sapiens protessome (proseure, macronair) subunit, appra type, 2 (PSMA2) mKNA	Homo sapiens diacyddycerol kinase, gamma (gokh) (DGKG) mRNA	Homo sapiens diacylolycerol kinase, gamma (90kD) (DGKG) mRNA	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (I IRE2/11) mRNA	Homo saplens Xq pseudoautosomal region: segment 1/2	Homo sapiens chromosome 21 segment HS21C100	Homo saplens chromosome 21 segment HS21C010	43c5 Human retina cDNA randomly primed sublibrary Home saplene cDNA	601886575F2 NIH MGC 17 Homo saniens CDNA chora IMAGE-4120338 K	PM1-HT0603-090300-001-408 HT0603 Homo seniens cDNA	Homo sapiens chromosome 21 segment HS21C084	Human endogenous retrovirus pHE.1 (ERV9)	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo saplens syntaxin-hinding graphs (STXRB4) mBNA and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sensitive and sen
JIE CXOLI PIO	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	LZ LZ	EST HUMAN	EST_HUMAN	1	LN PA	TN	N-	N _T	LN LN	Ę	EST HUMAN	1	F	LZ LZ	14691111	ES L'HOMAN	 	5	17	5	LN	NT	N.	EST HUMAN	EST HUMAN	EST HUMAN	N	FX	NT	
SIIIO	Top Hit Acession No.	7.0E-55 AI561056.1	7.0E-55 AI561056.1		7.	7		4502240 NT	4502240 NT	4506302 NT	1.1	1.1	5453765 NT	11417972 NT	4.0E-55 AW957994.1	4826973 NT	7661713 NT	7661713 NT	, 4	4506180	4506180 NT	4503314 NT	4503314 NT	4507794 NT	Γ	4.0E-55 AL163300.2								4507296 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-55	7.0E-55	7.0E-55 H23396.1	6.0E-55 AB04093	5.0E-55 AA70497	5.0E-55 AA70497	6.0E-55	5.0E-55	5.0E-55	5.0E-65 AB01451	5.0E-55 AB01451	5.0E-55	5.0E-55	4.0E-55 /	4.0E-55	4.0E-55	4.0E-55	4 OF SE DEDEA 44	4.05-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55 W28189.1	4.0E-55 BF303941	3.0E-55 E	3.0E-55 AL163284	2.0E-55 X57147.1	2.0E-55 M10976.1	2.0E-55
	Expression Signal	12.75	12.75	. 4.3	1.98	1.12	1.12	1.82	1.82	2.06	1.86	1.86	1.19	2.13	1.36	33.95	1.89	1.89	4. 0.	12	1.53	7.73	7.73	1.25	1.04	1.38	6.44	4.46	2.38	2.76	1.65	2.3	0.89	3.08
	ORF SEQ ID NO:	28679	28680		28908	21500			25970		27851	27852	27965		19843	20409	21193	21194		21763	21764	21824	21825	22046		22964						20150		20383
	Exon SEQ ID NO:	18413	18413	19648	18617					17106	17620		17719	18985	12658	10591	11328	11328	11402	11872	11872	11930	11930	12146	12419	13165	16736	18429	18933	18894	19356	10327	10480	10570
	Probe SEQ ID NO:	8541	8541	9823	8803	1732	1732	5941	5941	7229	7770	7770	7869	9283	49	656	1422	1422	1498	1979	1979	2039	2039	2262	2545	3242	6857	8559	9200	9138	9866	373	239	633

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Table 4
Single Exon Probes Expressed in Heart

f							_				_		_																			
	Top Hit Descriptor	Homo saplens ublquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains	THR.b2 THR repetitive element;	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5	Homo sapiens mannose-8-phosphate receptor (cation dependent) [M6PR] mRNA	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rahedia?) mBNA	Homo sapiens mRNA for KIAA0903 protein, partial cels	601120116F1 NIH MGC 20 Homo sepiens cDNA clone IMAGE-2967027 F	601120116F1 NIH MGC 20 Homo serviens cDNA clone INJAGE-3087027 E	Homo sapiens SMA3 (SMA3), mRNA	Homo saplens testis-specific Testis Transcript V 4 (TTV4) mDNA martial ad-	Human mRNA for HLA-A11E, a MHC class I molecule (maior histocomnatibility complex)	Homo sapiens mRNA for KIAA0406 protein, partial cals	Homo sapiens mRNA for KIAA0406 protein partiel cds	Homo sapiens CLP mRNA, partial cds	43c5 Human retina con A randomly nrimed sublitizary Homo serviens - DNA	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens DSCR5b mRNA, complete cds	Homo sepiens DSCR5b mRNA, complete cds	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	Human infant brain unknown product mRNA. complete cols	Homo sapiens DNA-binding protein (LOC56242), mRNA	601237702F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE 38nox52 5	yn82g03.r1 Soares adult brain N2b5HB55Y Homo saplens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
	Top Hit Database Source	뉟	EST_HUMAN		EST_HUMAN	EST_HUMAN	N F	M	N	EST HUMAN	EST HUMAN	N	LZ LZ	N-	F	N	Z		N	Z-	N.	F	¥	ξ	7	N.	·	¥	5	T HUMAN	EST HUMAN	$\Box$
,	Top Hit Acession No.	4507798 NT	3E719986.1		1002836.1	\U119344.1	4505060 NT	109823.1	10.1	31.1	31.1	5803174 NT	1.0E-55 AF000990.1		86.2				1.0E-55 AL163267.2			1.0E-55 AB037163.1	8923125 NT	11433046 NT	11433046 NT	0.2	10.2	-	10567821 NT	4.1		13.1
	Most Similar (Top) Hit BLAST E Value	2.0E-55	2.0E-55 BE71998		2.05-55/	2.0E-55 AU11934	1.0E-55	1.0E-55 U09823	1.0E-55 AB0207	1.0E-55 BE2778	1.0E-55	1.0E-55	1.0E-55/	1.0E-55 X13111.	1.0E-55	1.0E-55 /	1.0E-55 L54057.1	1.0E-55 W28189.1	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55 AL16321	1.0E-55 AL16321	1.0E-55 U50950.	1.0E-55	9.0E-56 BE37907	7.0E-56 H19934.	7.0E-56 AW3612
	Expression Signal	0.79	2.97	,	4.3	2.2	1.6	11.9	3.55	0.86	98.0	23	1.03	33.19	4.71	4.71	1.35	1.15	3.47	1.04	96.0	0.98	1.19	5.75	5.75	4.74	4.74	2.58	2.04	1.81	5.18	1.84
	ORF SEQ ID NO:		24342				19891	19969		21680	21681		22071	22238	22271	22272	22331	23082	23597	23878	24392	24393	24727	25809	25810	28405	28406	28138	28959	26383	22457	26538
ſ	Exon SEQ ID NO:	12855	14551	17460	3	18196	10075	10154	11046	11802	11802	12161	12651	12346	12381	12381	12439	13282	13817	14097	14607	14607	14951	15700	15700	18163	18163	17894	18671	16221	12567	16363
	Probe SEQ ID NO:	2928	4665	7007	1,204	8319	9	182	1132	1907	1907	2277	2290	2470	2507	2507	2568	3363	3907	4197	4721	4721	5081	5794	5794	8284	8284	8745	8859	6358	2703	6504

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA	43c5 Human retina cDNA randomly primed sublibrary Homo saniens cDNA	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22 55 51	Homo sapiens beta-tubulin mRNA, complete cds	Homo sapiens befa-tubulin mRNA, complete cds	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens X-linked anhidrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	Homo sapiens uncharacterized bone marrow profein RMA34 mBNA complete add	Homo sapiens uncharacterized bone marrow protein RMr31 mRNA Commists Adv	Homo sapiens lymphocyte-specific protein 1 (1.SP1) nene 1 SP1-7 allala matrial pub.	tm65d12.xt NCI CGAP British Homo seniens critish china iMACE shaped 21	tm65g12.x1 NCI_CGAP_Bm25 Home sablens cDNA clone IMAGE: 2183045 3'	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA	Homo saplens oncogene TC21 (TC21), mRNA	EST28889 Cerebellum II Homo sapiens cDNA 5' end	EST28889 Cerebellum II Homo sapiens cDNA 5' end	Homo sapiens MHC class 1 region	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens superkiller viralicidic activity 2 (S. carevisiae homolon) liika (SKIV2) 1 mBNA	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA	Homo sapiens sparciosfeonectin rwrv and kozal like domains and colored and services.	omo sanjena karecnal associated mandenna manifesta (1810-1810) (SPOCK) MKNA	Homo sabiens bone monthogenetic profets & (RMDE) TONA	Homo sapiens KIAA0317 dene product /KIA 402477 mPNA	Homo sapiens mRNA, similar to ret myomenafin, monthlyte ode	Homo sapiens nuclear bare complex interaction protein (NPIP) mPNA	Homo sapiens nuclear pore complex interacting profesion (NPIP) mRNA	Homo sapiens caveolin 3 (CAV3), mRNA	Homo sapiens caveolin 3 (CAV3), mRNA
	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	NT	TN	N.	TN	- L	N	TN	Z	EST HUMAN	EST HUMAN	IN	N	EST_HUMAN	EST_HUMAN	Z	NT	TN	TN	Į	L	L	Z	Ę	Į.	N N		
	Top Hit Acession No.	7.0E-56 AW361213.1	4W997712.1	N 28189.1	155099.1	4.0E-56 AF141349.1	VF141349.1	4507728 NT	4507728 NT	4.0E-56 AF003528 1	4.0E-56 AF217508.1	8.1		4.0E-56 AI498066.1	1498056.1	8924029 NT	6912697 NT			3.0E-56 AF055066.1	8.2	590Z085/NT	4759163 NT	4759163 NT	11421124 NT	11418704 NT	11434956 NT	6.1		5902013 NT	11434876 NT	11434876 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-56	5.0E-56 AW9977	5.0E-56 W28189	6.0E-56 H55099.	4.0E-56	4.0E-56 AF14134	4.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56 AF21750	4.0E-56	4.0E-56	4.0E-56 AI498066	3.0E-56	3.0E-56	3.0E-56 AA32582	3.0E-56	3.0E-56 A	3.0E-56 AL16326	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56 AB04255	3.0E-56	3.0E-56	3.0E-56	3.0E-56
	Expression Signal	1.84	2.26	1.31	2.68	6.15	6.15	4.11	4.11	3.05	6.29	6.29	1.23	8.75	8.75	9.85	2.7	1.58	1.58	1.39	4.05	2.14	1.57	1.57	6.34	5.74	1.52	10.72	3.89	3.89	2.3	2.3
	ORF SEQ ID NO:		21434			19805		22431	22432	20268	25802	25803	28090	28417	28418		21892	22804	22805		24006	24154	25467	25468	26141	27185	28078	28259	28771	28772	25315	25316
	Exan SEQ ID NO:		11568	17790		10012			12541	10457	15694	15694	17849	18174		11225	11992	13013	13013	13674	14224	14364	15405	15405	16003	16994	17837	18012	18497	18497	18955	18955
	Probe SEQ ID NO:	6504	1666	7940	9375	25	25	2676	2676	2781	5788	5788	7999	8295	8295	1318	2183	3086	3086	3761	4327	4470	5486	5486	6109	7117	7987	8124	8632	8632	9240	8240

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Γ		Т	Т	Т	Т	Т	Т	T	$\neg$	Т	┪	Т	7	Т	Т	一	_	$\overline{}$	7	Ť	Ť	-	┰	·	777	T	7	Ť	7	<del></del>	<del></del>	·····		
	Top Hit Descriptor	zq52a08.s1 Stratagene neuroepithelium (#937231) Homo saniens cDNA clone IMA CE GARONG 21	RC4-BT0310-110300-015-f10 BT0310 Homo saniens cDNA	RC4-BT0310-110300-015-f10 BT0310 Homo saplens cDNA	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA complete As	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA complete cus	Homo saplens mRNA for KIAA1414 protein, partial cds	AV703184 ADB Homo saplens cDNA clone ADRCFC10 5	Macaca fascicularis protein tyrosine phosphatase (PRI -1) mRNA complete cdc	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA_clone IMAGE-3046453 3'	hg23c11.x1 NCI_CGAP_GC6 Homo septiens cDNA_clone IMAGE: 3046463 3	QV-BT077-130199-079 BT077 Homo sepiens cDNA	RC2-CT0163-220999-001-F02 CT0163 Homo caniens chNA	QV0-OT0033-070300-152-h03 OT0033 Homo saniens cDNA	Homo sapiens EbhA4 (EPHA4) mRNA	Homo saplens EphA4 (EPHA4) mRNA	Homo saplens hypothetical protein FLJ20371 (FLJ20371) mRNA	QV4-ST0234-181199-037-105 ST0234 Homo septens cDNA	x05d10x1 NCI_CGAP_Brn53 Homo septens cDNA clone IMAGE:2759251 3' sImilar to gb:U05875 INTERFERON-GAMMA RECEPTOR RFTA CHAIN PRECLIDE OF ALLIMANN.	zv51b12.r1 Soares testis NHT Homo sabiens cDNA clone IMAGE-757454 5	Homo sapiens EphA4 (EPHA4) mRNA	Homo sapiens EphA4 (EPHA4) mRNA	op67h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15819393'	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sapiens mRNA for KIAA0837 protein, partial cds	Homo saplens mRNA for KIAA0837 protein, partial cds	Homo sapiens hypothetical protein FLJ20371 (FLJ20371) mRNA	Homo sapiens monocarboxylate transporter 3 (SI C16A8) mRNA	Homo saplens SH3-domain binding protein 1 (SH3RP1) mRNA	Homo sapiens SH3-domain binding protein 1 (SH3RP1) mRNA	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
	Top Hit Database Source	EST HUMAN	EST HUMAN	Π		N	LN LN	EST HUMAN		EST HUMAN	Т	HUMAN	HUMAN	Т				T HUMAN		Т			EST_HUMAN C			NT	IN IN							
	Top Hit Acession No.	AA199818.1	2.0E-56 BE064386.1	2.0E-56 BE064386.1	M26061.1	M26061.1	2.0E-56 AB037835.1		1.0E-56 AF190930.1	1.0E-56 AW 589833.1	1.0E-56 AW 589833.1	Γ		9.0E-57 AW880885.1	4758279 NT	4758279 NT	8923349 NT	05.1	8.0E-57 AW 264599.1		4758279 NT	4758279 NT	AA971001.1	11418185 NT	7.1				8923349 NT	7019528 NT	11545732 NT	11545732 NT	7657592 NT	7657592 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-56 AA1998	2.0E-56	2.0E-56	2.0E-56 M26061	2.0E-56 M26061.	2.0E-56	2.0E-56	1.0E-56	1.0E-56	1.0E-56	1.0E-56	1.0E-56 /	9.0E-57	9.0E-57	9.0E-57	8.0E-57	8.0E-57 AW8164	8.0E-57	8.0E-57	8.0E-57	8.0E-57		8.0E-57	8.0E-57 AB02317	8.0E-57 AB02317	8.0E-57	8.0E-57	8.0E-67	8.0E-57	8.0E-57	8.0E-57	7.0E-57	7.0E-57
	Expression Signal	2.94	1.19	1.19	1.02	1.02	0.93	1.08	1.44	1.79	1.79	1.52	1.86	1.97	1.17	1.17	1.55	2.91	5.79	1.63	1.02	1.02	96'0	6.35	11.76	11.76	67.78	67.76	3.32	1.27	2.02	1.39	2.02	2.02
	ORF SEQ ID NO:					22114	22684	23210		23321	23322	24606	27863		23786	23787	19790	20079	20642	21651	23060	23061	24750	25004	25915	25916	26594	26595	19790		25251	25251	22353	22354
	Exan SEQ ID NO:		12675			12215			10887	13536	13536	14838	17630	10545	14009	14009	6666	10258	10792	11673	13255	13255	14975	19624	15794	15794	18415	16415	6666	19097	19188	19188	12462	12462
	Probe SEQ ID NO:	513	718	716	2334	2334	2959	3489	964	3622	3622	4963	7780	609	4109	4109	13	294	866	1774	3335	3335	5107	5207	2888	2888	6557	6557	8774	9468	9607	9622	2592	2692

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Table 4
Single Exon Probes Expressed in Heart

		Т	T	7	Т	Т	Т	Т	7	7		$\neg$	_	<del></del> -	_	Ť	_	<u>-</u> -	<u>.</u>	_	Ť	ï	_	Ť	Ť	-	<del></del>	<del></del> -	<del></del>
Single Exort Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens NME7 (NME7), mRNA	Homo sapiens NME7 (NME7), mRNA	Homo sapiens Kruppel-like factor 8 (KI F8) mRNA	Homo sapiens phosphatid/linesitnl 4-kinasa 230 (pidk/230) mBNA	Homo sapiens phasphatidylinositol 4-kinase 230 (pi4K230) mBNA	Homo sapiens Xq pseudoautosomal region: segment 1/2	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	601471226F1 NIH MGC 87 Home serviens CDNA class (MACE:2674425 F1	Homo saplens ubleditin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	nc13f07.s1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN P46788 ans RIBOSOMAL BECTEIN S44	EST64770 Hippocampus II Homo sapiens - ONA 5' ond	783510.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263:	733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20283 :	Homo saplens celline tsA201a chloride ion current inducer actes: 1/01.	RC3-CT0254-110300-027-410 CT0254 Home seniors CONA	601589896F1 NIH MGC 7 Homo septiens cDNA clone IMA GE-20142A2 F1	42f6 Human retina cDNA randomly primed sublibrary Homo saniens cDNA	Homo sapiens hypothetical protein FLJ11656 (FLJ11656). mRNA	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA	AU117659 HEMBA1 Homo seplens cDNA clone HEMBA1001910 5	2820473.5prime NIH MGC 7 Homo sapiens cDNA clone IMAGE-2R20479 だ	2545d11,r1 Soares fetal lung NbHL19W Homo saplens cDNA clone IMAGE 308540 FT	RC0-HT0112-080999-001-C06 HT0112 Homo sapiens cDNA	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:14047473' similar to	contains Alu repetitive element contains element MER2z repetitive element ; Homo canians, chromosome, 24	Meg8h01 of Scares fatal liver and contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains t	yedsh01.11 Soares fetal liver spleen 1NFLS Home saniams CDNA clone IMAGE:125809 5:	Homo sapiens chromosome 21 segment HS21C083
JIG EVOII LIOI	Top Hit Database Source	TN	¥	Z	Į.	NT	TN	L L	EST HUMAN	L	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	Г		누		EST_HUMAN	П	HUMAN		ES HOMAN	T HIMAN		
	Top Hit Acession No.	7242158 NT	7242158 NT	TN 6005979 NT		2.1	5.1		<u> </u>	4507798	,	5.4		7.	-		3.0E-57 BE796537.1		11545798 NT	11545798 NT	.1	4.1		5.1		2.0E-57 AI 163204.2			2
	Most Similar (Top) Hit BLAST E Value	7.0E-57	7.0E-57	7.0E-57	7.0E-57 AF01287	7.0E-57 AF01287	5.0E-57	4.0E-57 AB02689	4.0E-57 BE78364	3.0E-57	3.0E-57 AA23027	3.0E-57	3.0E-57 BE67662	3.0E-57 BE67662	3.0E-57 /	3.0E-57	3.0E-57	3.0E-57 W28130.	3.0E-57	3.0E-57	3.0E-57 AU117659	3.0E-57 AW24837	3.0E-57 W23871.	3.0E-57 AW 17857	2 20 0	2.0E-57 A	2.0E-57 R07702.1	2.0E-57 R07702.1	2.0E-57 AL163283
	Expression Signal	0.92	0.92	6.49	2.17	2.17	2.39	123	96.0	0.79	11.34	2.83	1.62	1.62	1.15	115.94	3.34	3.95	1.95	1.95	4.65	20.31	5.2	2.15	7	291	0.84	0.84	6.88
	ORF SEQ ID NO:	22937			23500			23393		20558		22119	22425	22426	23230		25733	26805	26817	26818	27212	28400	24907		22453		23223	23224	24086
	Exon SEQ ID NO:	L	13136				19656	13608	L	10716	11215	12222	12535	12535	13430	13553	15630	16615	16630	16630	17019	18159	19721	19628	12563	13309	13421	13421	14303
	Probe SEQ ID NO:	3212	3212	3233	3801	3801	9934	3694	4935	787	1309	2342	2670	2670	3514	3639	5723	6736	6751	6751	7142	8279	9247	9608	2699	3392	3504	3504	4409

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		ins L1.t3 L1	TAR1.H						246 000246	THR.b3			75 015475	75 015475				2B)					/ Homo	\ Homo		
Single Extra Flobes Expressed in Rear	Top Hit Descriptor	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 6' similar to contains L1.t3 L1 repetitive element;	7n80104.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE;3570966 3' similar to contains TAR1.t1 MER22 repetitive element:	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA complete ade	Homo saplens 17-beta-hydroxysterold dehydrogenase IV (HSD1784) gene exchrs 3 and 4	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA	UFHF-BN0-akt-g-07-0-ULT NIH MGC 50 Homo sapiens cDNA clone IMAGE:3078348 51	ho32a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN:	he33d06.x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element :	601309465E1 NIH MGC 44 Home sablens CDNA clans IMAGE 3631000 E	601445948F1 NIH MGC 65 Homo saplens cDNA clone IMAGE:3850211 5	tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN:	t34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:015475 O15475	Homo saplens rulative profein O-mannos drons fasson (DONATO) DNIA	Homo saplens butative protein O-mannosyltransferese (POMIZ), mDNA	Homo saplens DHHC1 protein (LOC5/304), mRNA	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)	(MEFZB) MKNA	OH IT-BIND-all-9-TU-0-ULT I NIT MCC 60 USES CON Clane IMAGE:3079867 5'	601309465E1 NIH MGC 44 Hrms senions CNN class INACE 23079867 5	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 A	TCAAP1E1219 Pediatric acute myelogenous leukernia cell (FAB M1) Baylor-HGSC project=TCAA Homo saniens cDNA clune TCAAP1919	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo	September Liver   CART 12.19	control septembly by control prosphatase, non-receptor type 21 (PTPN21), mRNA
וופ באסוו רינסם	Top Hit Database Source	EST_HUMAN	EST HUMAN	NT.	TN	F	F	EST HUMAN	EST HUMAN		Т	T		$\Box$	NEWPORT				T CI MAN	Т	1	HUMAN	EST HIMAN		NOMO!	
Jillo	Top Hit Acesston No.	31.1	66.1	52.1	Γ	11424084 NT	11424084 NT	208.1	1.0E-57 BE043031.1				6.1		11434921	11434921 NT	7706132 NT		7.0E-58 AW 504100 1		6.0E-58 BE395061 1		50.1	5.	1143474B	
	Most Similar (Top) Hit BLAST E Value	2.0E-57 AA0161	2.0E-57 BF1152	2.0E-57	2.0E-57 AF0577	2.0E-57	2.0E-57	1.0E-57 AW503;	1.0E-57	1.0E-57	9.0E-58	8.0E-58 BE8687	8.0E-58 A179837	8 0E.58 A170837	8.0 = 58	8.0E-58	8.0E-58	1	7.0E-30	7.0E-58	6.0E-58	6.0E-58	6.0E-58 BE2424	8 0E-58		
	Expression Signal	1.43	28.14	1,29	1.71	2.22	2.22	1.12	2.08	3.47	1.43	1.41	2.62	2 62	223	2.23	2.83	9	3.25	3.25	0.9	2.96	1,19	67	13	
	ORF SEQ ID NO:			27084	27742	28729	28730	21973			25238		20389	20390	21588	21589		•	28425	28426	21997	22105	22592	22593	28000	
	Exon SEQ ID NO:	15398	15585	16894	17515	18460	18460	12071	16922	19055	19223	10512	10575	10575	11710	11710	12872	18112	18179	18179	12094	12205	12798	12798	17759	1
	Probe SEQ ID NO:	5478	5676	7017	7665	8592	8592	2184	7045	9401	9663	574	638	638	1813	1813	2945	823	8300	8300	2207	2324	2871	2871	7909	

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Table 4
Single Exon Probes Expressed in Heart

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בינון יפטר דילונסספת ווויםפון	Top Hit Descriptor	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	CM3-UM0043-240300-127-e07 UM0043 Hamo sapiens cDNA	CM3-UM0043-240300-127-e07 UM0043 Homo saplens cDNA	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	or98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'	Homo sapiens placenta-specific 1 (PLAC1), mRNA	ym51h07.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:52071 5	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA	Homo saplens hypothetical protein FLJ10826 (FLJ10826), mRNA	Homo sapiens chromosome 21 segment HS21C018	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity	conferring protein) (ATP50) mRNA	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA	Homo sapiens ublquitin-conjugating BIR-domain enzyme APOLLON mRNA complete cde	Human beta-prime adaptin (BAM/22) gene, exon 3	Human mRNA, Xq terminal portion	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA	Homo sapiens E18-55kDa-associated protein 5 (E18-AP5), mRNA	yg10e02.r1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'	Homo sapiens peptide YY (PYY) mRNA	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 51	AV712977 DCA Homo sapiens cDNA done DCAAZG04 5'	Homo saplens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds	be08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE):	601499961F1 NIH MGC 70 Homo saniens CDNA clone IMA CE 3001614 F1	
201 11000 21611	Top Hit Database Source	LN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	EST HUMAN	ΙŻ	N	Į.	ĬZ.	ΙΣ		본	NT	F	F	닐	۲	N	NT.	EST_HUMAN	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST HUMAN	
5	Top Hit Acession No.	4507334 NT	BE763984.1	AW 797948.1	AW 797948.1	AW797948.1	AW 797948.1	AA988183.1	11496282 NT	5.0E-58 H23072.1	11421330 NT	8922693 NT	5.0E-58 AL163218.2	11528293 NT	11418177 NT		4502302 NT	4504634 NT	4503648 NT	4.0E-58 AF265555.1	U36251.1	4.0E-58 D16470.1	5031660 NT	11424059 NT	R17879.1	4758981 NT	3.0E-58 BF569848.1	3.0E-58 BF569848.1	3.0E-58 AV712977.1	AF068624.1		١.	
	Most Similar (Top) Hit BLAST E Value	5.0E-58	5.0E-58 BE763	5.0E-58 AW 797	5.0E-58 AW 797	5.0E-58 AW797	5.0E-58 AW797	5.0E-58 AA988	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58		4.0E-58	4.0E-58	4.0E-58	4.0E-58	4.0E-58 U36251	4.0E-58	4.0E-58	4.0E-58	3.0E-58	3.0E-58	3.0E-58	3.0E-58	3.0E-58	2.0E-58	2.0E-58	2.0E-58 BE9071	
	Expression Signal	2.9	28.87	4.47	4.47	2:89	2.99	3.56	2.21	5.86	1.45	6.77	1.56	3.26	2.49		17.97	1.58	1.24	76.0	2.7	1.1	2.11	7.54	1.17	2.34	2.91	2.91	1.39	8.16	1206	4.42	
	ORF SEQ ID NO:		20451	20932			20933	23002		25764	25924	26721	27923					20548	21221	22297	22351	23004	23380	28798		21129	22864	22865	26031	20698		24986	
	Exan SEQ ID NO:	10261	10626	11088		11088	11088	13202	15378	15656	15800	16527	17679		19362		- 1	10709	11357	12405	12461	13204	13594	18515	10291	11273	13066	13066	15907	10850	11175	19441	
	Probe SEQ ID NO:	297	693	1176	1176	1177	1177	3281	5458	5748	5894	6647	7829	9215	9876		369	779	1452	2531	2590	3283	3680	8651	332	1367	3141	3141	6002	925	1268	5288	

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Table 4
Single Exon Probes Expressed in

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	601499961F1 NIH MGC 70 Homo sapiens cDNA clone IMAGE-3001011 F	am57e02.x1 Johnston frontal cortex Homo saplens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYMEI; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINITING DECTEIN.	Homo sapiens endocyfic recentor Endo/80 (ENIDO/80) DNIA	Hamo sapiens endocvira recentor Endo(480/ENDO) - PAIA	601890812F1 NIH MGC 17 Home seniers 2DN 4 class 140 E-4424604 F1	hm25f08.x1 NC   CGAP Thy4 Homo saniers cDNA clare INA DE 201251	Human complement component C5 mRNA, 3'end	Homo saplens NADH dehvelrozensee (rithisr invan) 4 Lets	FST36925 MAGE recentioned MACD Lives and December, 9 (22KD, 922) (NDUFB9), mRNA	EST369252 MAGE resemblences MACD Lights continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the continued to the	Homo sabiens partial AE-4 dene exone 2 to 7 and All	HV10008.X1 NCI CGAP GCB Homo seriem ANA Alma Str. 2000.	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	Expression Signal	4.42	1.74	2.76	2.76	10.79	2.26	0.93	5.45	2.17	2.17	1.07	202	96.0	96.0	0.98	0.84	0.89	4.86	6.7	3.46	27.47	1:2	1.83	6.21	5.85	7.48	2 7	- 00	242	12	
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	Exan SEQ ID NO:	19441	15628	16112	16112	18011	18209	10638	10969	11212	11212	11281	11545	12633	13409	13409	13573	14515	14775	17023	18790	12069	16638	12660	13015	14451	15130	17447	18158	10706	14571	
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Page 246 of 413 Table 4 Single Exon Probes Expressed in Heart

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	Expression Signal	12	2.16	96.9	4.12	18.6	9.87	7.68	7.68	3.71	3.71	1.17	1.07	1.85	2.03	1.82	1,23	1.23	1.64	3.9	5.01	2.47	1.84	1.84	5.14	2.75	3.58	2.46	<u>55</u>	122	8.32	2.71
	ORF SEQ ID NO:	24369			20002	21455	21456	21866	21867	22811	22812	23449	24366	24406	25786	26377	26697	26698					28341	28342	25359	24997		·	26488	27524	26488	21224
	Exan SEQ ID NO:	14571	19586	9995	10191	11584	11584	11972	11972	13017	13017	13666	14569	14619	15679	16215	16509	16509	19014	19101	17406	17853	18089	18089	18953	19611	10131	12446	16322	17318	16322	11360
	Probe SEQ ID NO:	4685	9356	6	221	1682	1682	2082	2082	3080	3090	3753	4683	4734	5772	6352	629	6629	9333	9474	7555	8003	8205	8205	9235	9756	157	2575	6463	7400	8229	1455

Page 247 of 413 Table 4 Single Exon Probes Expressed in Heart

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Page 248 of 413
Table 4
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I LIGHT I LIGHT LIGHT LIGHT	Top Hit Descriptor	ಂಪಕೆಕೆ09೨ನ Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM Mol ISF Oncaso Fobiana .	Homo sapiens profine dehydrogeness (avaline and 1995) (1995) 11	601646227F1 NIH MGC 60 Homo saniens china chara MAGE 2020 F1	Home continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continu	Histories souther carrier (SLC25A18) mKNA, complete cds; nuclear gene for mitochondrial product Historiens 41k/18 protein kinase related to not complete cds; nuclear gene for mitochondrial product	Himen has nadein mRNA 51 and	Homo sanjans chromocema 21 university and 14	Home saplens pro-alpha 200 collection (CO) 4 800	Homa saniens conficutionin reference has	Home sentens contractoring the sentence of the sentence of the sentence contractoring the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sentence of the sent	EST181949, Inrikat T.cells V. 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3'	wt05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA dane IMAGE:2506555 3'	Human endogenous retrovirus pHE.1 (ERV9)
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	Top Hit Acession No.	Aló40235.1	5174644 NT	3.0E-60 BF102612.1	2.0E-60 AY008285 1	2.0E-60 Z11694.1	M24603.1	2.0E-60 AF231919.1	AF004877.1	4503044 NT	4503044 NT	2.0E-60 AA311159.1	AA311159.1	2.0E-60 L36033.1	11991659 NT	11991659/NT	TN 2618171	2.0E-80 AF068757.1	11418068 NT	9.1	11418157 NT			1.0E-60 AL163285.2		7		4.1	8.1	78.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-60 A104023	3.0E-60	3.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60 AF0048	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-80	2.0E-60	2.0E-80/	2.0E-60	2.0E-60 AB01139	2.0E-60	1.0E-60	1.0E-60	1.0E-60 /	1 05 80 7	1.05-00	1.05-90	8.0E-01	8.0E-61 AW 0064	8.0E-61 AW0064	8.0E-61 X5/147.1
	Expression Signal	2.59	4.7	3.84	1.79	2.89	1.28	0.78	1.57	2.44	2.44	3.22	3.22	3.86	1.89	1.89	2.86	1.31	1.46	1.47	1.4	1.56	1.12	1.1	00	1 58	3 0	2 8	36.	1.39	
	ORF SEQ ID NO:	27061		27637	19810	21171	21462	23543	25941	24880	24881	26238	26239	27216	27806	27807		-			25169	20264	23531	24533		27170	20840	2007	2220	74030	1
	Exon SEQ ID NO:	16867	16954	17420	10015	11310	11593	13750	15816	15103	15103	16088	16088	17022	17582	17582	19123	19573	19209	19220	19420	10453	13738	14754	16963	16978	1000	12502	12502	12848	17[7]
	Probe SEQ ID NO:	0669	7077	7669	78	1405	1691	3839	5910	6093	6093	6222	6222	7145	7732	7732	9509	9639	9641	9658	9957	511	3827	4874	7086	7107	1083	2635	2635	2921	

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Table 4.
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo saplens PXR2b profein (PXR2b) mRNA	Homo sapiens PXR2b protein (PXR2b) mRNA	Homo sapiens PXR2b protein (PXR2b) mRNA	601300938F1 NIH MGC 21 Homo saniens cDNA doma MAAGE 2825488 ET	6013009338F1 NIH MGC 21 Homo Septiens CDNA Alone IMAGE: 3635490 5	Homo sapiens PRO2014 mRNA complete cds	601109238F1 NIH MGC 16 Homo sanians CONA class MA CE 225044E ET	nn66h09.st NCI CGAP Lart Homo sepiens ADNA character of NCI CGAP Lart Homo sepiens	AU130689 NT2RP3 Home saniers cDN4 clear NT2DP304322 E	Id-beta/829=CD795 (alternatively spliced) [himan B cells mDNA Bostol 275	Human autosomal dominant naturovetic kidness alsease arctein 4 (OKCA)	Homo sapiens general transcription factor 2J (CTF2)/ mPNA completed.	601300938F1 NIH MGC 21 Home serviers child Alexa MA CE 2555120 E1	Homo saciens protein phosphatase 1 regulatory cultural 40 (000404)	Homo sapiens chromosome 21 segment HS24 PA70	Homo sabiens mRNA for KIAA0825 profein partial cals	Homo canione aminist hote (AA) assess	Homo sepiens 959 kh confir heliusen AMI 1 - 1 Opps	AV73140 HTF Homo saniens cDNA Alone HTFABBA E.	601309785F1 NIH MGC 44 Homo sapiens china Mace pearance	Homo sapiens hypothetical protein FL/11026 /FI. 111026 / mRNA	QV3-HT0513-060400-147-d01 HT0513 Homo saplens cDNA	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA	yv53d11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to	Homo septens calmed to Colon mRNA	W03f11 f1 Soares melancade 2NkHM Home conjune and all all all and another and all all all and another and all all all and another and all all all and another and all all all all and another and all all all all all all all all all al	Homo sapiens ATPase, the transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 14 (140/146/D) (ATPANA)	AV694317 GKC Home canions anno CKCEL Coc 51	ULHF-BN0-akd-f-12-0-ULH NIH MGC 50 Home senions of the last of consensus	Homo saplens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
Top Hit Database Source	LN.	Z	F	FA	EST HUMAN	EST HUMAN	Z	EST HUMAN	EST HUMAN	EST HUMAN	Ŀ	Ę	LN L	EST HUMAN	1	NT	N.	Ę	Į.	EST HUMAN	EST HUMAN	N.	EST_HUMAN	EST_HUMAN	FST HIMAN	NICON I	T HUMAN		T HUMAN	HUMAN	
Top Hit Acession No.	T706670 NT	7706670 NT	7706870 NT	T706670 NT	6.0E-61 BE409310.1	6.0E-61 BE409310.1	6.0E-61 AF119860.1	6.0E-61 BE257400.1	AA596033.1	6.0E-61 AU130689.1	S79249.1	U24498.1	AF035737.1	BE409310.1		AL163279.2	AB020632.1	4502466 NT	5.0E-61 AJ229041.1	4.0E-61 AV731140.1	BE396279.1	8922829 NT	3E168410.1	3E168410.1	V53039.1	4758003 NT	12	11426166INT	7.1	56.1	1421778
Most Similar (Top) Hit BLAST E Value	7.0E-61	7.0E-61	7.0E-61	7.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61 AA5960	6.0E-61	6.0E-61 S79249	6.0E-61 U24498.	6.0E-61 AF0357	6.0E-61 BE4093	5.0E-61	5.0E-61 AL16327	5.0E-61 AB0206	5.0E-61	5.0E-61	4.0E-61	3.0E-61 BE39627	2.0E-61	2.0E-61 BE16841	2.0E-61 BE1684	2.0E-61 N53039	2.0E-61	2.0E-61 N39397	2.0E-61	2.0E-61 AV69431	2.0E-61 AW 5002	2.0E-61
Expression Signal	0.94	0.94	0.86	98.0	2	1.69	10.28	0.95	2.12	8.19	2.92	1.93	2.03	1.43	1.78	1.92	0.84	1.9	1.68	2.76	1.13	1.5	1.35	1.35	1.31	1.41	1.16	1.7	1.33	1.62	3.09
ORF SEQ ID NO:	19918	19919	19918	19919	20045	20564	21060	21376	21392	22987	25684	26370	26521	20564	21421	22720	22835	22890			23797	20246	20950	20951	21407	21897		25896	27279	27783	27979
Exon SEQ ID NO:	10098	10098	10098	10098	10230	10723	11206	11516	11532	13189	15583	16207	16351	10723	11558	12928	13039	13086	13809	18941	14019	10433	<del>1</del> 4	11104	11546	11998	12472	15777	17089	17557	17735
Probe SEQ ID NO:	122	122	123	123	265	794	1299	1612	1628	3266	5674	6344	6492	9417	1655	3000	3114	3161	3899	9213	4119	98	1194	194	1642	2109	2604	5871	7212	7707	7885

Page 250 of 413 Table 4 Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiane ribacomal avolata (14/00) (4/ -0)(4	Home evaluation the countries to compare the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the 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rell mouth forbat (PD40)	Homo sapiens hypothetical profein F1 120128 /F1 120129 1 - DN A	Homo sapiens hypothetical protein El 120128 (El 120128) El 120128	Homo sapiens growth hormone releasing hormone (GHRH) mRNA	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	WRO-BN0070-040400-010-bn1 BN0070 Home continue - ENTA	Homo sapiens KIAA0971 protein (KIAA0971) mRNA	Homo saplens actinin, alpha 4 (ACTN4), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens low density lipoprotein-related motein 2/1 RD2), mBNA	Homo saplens fow density linear-related process 2 (Lnt Z), IIINNA	Human kappa-immunodlobulin germling pseudosena (Chr.2), mixhb.	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	oc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POI_MI_VRK	121331 OL TOLITAN I SIN ;	AV714334 DCB Harno saplens cDNA clone DCBAMA08 5'	
gie Exon Pro	Top Hit Database Source	LN.	TN.	FN	N.T.	L	LN L	EST HIMAN	FST HIMAN	LN	EST HUMAN	4	L	EST HUMAN	EST HUMAN	N	IN IN	NT.	NT	H	LN LN	EST HUMAN	TZ	NT	N	ト		ĮN.	F	EST HIMAN	Т	$\top$	
115 H	Top Hit Acession No.	TN 92291NT		FARAR20 NIT	4 0E-64   A1 163203 2	U32657.1	6005983 NT	AW827281 1	3E386363.1	7862319 NT	BE174455.1	4759249 NT	4759249 NT	1==	4W298181.1	10.2	-	8923130	8923130	11034840 NT	1.0E-61 AF224669 1	26.1	11428892	11425578 NT	1.0E-61 AB011399.1	11430460 NT	1143046D NT	-	11418127 NT	8.0E-62 AA830420 1		7.0E-62 AV714334.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-61	1 0F-61 AI 1632	10F-61	1 0E.81	1.0E-61 U32657	1.0E-61	1.0E-61 AW827	1.0E-61 BE3863	1.0E-61		1.0E-61	1.0E-61	1.0E-61 AW 2981	1.0E-61 AW298	1.0E-61 AL1632	1.0E-61 M30135	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61 AW9997	1.0E-61	1.0E-61	1.0E-61 A	1.0E-61	1.0E-61	1.0E-61 M20809.	1.0E-61	8.0E-62	8.0E-62 A	7.0E-62 A	
	Expression Signal	7.14	0.85	132	180	76.0	4.47	1.49	1.67	0.88	1.47	0.95	0.95	7.63	7.63	0.85	7.19	1.4	1.4	3.38	3.59	2.79	6.28	1.96	1.26	2.96	2.96	1.8	8.25	0.79	1.56	1.27	
	ORF SEQ ID NO:			20524			21590	21935	22533	23055	23372	24019	24020	24422			26107	26287	26288	26800	26910		27840	28169		25002	25003	25261	25205	24138		20848	
	Exen SEQ ID NO:	18138	10373		L	11632	11711	12038	12734	13250	13585	14236	14236	14636	14636	14758	15971	16133	16133	16609	16717	17216	17613	17923	19631	19620	19620	19128	19317	14345	19417	11007	
	Probe SEQ ID NO:	8228	428	756	1377	1731	1814	2150	2804	3330	3671	4339	4339	4751	4751	4878	6124	9528	6268	6729	6838	7348	7783	8031	9110	9149	9149	9515	9805	4451	9953	1091	

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au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 nx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN au71d03.y1 Schneider fetal brain 00004 Homo saplens cDNA clone IMAGE:2781701 5' similar to gb:M37104 au71403.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 zw78e09.s1 Soares_testls_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT gg56a04.x1 Soares_testls_NHT Homo saplens cDNA clone IMAGE:1839150 3' similar to TR:O15103 wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to vf12b08.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE.2350359 3' similar to NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); wi04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE;2389251 3 wi04d02x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3 h07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981616 6 Q08379 GOLGIN-95. ;contains element MER22 repetitive element ; Top Hit Descriptor MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end Homo sapiens Xq pseudoautosomal region; segment 1/2 Homo sapiens Xq pseudoautosomal region; segment 1/2 Human zinc finger protein ZNF131 mRNA, partial cds Homo sapiens CGI-18 protein (LOC51008), mRNA Homo sapiens ryanodine receptor 3 (RYR3) mRNA Homo sapiens muscle specific gene (M9), mRNA Homo sapiens muscle specific gene (M9), mRNA 015103 HYPOTHETICAL 27.3 KD PROTEIN. Homo sapiens CGI-56 protein (CGI-56), mRNA gb:X57138_ma1 HISTONE H2B.2 (HUMAN); gb:X57138 ma1 HISTONE H2B.2 (HUMAN): Homo sapiens keratin 18 (KRT18) mRNA Single Exon Probes Expressed in Heart (AUTOANTIGEN NOR-90) P47245 NARDILYSIN; EST_HUMAN NT EST_HUMAN EST_HUMAN EST HUMAN **EST HUMAN EST HUMAN** EST_HUMAN **EST HUMAN EST HUMAN** Top Hit Database SWISSPROT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN Source 눋 11418255NT 눋 11425574 NT 4506758 NT 11425574 NT 4557887 NT 11431139 Top Hit Acession 6.0E-62 AW814393.1 5.0E-62 AW410687.1 4.0E-62|AW161479.1 4.0E-62 AW 161479.1 4.0E-62 AW 161479.1 4.0E-62 AW 161479.1 5.0E-62|AA431093.1 5.0E-62 AJ271735.1 4.0E-62 AA311281.1 5.0E-62 AJ271735.1 7.0E-62 AIZ08681.1 6.0E-62 AI762801.1 4.0E-62 AI827900.1 4.0E-62 AI827900.1 5.0E-62|A1950528.1 6.0E-62 U09410.1 7.0E-62|P17480 6.0E-62 6.0E-62 6.0E-62 4.0E-62 5.0E-62 5.0E-62 Aost Similar BLASTE (Top) Hit 0.79 3.93 3.33 3.26 3.26 2.76 1.65 4.91 3.47 4.63 1.07 3.47 4.63 0.89 1.39 1.39 6.8 6.17 4.91 Expression Signal 23184 28829 20183 22132 22133 26526 26873 27460 23090 23907 28723 27556 20597 20598 20598 22183 ORF SEO 22184 28724 20597 ÖΝΩ SEQ ID 13378 12896 13258 16355 16355 16683 10356 12236 14131 17352 18455 18455 10750 10750 10750 10750 12286 12286 13291 13273 17255 12236 11351 ë 3338 3462 8657 2969 6496 2356 2356 4233 7482 2409 3353 6496 6804 410 3372 2409 SEQ ID 8587 8587 822 822 1446 7386 823 823 ë

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Table 4
Single Exon Probes Expressed in Heart

					_		_	_		_	_	_						_				,-	4114	*****						
	Top Hit Descriptor	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA	Homo saniens uhim timemeritin andesse d. V. Akamassa (1).	Homo saplens phosphorthosy procedures a mitotage of the saplens and activities of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of the saplens of	Homo sepiens eukarvolic translation initiation factor 28 euhrm 2/hata 20/m / zirzba) - maxa	Homo sepiens eukanofic translation initiation factor 28 subumit 2 (beta, 38kD) (E17252), mKNA	Homo sapiens mRNA for KIAA1263 protein partial cide	H.sapiens flow-sorted chromosome 6 Hindlil fragment SCR-248D3	H.sapiens flow-sorted chromosome 6 Hindill fragment SCB-145D3	Homo sapiens butative nuclear profess (HRIHERS) - MENA	Homo sapiens non-histone chromosome brotein 2 (S. ceraniciae) like 4 (NIDD) 4)DNA	Home sapiens cadharin EGF (AG seven-pass G-has according 1 (NT) 21), IIINNA	Homo sapiens calcineurin binding protein 1 (KIAA0330) mBNA	Homo sapiens calcineurin binding protein 1 (KIAA0330) mBNA	Homo sabiens low density inontratein related protein 2 (I DD2). TONA	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NES)	Homo saniens mRNA for KIAA478 profess control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and cont	Homo sepiens mRNA for KIAA 4476 models models	Human cyclophilin-related processed pseudocene	ws33f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.t2 THR remetitive element	Homo satiens chromosome 21 segment HS21 Cosu	RC0-BN0284-300500-031-e05 RN0284 Home seniers conta	RC0-BN0284-300500-031-905 BN0284 Homo sapiens cDNA	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete ode	10/4 PT0757 / R84 000 / 17 / 02 BT0267 U	Homo sanjens infersectin 2 (SH2DAB) mBNA committee a	Homo sapiens ADP/ATP carrier protein (ANT-2) gans complete cds	af70e/1.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453:	DKFZp566F104_r1 566 (synonym: hfkd2) Homo saplens cDNA clone DKFZp566F104 5'
S: : 6	Top Hit Database Source	NT TN	F	Ā	LZ	N.	N.	NT	NT	L	PN PN	IN	N	Z	N.	Į.	Į.	N.	TN	Z	FST HIMAN	IN	EST HUMAN	EST HUMAN	L	EST HIMAN	LN	N.	EST HUMAN	1 1
	Top Hit Acession No.	4.0E-62 AJ243213.1	4506978 NT	11420654 NT	11421041 NT	7657057 NT	7657057 NT	AB033089.1	Z78766.1	78766.1	11418086 NT	11418192 NT	11418322 NT	11417862 NT	11417862 NT	11430460 NT	4557794 NT	3.0E-62 AB040909.1	Γ		-	2	-	-	_		1.0E-62 AF248540.1		-	
	Most Similar (Top) Hit BLAST E Value	4.0E-62	4.0E-62	4.0E-82	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62 Z78766.1	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	3.0E-82	3.0E-62	3.0E-62	3.0E-62 X52858.1	3.0E-62 A1632733	2.0E-62 AL163284	2.0E-62 B	2.0E-62 BF329911	2.0E-62 A	2.0E-62 B	1.0E-62 A	1.0E-62 L78810.1	1.0E-62 AA625207	1.0E-62 AL039044.
	Expression Signal	2.03	1.66	2.42	1.88	221	221	6.3	2.43	2.43	2.95	2.98	1.99	4.2	4.2	1.51	1.12	0.95	0.95	1.92	4.35	1.5	4.8	4.8	3.94	8.93	1.24	6.83	1.02	1.12
	ORF SEQ ID NO:		25606	25822	26273	26528	26529	27204	28505	28506	28792		25201	25198	25199	25210	19868	22728	22729	23340	27038	20969	27165	27166		-   	20791	21288	21528	22606
	Exan SEQ ID NO:	14824	15524	15709	16120	16357	16357	17011	18254	18254	18891	19578	19305	19302	19302	19335	10053	12936	12936	13554	16846	11120	16973	16973	17696	18744	10946	11431	11657	12811
	Probe SEQ ID NO:	4947	5609	5804	6254	6498	6498	7134	8377	8377	9135	9355	9743	9792	9792	9835	89	3008	3008	3640	6969	1211	7096	7096	7846	8936	1028	1526	1758	2884

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Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof.   Prof			_	$\overline{}$	_	-	-	-	_	~	_,_	-	_	_		_	<del></del> -						_	_	-									
Exon NO:         ORF SEQ ID SIGNAL         Most Similar (Top) Hit Allos         Top Hit Accession Allos         Allos         Allos         Allos         Allos         Allos         Allos         Allos         Allos         Allos	oes cypressed in near	Top Hit Descriptor	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA	298910.s1 Soares fetal heart NbHH19W Home seniens cDNA clume IMAGE 200774 9	Zg89f10.s1 Soares fetal heart NbHH19W Homo saniens cDNA clone IMACE-700774 2	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9	aa33d08.s1 NCI CGAP GCB1 Homo septens cDNA clone IMAGF-815055.3'	H.sapiens flow-sorted chromosome 6 Hindill fragment. SC60A14D8	Homo saplens cadherin EGF LAG seven-pass G-twe recentor 1 (CEI SR1) mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2). mRNA	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA	C18159 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GFN-558C10 5'	Homo sapiens mRNA for KIAA0350 protein, partial cds	Homo saplens mRNA for KIAA0350 protein, partial cds	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for PkB kinase	Homo saplens nucleoportn 88kD (NUP88), mRNA	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSE2) mRNA	Homo saplens monoamine oxidase A (WAOA) nuclear nane encoding mitochandatal sector	Homo sapiens II.2-inducible T-cell kinase (TTK), mRNA	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21 C068	wm55g11x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'	nc63f02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUMAN):	Homo sapiens chromosome 21 segment HS21C078	CM3-BT0595-190100-072-a09 BT0595 Homo saniens cDNA	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE: 2712482 3	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE-2712482 3	Homo sapiens mRNA for KIAA0717 protein, partial cds
Exam NO: 16102         ORF SEQ 225261         Expression Signal         (Top) Hit Value         Top Hit Acess No: 1.0E-62         Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess Acess	אופ באטון רוט	Top Hit Database Source	LN L	EST HUMAN	EST HUMAN	LN TN	N	NT	E	EST HUMAN	TN	K	TN	EST HUMAN	EST HUMAN	N-	N F	F	NT.	N-	NT	     	FN	TN.	TN.	TA.	EST_HUMAN	EST HUMAN	N-	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę
Exon No:         ORF SEQ Expression (Total Signal No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:         Mossional No:			8923201		AA722878.1	7662289	7662289		_			11418322	11430460	05.1	_			11418185	1	11426985	11421160	4557734	5031810	Γ	9.1	3.2	۲.		8.2	72.1	72.1	09.1		П
Exam         ORF SEQ         Expression           NO:         ID NO:         Signal           14321         24108         1.32           16102         26251         2.17           16102         26251         2.17           16102         26251         2.17           16102         26251         2.17           1716         27331         1.53           1716         27331         1.81           17300         27507         2.81           16561         28845         2.13           16730         27507         2.81           16794         20109         2.14           1730         27507         2.81           1679         2.009         2.3           1679         2.009         2.3           1670         2.009         2.14           1270         2.200         2.17           1672         2.6017         1.52           1672         2.6017         1.52           1672         2.6017         1.52           1672         2.6017         1.78           1672         2.6017         1.78           1672         2		Most Similar (Top) Hit BLAST E Value	1.0E-62	1.0E-62/	1.0E-62	1.0E-62	1.0E-62	1.0E-62	1.0E-62)	1.0E-62	1.0E-62	1.0E-62	1.0E-62	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	8.0E-63	8.0E-63	8.0E-63 A	8.0E-63	8.0E-63	7.0E-63	6.0E-63 A	4.0E-63	4.0E-63 A	4.0E-63	4.0E-63 A	4.0E-63 A	3.0E-63
Exan SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		<del></del>	1.32	2.17	2.17	1.53	1.53	1.81	1.81	2.81	2.13	1.94	2.3	2.14	1.51	7.42	7.42	6.51	1.31	4.39	1.37	1.52	2.17	3.81	3.81	3.37	1.78	40.61	0.98	2.86	2.86	2	2	1.97
		ORF SEQ ID NO:	24108	26251	26252	27310	27311	27331	27332	27507	28845		25206	20109		23638	23639	29106	25104	26281	26917	22077	22102	23134	23135	23843			23001	25905	25906	28611	28612	21666
Probe SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Exon SEQ ID NO:		1		17116	17116	17139	17139	17300	18561	19199	19322	10294	12179	13863	13863	15088	15274	16127	16724	12178	12203	13332	13332	14068	10837	15196	13200	15785	15785	18347	18347	11788
		Probe SEQ ID NO:	4426	6236	6236	7239	7239	7262	7262	7512	8673	9623	9815	335	2297	3955	3955	5210	5354	6262	6845	2296	2322	3415	3415	4168	913	5274	3279	5879	5879	8474	8474	1893

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	ON A close o middle		Value of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state		MA OF CAST OF	OII BINAGE: 2101020 5:	B 1846 CE 204053 5	AB4) mBMA	DNA class MACE: 2002 FI	MAACE SESSON EI	וויואו לבני אסטטטענים איני איני איני איני איני איני איני א			wb61e07.x1 NCI_CGAP_GC6 Homo septems cDNA done IMAGE:2309220 3' similar to gb:M16182 BETA-	WESTED XI NOI CGAP GOS Home seniors of NA Alma MAICE (2002) 2: 1: 1	ine invade: 2509220 3 similar to gb:M15182 BETA-	ma 1140 CE 25500 400 01	THE INVINCE COSTAGE OF	GIB INVACE 2028430 3		JRNA complete cale	SNA SAMPHER CAS	NA	A)	nBNA complete ada	יייייייייייייייייייייייייייייייייייייי			SALA	With the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of		VRD) nene complete ede	in a ferre, complete cas
Ilian III passardy a sant I may call	Topt	HSCZVD111 normalized infant brain cDNA Homo saniens cDNA clarace zada	QV0-ST0215-060100-083-b09 ST0215 Home series SANA	Homo saplens chromosome 21 seriment HS21C047	Homo sapiens chromosome 21 sogment DC21/2007	Im50b07.x1 NCI CGAP Kid41 Home carions - DNA class 1844 OFF-04 CAP CO	601155232F1 NIH MGC 21 Home seniens china MAGE 213191925	601508968F1 NIH MGC 71 Homo saplens CDNA clone IMAGE 200202 ET	Homo sapiens Ran GTPase activating protein 1 (BANGABA) BNA	Vb98b02.r1 Strategene lung (#937210) Home seniers CDNA class (MACE 2752 75 5	601311455F1 NIH MGC 44 Homo saniers COMA class INVACE 2523274 El	Homo sabiens thimet oligopentidese 1 (THOP1) went	Homo sapiens thimef oligonentidese 1 (THOP1) mBNA	Homo sapiens EWS dar22 mp2 and ham22 comes	wb61e07x1 NCI_CGAP_GC6 Homo septimes cDN/	wb51e07.x1 NCI CGAP GC6 Homo sanians clink	GLUCURONIDASE PRECURSOR (HUMAN)	wv13e03.x1 NCI CGAP Brn23 Homo saniens chNA clare 11/1/ACE:25:20/122 21	WY13e03.X1 NCI CGAP Bin23 Home sariens CDNA clara MAGE: 252436 3	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA complete cata	Homo sapiens mesenchyme homeo box 1 (MEOX1) mRNA	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA	Homo sapiens progressive ankylosis-like protein (ANK) mRNA complete and	trkC [human, brain, mRNA, 2715 nt]	Homo sapiens stromal antigen 3 (STAG3) mRNA	Homo sapiens stromal antigen 3 (STAG3), mRNA	Homo sapiens interleukin 10 recentor beta (II 10RB) mBNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens phosphodiucomutase-related protein (PGMRP)	Home costs
מון ווסעד סופ	Top Hit Database Source	EST HUMAN	EST HUMAN	N	N.	EST HUMAN	EST HUMAN	EST HUMAN	N-	EST HUMAN	EST HUMAN	L L	IN	NT	FOT LIMAN	NUMBER OF THE	EST HUMAN	EST HUMAN	EST HUMAN	N L	N	N	L	NT	TV	IN	IN	Þ	F	5	NT	L	N	NT.
5	Top Hit Acession No.	F08485.1	AW 582266.1	1.0E-63 AL163247.2	1.0E-63 AL163207.2	9.0E-64 AI478186.1	8.0E-64 BE280796.1	8.0E-64 BE885755.1	11418177 NT	T60651.1	BE394321.1		45074901NT	1	-		AJ651992.1	6.0E-64 AW026445.1				-	11525879 NT	11525879 NT	1420555	3.1	S76475.1	11420197 NT	11420197 NT	11526198 NT	9.1	1.		
	Most Similar (Top) Hit BLAST E Value	1.0E-63 F08485.	1.0E-63 AW 5822	1.0E-63	1.0E-63	9.0E-64	8.0E-64	8.0E-64	8.0E-64	8.0E-64 T50651.1	7.0E-64 BE39432	7.0E-64	7.0E-64	7.0E-84 Y07848.	B 0F-64 AIR5190		6.0E-64 AI651992	6.0E-64 /	6.0E-64	6.0E-64 Y18933.1	6.0E-64 Y18933.1	6.0E-64 M13975	6.0E-64	6.0E-64	6.0E-64	6.0E-64 AF27475	6.0E-64	6.0E-64	6.0E-64	6.0E-64	5.0E-64 AF23191	5.0E-64 AF23191	5.0E-64 L40933.1	5 0F-64   40933 4
	Expression Signal	2.91	1.39	2.3	3.02	4.78	7.89	3.16	2.61	2.56	0.99	2.44	2.44	2.13	1.7		1.7	3.7	3.7	2.64	2.64	4.41	2.58	2.58	7.8	2.06	2.34	7.57	7.57	4.08	2.44	2.44	2.42	2.42
	S C					26661		25747				24303	24304	27844	21463	-	21464	22801	22802	25433	25434	25444	26312	26313	27451	27538	27669	28287	28288	25321	20574	20275	21167	21168
	S		15443	16813	19633	16471			18841	18875	13402	14513	14513	17616	11594		11594	13011	13011	15375	15375	15384	16157	16157	17245	17332	17455	18039	18039	18967	10732	10732	11307	11307
	Probe SEQ ID NO:	4246	5526	6935	9879	6591	1030	5733	8028	9111	3486	4625	4625	7766	1692		1692	3084	3084	5454	5454	5464	6293	6283	3/8	7472	26 26	8151	8151	3262	803	88	1402	1402

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Human (/3)mbt protein homolog mRNA, complete cde	Homo sapiens KIAA0618 gene product /KIAA0648 mRNA	Homo saplens KIAA0618 cene product (KIAA0618) mRNA	Homo sapiens putative transcription factor CR53 (CR53) mBNs and adv	RC3-ST0197-120200-015-a03 ST0197 Home sahiens cDNA	RC3-ST0197-120200-015-a03 ST0197 Homo saniens cDNA	C18895 Human placenta cDNA (TFuïwara) Homo saniens cDNA clone GEN 560502 51	601569565F1 NIH MGC 7 Home septems CDNA clane IMAGE 3049577 E1	AV711714 DCA Homo saplens cDNA clone DCAAMCM 5	AV711714 DCA Homo sapiens cDNA clone DCAAMCA1 5'	H.sapiens isoform 1 gene for L-type calcium channel exem 28	RC8-FN0019-290600-011-G-11 FN0019 Home serviers ANA	Homo sapiens goldi matrix nrotein GM430 (GOI CA2) TDMA	Homo saplens gold matrix protein GM130 (GOL GA2) mBNA complete da	bb/2k12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ	PROTEIN HOWOLOG 2 (HUMAN);	bb/2n12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN):	Homo sapiens chromosome 21 segment HS24Ch48	Homo sapiens chromosome 21 segment HS24 Code	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21C046	Hamo sapiens chromosome 21 segment HS21C027	at09d08.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE-1034151 2	Homo saplens elF4E-like cap-binding protein (4EHP) mRNA	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element	Hamp sapiens changeans 21 serment HS34CA48	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2),	EST370245 MAGE recommend MAGE L	EST370215 MAGE resequences, MAGE Home series only	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
Jie Exon Proi	Top Hit Database Source	L	TN	N.	TN.	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	LN LN	EST HUMAN	¥	LN N	Cot Children	ES HOMAN	EST_HUMAN	N	NT	N.	NT	NT	EST_HUMAN		FST HIMAN	TN TN	N-		T HUMAN	Т	П
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	Most Similar (Top) Hit BLAST E Value	5.0E-64	5.0E-64	5.0E-64	5.0E-64 AF017	4.0E-64	4.0E-64	3.0E-64	3.0E-64 BE794	3.0E-64 AV711	3.0E-64 AV711	3.0E-64	3.0E-64	3.0E-64 AF2489	3.0E-64 AF2489	3 DE 64	200	3.0E-64	3.0E-64	3.0E-64	3.0E-64 /	3.0E-64	3.0E-64	2.0E-64 /	2.0E-64	2.0E-84	2.0E-64	2.0E-64	2.0E-64	2.0E-64 AW958	2.0E-64 AW958	2.0E-64
	Expression Signal	1.67	2.66	2.66	5.61	3.9	3.9	3.85	0.95	1.51	1.51	1.34	3.39	1.81	1.81	13	2	1.3	1.26	1.26	1.76	1.76	4.59	0.94	1.32	1.78	3.03	3.03	2.56	1.33	1.33	2.62
	ORF SEQ ID NO:	21457	21235									25713	25942	27005	27006	27016		27017	27497	27498	28703	28704	29040	20831	21137		22252	22253	22823	23416	23417	25662
	Exen SEQ ID NO:	11585	11370	11370	13787		- 1	12039	13140	13313	13313	15611	15817	16811	16811	16824		16824	17289	17289	18434	18434	18746	10988	11282	12354	12359	12359	13027	13631	13631	15565
	Probe SEQ ID NO:	1683	2796	2796	3876	8188	8188	2151	3216	3396	88	5703	5911	6933	6833	6946		6946	7422	7422	8565	8265	888	10/2	1376	2478	2484	2484	3101	3719	3719	5653

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Table 4
Single Exon Probes Expressed in Heart

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Story of the second in Figure 1	Top Hit Descriptor	Homo sabiens anaicocleiin 4 (ANG4) mRNA norial Ac	1802123474F1 NIH MGC 56 Homo sanians cityla class (17300005 F)	0229b03.x1 Sogres total fetus Nb2HF8 ow Home senions a DNA Aless IMA DE 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRACT OF 12 CONTRA	H. 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DNA	AV721898 HTB Homo sapiens cDNA clone HTBR2708 5'	ng6d10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN):	xc07b09.x1 NCI_CGAP_Co21 Homo sepiens cDNA clone IMAGE:2683545 3' similar to TR:Q63306 Q63306	LONG IN IERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S. contains L1 b2 L1 renetitive element	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMACE-7737477 2	zw53b06.s1 Soares_total_fetus_NbZHF8_9w Homo sapiens cDNA clone IMACE:773727 2	601340485F1 NIH MGC 53 Homo sapiens cDNA clone IMAGE 3682677 5	Homo sapiens chromosome 21 segment HS21C010
200	Top Hit Database Source	N	EST HUMAN	EST HUMAN	Į.	EST HUMAN	EST HUMAN	EST HUMAN	F	EST HUMAN	NT	EST HUMAN		FZ.	N	NT	LN	LN.	N.	T HUMAN		T	7	EST_HUMAN		П			EST_HUMAN	П
	Top Hit Acession No.	2.0E-64 AF113708.1	2.0E-64 BF668537.1		2.0E-64 M77185.1	2.0E-64 BF528114.1	2.0E-64 AI922911.1	2.0E-64 Al922911.1	8567387 NT	2.0E-64 H55162.1	2	1.0E-64 Al929419.1		1.0E-64 AF196779.1	1.0E-64 AF228527.1	1.0E-64 AF228527.1		(89211.1	(89211.1	9.0E-65 BF330676.1	1929244.1	7.0E-65 BE081653.1	6.0E-65 AV721898.1	6.0E-65 AA550929.1	A DE AS AWORDS	T		_	_	2
	Most Similar (Top) Hit BLAST E Value	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	1.0E-64	1.0E-64		1.0E-64	1.0E-64	1.0E-64	1.0E-64	9.0E-65 X89211.1	9.0E-65 X89211.1	9.0E-65	8.0E-65 A1929244.	7.0E-85	6.0E-65	6.0E-65	80 20	0.00	6.0E-65 AA427878.	6.0E-65 AA427878.	6.0E-65 BE567816.	6.0E-65 AL163210.
	Expression Signal	1.3	4.97	1.31	3.86	2.85	6.4	6.4	1.73	2.68	1.74	5.88		5.61	1.32	1.32	1.62	0.93	0.93	15.1	10.83	2.05	1.52	8.32	0.50	707	4.25	4.25	6.18	4.76
	ORF SEQ ID NO:		25938		26060	28279	28534		25347		20039	21508		23188	23248	23249		22017	22018		28903	27936	20801		27150	2707E	6/7/2	27276	28375	28892
	_ O					18032		18282	18921	19195	10224	11641		13382	13452	13452	18904	12115	12116	18635	18613	17691	10958	11776	16957	47000	000/-	980/1	18127	18602
	Probe SEQ ID NO:	6783	5906	5976	6024	8144	8406	8406	9182	9617	258	1740		3466	3536	3536	9154	2230	2230	8822	8789	7841	\$	1880	7080	7200	2007	200	8247	8/8/

Page 258 of 413 Table 4 Single Exon Probes Expressed in Heart

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Oligie Lyon Flobes Expressed III near	Top Hit Descriptor	Homo saplens KE03 protein mRNA, partial cds	Homo sapiens KIAA0158 gene product (KIAA0156), mRNA	Homo saplens KIAA0156 dene product (KIAA0156) mRNA	Homo sapiens hPAD-colony10 mRNA for pentidylarmining deimingse has I commission and	Homo sapiens ubiquitin specific protease 13 (isopertidase T-3) (i (SP43) mRNA	Homo sapiens ubiquitin specific protease 13 (Isonentidase T-3) (11SP13) mRNA	DKFZp761G108_r1 761 (synonym; hamy2) Homo sapiens cDNA_clone DKFZp761G108_F7	qm46e01.x1 Soares, placenta, 8to9weeks, 2NbHP8to9W Homo sapiens, cDNA cirne, IMAGE-1864800 2	am46e01.xf Soeres placente Broweeks 2NhHDRhow Home and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant	Homo saniens franile X mental reterdation autocomed to the National April 1991800 3	Homo sapiens ribosomal protein i 34 (RPI 34) mRNA	hu25e04.x1 NCI CGAP Mel15 Homo saniens cDNA clene MAACE:3474402.21	hu25e04.x1 NCI_CGAP_Me115 Homo sapiens cDNA clone IMAGE:3174102.3	Homo sapiens low density liboprotein recentor related undein-delated in time (1 popular)	Homo sapiens low density lipoprotein receptor related protein-deleted in himor (LIDDAIT) - BALA	Homo sapiens mRNA for KIAA1267 profein, parfial cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA	Homo saplens WEE1 gene for protein kinase and partial 7NF143 name for zinn finner transceinden forden	Homo sapiens PRO1474 mRNA, complete cds	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1) mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	H. sapiens HZF9 mRNA for zinc finger protein	ov23/03.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element	Homo sapiens faminin, beta 1 (I AMB1) mRNA	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element :	Homo septiens rab6 GTP assa activating probin /CAD and extraction	601479688F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
BIG LAUII P10	Top Hit Database Source	NT	IN	TN	N	NT	NT	EST HUMAN	EST_HUMAN	EST HUMAN	LZ	LZ LZ	EST HUMAN	EST HUMAN	₽ F	LN	N.	TN	TN	TN	Z	FN	NT	NT	EST HUMAN	4504950 NT	EST HUMAN	L L	EST HUMAN
	Top Hit Acession No.	5.0E-65 AF064604.1	7661951 NT	7661951 NT	180	4507848 NT	4507848 NT	AL120419.1	4.0E-65 Al266468.1	4.0E-65 AIZ66468.1	4826735 NT	4506636 NT	4.0E-65 BE221469.1		5269	, 9055269 NT	4.0E-65 AB033093.1	4.0E-65 AB033093.1	5780	16.2	46.1	4826735 NT	11430460 NT	1	3.0E-65 A1000692.1	4504950	VI000692.1	6912385 NT	36.1
	Most Similar (Top) Hit BLAST E Value	5.0E-65	5.0E-65	5.0E-65	5.0E-65 AB0337	5.0E-65	5.0E-65	4.0E-65 AL1204	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65 /	4.0E-65	4.0E-65	4.0E-65 AJ27754	4.0E-65 AF1198	4.0E-65	4.0E-65	3.0E-65 X78932	3.0E-65/	3.0E-65	3.0E-65 A100069	3.0E-65	3.0E-65 BE78730
	Expression Signal	0.91	1.62	1.62	1.02	1.91	1.91	1.09	1.56	1.56	1.88	8.28	1.03	1.03	0.95	0.95	3.93	3,93	2.29	2.17	7.47	1.34	1.58	5:37	1.14	1.39	0.98	1.41	1.43
	ORF SEQ ID NO:	20362			21898			19975	20491										26304		28579	20822	25152		21557	22962	23361	24228	27876
	Exan SEQ ID NO:	10551	11238	11238	11999	13141	13141	10158	10660	10660	10978	11375	12171	12171	15005	15005	15648	15648	16149	17870	18320	10978	19434	12646	11679	13162	13574	14444	17643
	Probe SEQ ID NO:	615	1331	1331	2110	3217	3217	186	728	728	1062	1470	2288	2288	5138	5138	5740	5740	6285	8020	8446	9471	9975	1212	1780	3239	3660	4551	7793

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Table 4
Single Exon Probes Expressed in Heart

Probe NO:         Exor NO:         ORF SEQ ID ID NO:         Expression Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal	Top Hit Acessian No. S AA430006.1 BE680294.1 BE568373.1 BF576922.1 AK024463.1 AK024463.1 AK024463.1 AK024463.1 AK024463.1 BF266086.1 BF266086.1 BF266086.1 BF266086.1	Top Hit Database Scurce THUMAN THUMAN THUMAN THUMAN THUMAN	Zw65a06.r1 Scares_testis_NHT Homo sepiens cDNA clone IMAGE:781042 5' 602155062F1 NIH_MGC_83 Homo sepiens cDNA clone IMAGE:359596 5' 601190883F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3534741 5' 602134359F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3534741 5' 602134359F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4289295 5' Homo sepiens mRNA for FLJ00056 protein, partial cds Homo sepiens mRNA for FLJ00056 protein, partial cds Homo sepiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA EST178755 Colon carcinoma (HCC) cell line Homo sepiens cDNA 5' end similar to similar to endogenous retrovinus 601854033F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:4026501 5' Homo sepiens pultative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo sepiens mRNA for KIAA1513 protein, partial cds hyzkang vi NCI CGAP GCS Homo sepiens cDNA clone IMAGE:300889 2' Homo sepiens mRNA for KIAA1513 protein, partial cds
17877         28119         9.69           13277         23078         6.27           16039         26247         23.12           17010         27202         1.27           17010         27202         1.27           17010         27203         1.27           17010         27203         1.27           17010         27203         1.27           17010         27203         1.27           10069         2.8189         2.85           10470         20282         1.32           10470         20282         1.32           13246         23052         0.89           13826         23606         2.13           14012         23789         2.37           14012         23789         2.37           16681         26870         1.58           16721         26871         1.58           16721         26816         2.38           17009         27201         1.76           17092         27282         1.62           17092         27283         1.62           17099         27283         1.62           17099         <	6.1 4.1 2.1 3.1 3.1 3.1 14.19247 4.1 6.1 6.1 6.1	T HUMAN T HUMAN T HUMAN T HUMAN	zw65a06.r1 Scares testis NHT Homo sapiens cDNA clone IMAGE:781042 67 602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295866 57 601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:4289296 57 602134359F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:4289296 57 Homo sapiens mRNA for FLJ00056 protein, partial cds Homo sapiens mRNA for FLJ00056 protein, partial cds Homo sapiens sW I/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 601763488F1 NIH_MGC_27 Homo sapiens cDNA clone IMAGE:4026501 57 Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo sapiens mRNA for KIAA1513 protein, partial cds homo sapiens mRNA for KIAA1513 protein, partial cds
13277         23078         6.27           15843         4.55           16099         26247         23.12           17010         27202         1.27           17010         27202         1.27           17010         27203         1.27           17010         27203         1.27           18874         4.15           19504         2.37           10069         1.06           10470         20282         1.32           13246         23052         0.89           13826         23607         2.13           14012         23789         2.37           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26814         2.38           17099         27201         1.76           17092         27283         1.62           17093         27283         1.62           17099         27283         1.62           17099         27283         1.62	4.1 2.1 2.1 3.1 3.1 1419247 14.1 6.1 6.1 6.1	T HUMAN T HUMAN T HUMAN T HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5' 601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:4289295 5' 602134359F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:4289295 5' 602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5' Homo sapiens mRNA for FLJ00056 protein, partial cds Homo sapiens mRNA for FLJ00056 protein, partial cds Homo sapiens SWUSNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA  EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus  801763493571 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4026501 5' Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo sapiens mRNA for KIAA1513 protein, partial cds  Homo sapiens mRNA for KIAA1513 protein, partial cds  Homo sapiens mRNA for KIAA1513 protein, partial cds
15843         4.55           16099         26247         23.12           17010         27202         1.27           17010         27203         1.27           17010         27203         1.27           18874         4.15         2.37           10069         1.06         1.06           10470         20282         1.32           11888         21781         0.91           13246         23052         0.89           13826         23607         2.13           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26814         2.38           16721         26815         2.38           17099         27281         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	3.1 2.1 3.1 3.1 1419247 4.1 6.1 6.1 6.1	T HUMAN T HUMAN T HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5' 602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5' Homo sapiens mRNA for FLJ00056 protein, partial cds Homo sapiens mRNA for FLJ00056 protein, partial cds Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4026501 5' Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo sapiens mRNA for KIAA1513 protein, partial cds homo sapiens mRNA for KIAA1513 protein, partial cds
16099         26247         23.12           17010         27202         1.27           17010         27203         1.27           17010         27203         1.27           18874         4.15           19504         2.37           10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23052         0.89           13826         23607         2.13           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26814         2.38           16721         26815         2.38           17099         27281         1.62           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62	2.1 3.1 1419247 14.1 6.1 6.1 6.1	T HUMAN T HUMAN	Homo sapiens mRNA for FLJ00056 protein, partial cds  Homo sapiens mRNA for FLJ00056 protein, partial cds  Homo sapiens mRNA for FLJ00056 protein, partial cds  Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA  EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovinus  801854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4026501 5'  Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA  Homo sapiens mRNA for KIAA1513 protein, partial cds  Homo sapiens mRNA for KIAA1513 protein, partial cds  Homo sapiens mRNA for KIAA1513 protein, partial cds
17010         27202         1.27           17010         27203         1.27           17010         27203         1.27           18874         4.15           19504         2.37           10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23605         2.13           13826         23607         2.13           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26814         2.38           17099         27281         1.62           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	3.1 3.1 1419247 4.1 6.1 7657495 6.1	T HUMAN T HUMAN	Homo saplens mRNA for FLJ00056 protein, partial cds  Homo saplens mRNA for FLJ00056 protein, partial cds  Homo saplens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA  EST178755 Colon carcinoma (HCC) cell line Homo saplens cDNA 5' end similar to similar to endogenous retrovinus  801854033F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4026501 5'  Homo saplens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA  Homo saplens mRNA for KIAA1513 protein, partial cds  homo saplens mRNA for KIAA1513 protein, partial cds
17010         27203         1.27           17039         28189         2.85           18874         4.16           19504         2.37           10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23605         2.13           13826         23607         2.13           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26815         2.38           17009         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	3.1 1419247 4.1 6.1 7657495	T HUMAN T HUMAN	Homo sapiens mRNA for FLJ00056 protein, partial cds  Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA  EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovinus  801854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4026501 5'  Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA  Homo sapiens mRNA for KIAA1513 protein, partial cds  homo sapiens mRNA for KIAA1513 protein, partial cds
17939         28189         2.85           18874         4.15           19504         2.37           10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23605         2.13           13826         23606         2.13           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26914         2.38           17099         27281         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	1419247 4.1 6.1 7657495 6.1	T HUMAN T HUMAN	Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovinus 601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4026501 5' Homo sapiens putative Rab5 GDP/GTP enchange factor homologue (RABEX5), mRNA Homo sapiens mRNA for KIAA1513 protein, partial cds harvano or Nich Cab GDS Home canings ANA changeline in the capiens of the control of the control of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of the capiens of th
18874     4.15       19504     2.37       10069     1.06       10470     20282     1.32       11888     21781     0.91       13246     23652     0.89       13826     23606     2.13       13826     23607     2.13       14012     23789     2.37       14012     23789     2.37       14012     23780     2.37       16681     26870     1.58       16721     26871     1.58       17009     27201     1.76       17092     27282     1.62       17099     27283     1.62       17099     27283     1.62       17099     27283     1.62       17099     27283     1.62       17099     27283     1.62	4.1 6.1 4.1 7657495 6.1	T HUMAN T HUMAN	FEST 1987 S. Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus servicional (HCC) cell line Homo sapiens cDNA clone IMAGE:4073769 5' 801763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5' Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo sapiens mRNA for KIAA41513 protein, partial cds
18874         4.15           19504         2.37           10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23052         0.89           13826         23606         2.13           14012         23789         2.37           14012         23789         2.37           16681         26870         1.58           16721         26871         1.68           16721         26814         2.38           17009         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62	6.1 4.1 7657495 6.1	T HUMAN	retrovirus  801854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'  801763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'  Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA  Homo sapiens mRNA for KIAA1513 protein, partial cds  522400 val NC1 CGAP GCS Home capiens cDNA clone IMACE:308888 2'
19504         2.37           10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23052         0.89           13826         23606         2.13           14012         23789         2.37           14012         23789         2.37           16681         26871         1.58           16721         26814         2.38           16721         26914         2.38           17099         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	6.1 4.1 7657495 6.1	T HUMAN	801854033F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4073769 5' 801763488F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:4026501 5' Homo saplens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo saplens mRNA for KIAA1513 protein, partial cds
10069         1.06           10470         20282         1.32           11888         21781         0.91           13246         23052         0.89           13826         23606         2.13           14012         23789         2.37           14012         23789         2.37           16681         26870         1.58           16721         26871         1.68           16721         26914         2.38           17099         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	4.1 7657495 6.1	T_HUMAN	801763488F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:4026501 57  Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA  Homo sapiens mRNA for KIAA1513 protein, partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial close the partial cl
10470         20282         1.32           11888         21781         0.91           13246         23052         0.89           13826         23606         2.13           13826         23607         2.13           14012         23789         2.37           16681         26870         1.58           16721         26871         1.68           16721         26914         2.38           17099         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	7657495 6.1		Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA Homo sapiens mRNA for KIAA1513 protein, partial cds
11888         21781         0.91           13246         23052         0.89           13826         23606         2.13           13826         23607         2.13           14012         23789         2.37           14012         23780         2.37           16681         26870         1.58           16721         26914         2.38           17099         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	6.1		Homo sapiens mRNA for KIAA1513 protein, partial cds
13246     23052     0.89       13826     23606     2.13       13826     23607     2.13       14012     23789     2.37       14012     23790     2.37       16681     26870     1.58       16721     26914     2.38       16721     26914     2.38       17099     27201     1.62       17092     27283     1.62       17099     27283     1.62       17099     27283     1.62       17099     27283     1.62			1724and or NCI COAD GCS Home canions of NA clone IMAGE: 3208999 2
13826         23606         2.13           13826         23607         2.13           14012         23789         2.37           14012         23780         2.37           16681         26870         1.58           16721         26914         2.38           17009         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         1.62	1.0E-65 BE466681.1 E	EST_HUMAN I	COODE TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
13826         23607         2.13           14012         23789         2.37           14012         23790         2.37           16681         26870         1.58           16721         26914         2.38           16721         26915         2.38           17009         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62	:-65 4504082 NT		Homo sapiens glypican 4 (GPC4) mRNA
14012         23789         2.37           14012         23790         2.37           16681         26870         1.58           16681         26871         1.68           16721         26914         2.38           17009         27201         1.76           17092         27283         1.62           17092         27283         1.62           17099         27283         1.62	:-65 4504082 NT		Homo sapiens glypican 4 (GPC4) mRNA
14012     23790     2.37       16681     26870     1.58       16681     26871     1.68       16721     26914     2.38       1701     27201     1.76       17092     27282     1.62       17092     27283     1.62       17099     27283     1.62       17099     27283     1.62			wx09c09.x1 NCI_CGAP_Gas4 Homo sapieris cDNA clone IMAGE:2543152.3'
16681         26870         1.58           16681         26871         1.68           16721         26914         2.38           17009         27201         1.76           17092         27282         1.62           17092         27283         1.62           17099         27283         1.62           17099         27283         2.83			wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
16681     26871     1.68       16721     26914     2.38       16721     28915     2.38       17009     27201     1.76       17092     27282     1.62       17092     27283     1.62       17099     27283     1.62			QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
16721     26914     2.38       16721     26915     2.38       17009     27201     1.76       17092     27282     1.62       17092     27283     1.62       17099     2.83			QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
16721     26915     2.38       17009     27201     1.76       17092     27282     1.62       17092     27283     1.62       17099     2.83		EST_HUMAN /	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5
17009     27201     1.76       17092     27282     1.62       17092     27283     1.62       17099     2.83			AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
17092     27282     1.62       17092     27283     1.62       17099     2.83	1.0E-65 BF698707.1   E	EST_HUMAN 6	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5
17092 27283 1.62 17099 2.83	1.0E-65 AU129040.1   E	EST_HUMAN /	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5
17099 2.83	1.0E-65 AU129040.1	EST_HUMAN /	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
	:-65 11431994 NT		Homo sapiens inosital 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
7456 17265 27469 6 1.0E-4	1.0E-65 Al191716.1 E	EST HUMAN	qd66e02x1 Soares _testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN);contains MER19.11 MER19 repetitive element :
7687 17537 27763 1.25 1.0E-4	3.1	EST_HUMAN A	AU153793 NT2RP3 Homo saplens cDNA clone NT2RP3004016 3'
8042 17933 28181 2.23 1.0E-(	1.0E-65 M26167.1		Human platelet factor 4 varation 1 (PF4var1) gene, complete cds
18046 28298 12.99	4506660		Homo sapiens ribosomal protein L7a (RPL7A) mRNA
8473 18346 28610 2.18 1.0E-4	1.0E-65 BF698707.1 E	T HUMAN	602126239F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE:4283313 5

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Table 4
Single Exon Probes Expressed in Heart

	iptor	MAGE:2237170 3' similar to gb:L15533_ma1	SNA	ther 1 (CEI SR4) mBNA	PNA			SOH4) mBNA	OH) mena	· VANILLAND	A2) mBNA complete ada	A2) mRMA complete cus	MADE: 787048 F	A	MAGE:2449597 3' similar to WP:F15G9.4A	MAGE:2449597 3' similar to WP:F15G9.4A	MAGE:2449597 3' similar to WP:F15G9.4A			(3) mRNA	you (Fmr1) mBNA				AD+ dependent), methenytetrahydrofolate				RENA (CAMP-GEFI) mRNA, complete cds	
ביליינים ביו וכמור	Top Hit Descriptor	ts76a08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L15533_ma1 PANCREATITIS ASSOCIATED PROTEIN 1 PRECI IRSOR (11 IMAN).	Homo saplens TNF-Inducible protein CG12-1 (CG12-1) mRNA	Homo sapiens cadherin EGF LAG seven-pass G-trae recentor 1 (CEI SR1) mBNA	Homo sapiens sulfotransferase-related protein (SI I) TX3 mRNA	Novel human gene mapping to chomosome 22	Novel human gene mapping to chomosome 22	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA	Homo sapiens 26S proteasome-associated nad1 homolog (POH1) mRNA	Human transposon-like element partial	Human calcium-dependent phospholipid-binding protein (PI A2) mBNA	Human calcium-dependent phospholinid-hinding protein (PI 42) mBMA complete 23	zv90c05.r1 Soares NhHMPu S1 Homo saniens chnA chne IMAGE-767048 F	RC4-BT0311-141199-011-h06 BT0311 Homo sepiens cDNA	wn57h07x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A	wn57h07 x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;	wn57h07 x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A	H.saplens mRNA for ribosomal protein 134	RC4-BT0311-141189-011-h06 BT0311 Homo Saniens CDNA	Homo sapiens thyroid hormone receptor binding protein (AIB3) mRNA	Mus musculus fregile X mental retardation syndrome 1 homolog (Fmr1) mBNA	H.sapiens DNA for endogenous retroviral like element	Homo sapiens germ-line DNA upstream of Jkappa locus	Human endogenous retrovirus, complete genome	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2) mRNA	QV1-DT0069-110200-067-410 DT0069 Home 5 amins 5 DNA	EST377546 MAGE reseduences MAGI Homo saniens CONA	Homo saplens cAMP-remitated mushing muchanist and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush and mush an	Homo sapiens hypothetical protein FJ20116 (FL)20116), mRNA	
	Top Hit Database Source	EST HUMAN	₽ F	Į.	L	FN	FN	F	TN	FX	TN.	IN IN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	N	EST HUMAN	1	F	Z	Z	Į.	Į.	EST HUMAN	EST HUMAN	IN	M	
	Top Hit Acession No.	AI621017.1	11418041 NT	11418322 NT	11418248 NT	9.0E-66 AL160311.1	AL160311.1	5031980 NT	5031980 NT	اما	M72393.1	9.0E-66 M72393.1	8.0E-66 AA424304.1	3E064410.1	6.0E-66 Al924653.1	6.0E-66 Al924653.1	6.0E-66 Al924653.1	(69181.1	5.0E-66 BE064410.1	11420557 NT	6679816 NT	(89211.1	54.1	9635487	11428643INT	119.1	173.1	-	11421638	
	Most Similar (Top) Hit BLAST E Value	1.0E-65 AI6210	1.0E-65	1.0E-65	1.0E-65	9.0E-66	9.0E-66 AL1603	9.0E-66	9.0E-66	9.0E-66 M8729	9.0E-66 M7239	9.0E-66	8.0E-66	7.0E-66 BE0644	6.0E-66	6.0E-86	6.0E-66	6.0E-66 X69181	5.0E-66	5.0E-66	4.0E-66	4.0E-66 X89211	4.0E-66 AJ2233	4.0E-66	4.0E-66	4.0E-66 AW939	4.0E-66 AW965	4.0E-66 U78168.	4.0E-66	
	Expression Signal	2.35	227	4.85	1.44	1.51	1.51	2.49	2.49	4.18	6.0	6.0	0.88	1.73	1.22	1.22	122	7.07	2.25	12.31	0.79	1.94	3.66	5.15	3.35	1.78	4.71	6.89	6.38	
	ORF SEQ ID NO:	28681		25318		19864		21096	21097				24266		23944	23945	23946	28636	21107	27424	20542	22022			25376	25494	24869	26246	26776	
	Exan SEQ ID NO:	18414	18905		19225			_ [	11239	11373	13738	13738	14479	18543	14168	14168	14168	18372	11250	17225	10703	12120	12302	14560	15326	15430	15106	16098	16588	
	Probe SEQ (D NO:	8542	9155	9254	9665	65	92	1332	1332	1468	3826	3826	4591	8654	4269	4269	4269	8486	1344	7357	773	2235	2425	4674	5407	5512	9609	6232	8029	

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Table 4
Single Exon Probes Expressed in Heart

		7	_	_				_	_		-,-				<del></del>		_									_	
יינים באירו ולקו מספר ווו ופמו	Top Hit Descriptor	UI-H-BW1-amr-a-10-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070747 2	Homo sapiens solute carrier family 25 (milochondrial carrier; adenine nucleotide translocator), member 5 (SLC2545), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein. mRNA	yz27g12.r1 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 IZI PIR-B56612.	727g12.r1 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:284326 5 similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1H2B_2 I2) IPIR-R5642.	yz27g12.r1 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:284326 5 similar to SW:H281 TIGCA P35068 HISTONE H28 1191 PIR-R6643.	Homo sapiens TGF(beta)-induced franscrintion forths 2/TGIE3) month	Homo sapiens KIAA0649 gene product (KIAA0649) mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo saplens profein phosphatase 2 remilation within the 1958 to 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 155 city of 1	Homo sapiens Misshaben/NIK-related kinase (Minik) mBnA	Homo sapiens Misshapen/NIK-related kinase (MINK) mRNA	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	Homo sapiens chromosome 21 segment HS21C101	H.sapiens pseudogene for the low affinity IL-8 recentor	Homo sapiens sodium/calclum exchanger isoform NaCa3 (NCX1) mBNA complete code	Homo sapiens HLA-B gene for human leucocyte antiden R	Homo sapiens HLA-B gene for human leucocyte antigen B	1959c02.r1 Soares multiple sclerosis 2NbHMSP Homo saniens cDNA clone IMAGE 277828 FI	Homo sapiens G-2 and S-phase excressed 1 (GTSE1) mRNA	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5	AV717817 DCB Hamo sapiens cDNA clone DCBADC07 5'	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5
21 1107 216	Top Hit Database Source	EST HUMAN	NT	TN	EST_HUMAN	EST HUMAN	EST HUMAN	N	N	LN LN	LN T	IN	F	NT.	NT	N	TN	NT	L	NT	NT	EST HUMAN		EST_HUMAN	П		EST_HUMAN
5	Top Hit Acession No.	4.0E-66 BF507493.1	4502098 NT	4502098 NT	3.0E-66 N55323.1	3.0E-66 N55323.1	N55323.1	11141880 NT	7662223 NT	11417946 NT	11417946 NT	5453949 NT	7657334 NT	7657334 NT	4505524 NT	4505524 NT			-		.2		11418318 NT		.1		1.
	Most Similar (Top) Hit BLAST E Value	4.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66 AL163301	2.0E-66 X65859.1	2.0E-66	2.0E-66 AJ133267	2.0E-66 AJ133267	2.0E-66 N45480.1	2.0E-66	1.0E-66 AV717817	1.0E-66	1.0E-66 AV717817	1.0E-66 AV717817
	Expression Signal	1.96	24.62	24.62	0.84	0.84	0.84	2.91	5.47	1.64	1.64	8.3	1.02	1.02	0.93	0.93	2.02	96.0	0.86	12.69	12.69	2.18	2.22	1.38	1.38	3.26	3.26
	ORF SEQ ID NO:	28193	21175	21176	21717	21718	21719	22430			25512	28904	19837	19838	19774	19775	21560	22669	23657	24233	24234	27205		22585	22586	22585	22586
	Exon SEQ ID NO:	17943	11313	11313	11834	11834		12540			15445	18614	10033	10033	866	9983	11682	12871	13882	14448	14448	17012	19712	12792	12792	12792	12792
	Probe SEQ ID NO:	8052	1408	1408	1939	1939	1939	2675	3079	5528	6528	8800	45	45	416	416	1784	2944	3975	4556	4556	7135	9475	2864	2864	4288	4288

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Table 4
Single Exon Probes Expressed in Heart

Most Similar  Top Hit Acession (Top) Hit Top Hit Acession Database  LAST E No. Source	6.36 1.0E-66 BF673088.1 EST_HUMAN 602152996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'	1.0E-66 BF328623.1 EST_HUMAN	1.37 1.0E-66 AA668858.1 EST_HUMAN aa80e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA cione IMAGE:827262.3'	2.39 1.0E-66 AF11167.2 NT Homo sapiens lun dimerization protein dene. partial cds: cfos gene. complete cds: and imbroum gene.	9.0E-67 11418177 NT	8.0E-67 M78158.1 EST_HUMAN	6.19 7.0E-67 AW 162232.1 EST_HUMAN ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HIMAN):	7.0E-67 AA383416.1 EST HUMAN	T	1 7.0E-67 W85947.1 EST HUMAN 2h58b05.r1 Soares fetal liver spleen 1NFLS S1 Homo saplens cDNA clone IMAGE-446040 F	7.0E-67 7657243 NT	7.0E-67 7657243 NT	7.0E-67 AW162232.1 EST_HUMAN	7.0E-67 11425572 NT	7.0E-67 11425572 NT	7.0E-67 11430460 NT	7.0E-67 11430460 NT	7.0E-67 AB011399.1 NT	7.0E-67 11421527	6.0E-67 X68968.1 NT	IM	6.0E-67 Y14320.1 NT	6.0E-67 4506434 NT	4507332 NT	1507332 NT	6.0E-67 AL163201.2 NT	6.0E-67 AL163201.2 NT	6.0E-67 7657020 NT	6.0E-67 7657020 NT
<del></del>	1.0E-66 BF	1.0E-66 BF	1.0E-66 AA	1.0E-66 AF	9.0E-67	8.0E-67 M7	7.0E-67 AV	7.0E-67 AA	7.0E-67 W	7.0E-67 W	7.0E-67	7.0E-67	7.0E-67 AW	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67 AB	7.0E-67	6.0E-67 X6	6.0E-67 Z1	6.0E-67 Y1	6.0E-67	6.0E-67	6.0E-67	6.0E-67 AL	6.0E-67 AL	6.0E-67	6.0E-67
Expression Signal	5.36	1.49	1.37	2.39	2.09	0.84	6.19	2.63	-	1	1.06	1.06	7.07	2.04	2.04	1,56	1.56	3.33	1.43	1.32	1.5	0.93	1.24	1.2	1.2	1.28	1.28	3.37	3.37
ORF SEQ ID NO:		1 26128	4 26998	9 28438	5	-	0 20184	6 21122			1 21773	1 21774		9 25807	9 25808			5 25292						8 23106					5 24284
Exan SEQ ID NO:			16804	18189	18965	14711	10360	11266	11439		11881	11881					$\Box$	_					_						14495
Probe SEQ ID NO:	5306	6143	6926	8312	9260	4829	376	1360	1535	1535	1988	1988	2779	5793	5793	9039	9039	820	9868	547	778	1252	3131	3391	3391	4035	4035	4607	4607

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	Top Hit Descriptor	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	-g04 BN0176 Homo sapiens cDNA	yn02d11.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'	-003 HT0934 Homo saplens cDNA	nw06a01.s1 NCI_CGAP_SS1 Home sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385 PPO_DI_DI_TDASE_DI_VEDATEM .	c Homo septiens CDNA 55 and	h06 BT0311 Homo sepiens cDNA	-f01 SN0066 Homo sapiens cDNA	hr81f05.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1.	om18b07.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGF-1541365 31	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9 CE09617	f05 ST0234 Homo seplens cDNA	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a 2, 3, and 4	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892 KIAA0798 PROTEIN.;	ba72g05.11 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN.:	finger protein ZFOR mRNA, complete cds	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:7453g2 3	e 21 segment HS21C100	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 57	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds	c07 BT0566 Homo saplens cDNA	c07 BT0566 Homo sapiens cDNA	ratein (KIAA0985), mRNA	601175762F1 NIH_MGC_17 Homo septens cDNA done IMAGE:3531038 5	c02 TN0103 Homo sapiens cDNA	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
sed in Heart	Top Hit Desc	s ubiquitin specific protease 13 (isopeptidase	s T cell receptor beta locus. TCRBV7S3A2 to	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA	oares adult brain N2b4HB55Y Homo sapiens	RC0-HT0934-150900-026-c03 HT0934 Homo saplens cDNA	nw06a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone	EST37903 Embryo 9 week Homo sapiens CDNA 57 end	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone Q61085 GTP-RHO BINDING PROTEIN 1:	Soares NFL T GBC S1 Homo sapiens cDN	NCI_CGAP_Lu24 Homo sapiens cDNA clone	QV4-ST0234-181199-037-f05 ST0234 Homo saplens cDNA	s double stranded RNA activated protein kings	VIH MGC_20 Homo sapiens cDNA clone IMA	VIH_MGC_20 Homo sapiens cDNA clone IM/	Homo saplens KRAB zinc finger protein ZFOR mRNA, complete cds	s developmentally regulated GTP-binding prot	oares_testis_NHT Homo sapiens cDNA clon	Homo sapiens chromosome 21 segment HS21C100	NIH_MGC_55 Homo sapiens cDNA clone IN	s mRNA for NADPH-cytochrome P-450 reduc	s mRNA for NADPH-cytochrome P-450 reduc	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA	Homo saplens KIAA0985 protein (KIAA0985), mRNA	NIH_MGC_17 Homo sapiens cDNA clone IN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA	s thyroid autoantigen 70kD (Ku antigen) (G22)
Single Exon Probes Expressed in Hear	Top Hit Database Source	Homo sapiens		T HUMAN	Г	П		EST HUMAN EST37903 En	т	Т	BST HUMAN Q61085 GTP-	Π		Т	Т	ba72g05.y1 NIH_MGC EST_HUMAN KIAA0798 PROTEIN.	ba72g05.y1 NIH_MGC EST HUMAN KIAA0798 PROTEIN.	П	Homo sapiens	HUMAN		HUMAN		Homo sapiens	EST_HUMAN RC4-BT0566-	EST_HUMAN RC4-BT0566-	Homo sapiens			
eignic	Top Hit Acession No.	7 4507848 NT	5.0E-67 AF009860.1 NT			4.0E-67 BF357321.1 EST	4 0E-67 A \$ 74 4 2 0 4 1		l				1.4		Π	2.0E-67 BE303037.1 EST	2.0E-67 BE303037.1 EST		4758795	2.0E-67 AA625755.1 EST_		2.0E-67 BF240758.1 EST		2.0E-67 AB051763.1 NT		AW602635.1	7 11436448 NT	2.0E-67 BE295714.1 EST	2.0E-67 BF377169.1 EST_HUMAN	
	Most Similar (Top) Hit BLAST E Value	6.0E-67			L										_						2.0E-67			2.0E-67	2.0E-67					2.0E-67
	Expression Signal	2.1	245	2.1	1.83	1.22	2.3	0.93	1.14	3.14	1.22	19.27	1.94	9	1.74	1.5	1.5	86.0	1.2	3.9	2.33	4.22	2.17	2.17	1.34	1.34	3.26	1.77	2.26	2.6
	ORF SEQ ID NO:		22913		21069			20365	23125	24270	26827		19967	20604		21614	21615	22116	22153	23144	23610	25734	25820	25821	27264	27265		28698	28144	25069
	Exen SEQ ID NO:	14761	13109	18229	11213	16762	18290	L	L	14484	16639	18451	10152	10754	11005	11737	11737		12261	13339	13830									19577
	Probe SEQ ID NO:	5125	3184	8352	1306	6883	8416	2782	3407	4596	6760	8583	180	827	1089	1841	1841	2336	2381	3422	3921	5724	5803	5803	7202	7202	8409	8558	8751	9388

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	Top Hit Descriptor	601458514F1 NIH MGC 66 Homo sepiens cDNA clone IMAGE 3862034 F	601437367F1 NIH MGC 72 Homo sepiens cDNA clone IMAGE 3022302 E	Homo sapiens meningloma (disminited in halanced transforcition) 4 (MM4)	OV4-ST0234-181190-037-475 ST0234 Home serious ability	Homo sapiens mRNA for KIAAA677 protein commissionals	Homo sapiens mRNA for KIA 40577 protein, complete cas	ULH-BI3-gik-f-01-01-11 st NCI COAP Subst Home annime ability at a management	601177002F1 NIH MGC 17 Homo sapieps CINA clone IMAGE-253741 F1	a47q12.s1 Soares NFL T GBC S1 Homo saniens chNA chare NAA GE14465520 21	Homo saplens cell recognition molecule Cashr? (KIAAARRR) mRNA	Homo sapiens phosphodiesterase 78 (PDE7R) mRNA	Homo sapiens phosphodiesterase 78 (PDF7R) mRNA	Homo sapiens MIF2 suppressor (HSMT3) mRNA complete cde	Homo saplens menindicima (disminted in halament complete out	Homo sapiens low density lipoprotein-related protein 2 (I RP2) mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PREF) mRNA	Homo sapiens pre-B-cell colony-enhanction factor (PREE) mixiva	Homo sapiens 26S proteasome-associated nad1 homolog (POH4) mPNA	Homo sapiens 265 professome-associated nad1 homolog (POLI1) m DNA	Homo saplens V-raf murine sarcoma viral oncorene homolog 84 / BDAC1 DNA	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA100008 デ	Homo sapiens RIBIIR gene (partial), exon 12	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN):	qe62h01.xf Soares_feta_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to	WINDSHITT NOT COMP THE LAW AND THE SECOND THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECON	wh57b08x1 NCL CGAP_Kkd11 Home sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137	OBBIS/ ACYL-COA I HIDESTERASE.;	rronno sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	From Sapiens larent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Homo saplens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds
Top Hit	Database Source	EST HUMAN	EST HUMAN	٧.	EST HUMAN	L L	Į.	EST HUMAN	EST HUMAN	EST HUMAN	N-	₽ F	N-	NT	Z	LN LN	N F	N-	L'A	N	N	EST_HUMAN	NT	NT	EST_HUMAN	ECT LIMAN	Т		LICMAN		T HI MAN	
Top Hit Acession	No.	BF035316.1	BE897376.1	· 4505222 NT	1.0E-68 AW816405.1	1.0E-68 AB011149.1	1.0E-68 AB011149.1	1.0E-68 AW451832.1	1.0E-68 BE296032.1	AA897343.1	7662349 NT	11418869 NT	11418869 NT	L76416.1	4505222 NT	11430460 NT	5031976 NT	5031976 NT	5031980 NT	5031980 NT	4757867 NT	۲:	8.0E-69 AJ237744.1	. 9966912 NT	-	,	_		1 4EE7720	TIN C27773A	3.0E-69 BF258012 1	
Most Similar (Too) Hit	BLAST E Value	2.0E-68	2.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68 AA89734	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0E-69 AU11724	8.0E-69	7.0E-69	6.0E-69 AI192764.	6 0F-69 A (192764	4.0E-69 AI873630	4 OF 80	4 05-69	4 OF 50	3.0E-69	3.0E-69 AF221712.
Expression	Signal	4.79	1.92	1.31	9:36	1.32	1.32	1.9	0.95	96.0	1.57	2.44	2.44	2.29	1.95	1.38	1.82	1.82	1.63	1.ස	0.78	9.27	1.21	6.08	3.61	3.64	1.88	445	2.43	2 43	2.81	1.64
ORF SEQ	D NO:	26095		19873	20078	21994	21995	22486	23617	24298		28361			19873	24991	19797	19798	20772	20773	23718			25852	26659	26660		25554	28024	26025	20187	20340
Exan	SEQ NO:			10056	10257	12092						- 1	- 1	- 1	10056	19669	10006	10006	10929	10929	13940	18143	13260	15740	16469	16469	10451	15481	15900	15900	10364	10532
Probe	SEQ ID	6202	9148	72	293	2205	2205	2728	3928	4954	5261	8226	8226	8275	9659	9862	19	9	5	101	4037	8283	3340	5834	6589	6289	509	5565	5995	5995	380	596

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Table 4
Single Exon Probes Expressed in Heart

							_	<del></del>	-		<del>_</del>		<del></del>		_					-						****				
Oligie Exon Probes Expressed in Heart	Top Hit Descriptor	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48836	Homo saniens humbalic viessel and other in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont	wheegoext NCI CGAP Kid11 Home seniers cDNA clare IMAGE:2385758 21	Homo saplens aconitase 2 mitro-handrial (ACO2) menu	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA Partial Ac	Homo sapiens TRAFG-binding protein TGRP mRNA complete add	EST88807 HSC172 cells II Homo seniens cDNA A' and similar to all all and seniens and similar to all all and seniens and similar to all all and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens and seniens are seniens and seniens and seniens and seniens and seniens are seniens and seniens and seniens and seniens are seniens and seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens and seniens are seniens and seniens are seniens and seniens are seniens and seniens are seniens and seniens are seniens and seniens are seniens are seniens and seniens are seniens are seniens and seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens are seniens	H.sapiens mRNA for N-acet/Iglucosamide (beta 1.4) calactos utransferase	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor	Homo seniens rihosomal protein S452 (RDS464) BNA	EST88807 HSC172 cells II Home cominers a DNA 51 and a million a	Homo sapiens HGC8.2 profein (HGC8.2) mRNA	Homo saplens KIAA0553 matein dens complete ade and alabalit	Homo sapiens KIAA0563 protein gene, complete cels, and alphalib protein accompanies.	Homo sapiens KIAA0553 profein gene complete cds: and alphalit profein gene, partial cds	Homo sapiens KIAA0553 protein game complete cds; and alphalit models gene, partial cds	601109444F1 NIH MGC 16 Home saniers cDNA clone MAACE 3250074 F1	ZW71g02.r1 Soares testis NHT Homo seniens CDNA clane MAGE-784889 F	Rattus norvegicus brain specific cortactin-binding protein CRP90 mRNA partial rate	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens mRNA for KIAA1147 protein, partial cds	Homo sapiens mRNA for KIAA1147 protein, partial cds	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens	CDNA clone TCBAP2678 TCBAP1F2678 Bedietic and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Book and Bo	r ODNA clone TCBAP2678 cDNA clone TCBAP2678	Homo sapiens keratin 8 (KRT8) mRNA	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE-4025785 5'
JIE EXON PIO	Top Hit Database Source	H H	LN	EST HUMAN	4	NT	N	EST HUMAN	N L	F	L	EST HUMAN	-1	N I	NT	IN	NT	EST HUMAN	EST HUMAN	NT	EST_HUMAN	TN	Į.	N	NT		EST_HUMAN	EST HUMAN	-	EST_HUMAN
	Top Hit Acession No.	3.0F-69 T80514 1	5729910 NT	3.0E-69 AI765888.1	11418185 NT		3.0E-69 AF268075.1		3.0E-69 X13223.1	3.0E-69 X06233.1	1432120	3.0E-69 AA376399.1	9157	2.0E-69 AF160252.1		1.7		7:		1.1	1.0E-69 AW393969.1	7662263 NT	7662263 NT		1.0E-69 AB032973.1		1.0E-09 BE2450/0.1	1.0E-69 BE245070.1	1918	1.0E-69 BF125887.1
	Most Similar (Top) Hit BLAST E Value	3.05-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	3.0E-69	2.0E-69	2.0E-69	2.0E-69	2.0E-69	2.0E-69	2.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	7 0		1.0E-69	1.0E-69	1.0E-69
	Expression Signal	1.35	0.88	,0.86	5.94	1.37	8.43	1.26	1.54	2.24	3.07	7.12	4.13	-	1	4.94	4.94	1.2	2.73	2.35	3.68	1.55	1.55	2.93	2.93	200	9.69	5.29	23.27	1.63
	ORF SEQ ID NO:			23674	29105	26410	26485		27491	27568	28174			20170	20171	20170	20171	21616		21445	26008	26211	26212	26173	26174	07070	24612	27943		28785
	Exan SEQ ID . NO:	11440	12206			16249	16318	16968	17284	17363		18099	18911	10344	10344	10344	10344	11738	12742	11577	15886	16083	16063	16633	16033	17697	3	17697	18126	18872
	Probe SEQ ID NO:	1536	2325	3890	5209	6387	6457	7091	7417	7493	8036	8215	9168	124	124	398	398	1842	2813	1675	2084		888	888	888	7847		7847	8246	9105

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Table 4
Single Exon Probes Expressed in Heart

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ongo rydi Tobes rypiessed II Teall	Top flit Descriptor	wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element contains element MIR repetitive element contains element of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of the separate of 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separate of the separate of the separate of the separate of the separate of the separate of the separate of	nc13d12_f NCI CGAP Pri Hamp sanians cDNA close 1846 CE - 1008022	Homo sapiens DGS-I mRNA 3' end	tm89f01xf NCI CGAP Brn25 Homo saniens cDNA clare IMACE:345236 91	tm89f01.x1 NCI CGAP Bm25 Home saniens cDNA close IMAGE: 3465305 3	Z15h04,r1 NCI CGAP GCB1 Homo saniens cDNA clane IMAGE:743226 F	Homo sapiens fumor suppressor deleted in oral cancer-related 4 (In Or Ab), ability	Homo sapiens adenylata cyclase 3 (ADCY3) mRNA	Homo saplens MIST mRNA, partial cds	Homo sapiens MIST mRNA partial cds	Homo sablens dene encoding splicing factor SE1 expns 2.8	Homo sapiens mRNA for KIAA1204 protein northal adv	Homo sabiens mRNA for KIAA1204 protein partiel ads	Human displacement protein (CCAAT) mRNA	Human displacement protein (CCAAT) mRNA	Human PBX3 mRNA	Human PBX3 mRNA	Homo saplens phospholipid scramblese 1 gene own 4 and 6' familian contra	Homo saplens karvonherin heta 2b transportin (TRNI2) DNA	Homo sapiens (arrobhern beta 2b fransnorth (TRN2), mRNA	Homo cantione HIP (histone call and a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second call a second 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second call a second call a second call a second call a second call a second call a second call a second	Commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of 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commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission of the commission o	Troing septents mirk (mistane cen cycle regulation defective, S. cerevisiae) hamolog A (HIRA), mRNA	Homo sapiens amyoid beia (A4) precursor profesio (matease navin II Altaniana).	Human Ku (p70/p80) subunit mRNA complete che	Homo saplens CMP-N-acelylneuraminic acid synthase (1 OC550n7) mRNA	Homo saplens KIAA0792 gene product (KIAA0702) m2NA	Homo sapiens KIAA0792 dene product (KIAA0792) mRNA	MR3-HT0487-150200-115-a06 HT0487 Home sabless cloud	RC0-BT0522-071299-011-a12 BT0522 Home saniers cDNA	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA	
gic Lydi I 10	Top Hit Database Source	EST HUMAN	EST HUMAN	Ę	EST HUMAN	EST HUMAN	EST HUMAN	NT.	LN LN	NT	N	NT	Į.	LZ	LN LN	N	LN	₩.	N.	LN	片	Į į	17		LN L	LN	NT	F	NT	EST HUMAN	П	П	
5	Top Hit Acession No.	AI809994.1	8.0E-70 AA230303.1	77566.1	7:	Ξ		5031668 NT	4757723 NT	7.0E-70 AB032369.1	7.0E-70 AB032369.1	4J000052.1	4B037715.1	AB037715.1		M74099.1	(59841.1	(59841.1	NF153715.1	11525964 NT	11525964 NT	11526319 NT	1152834D NT	01000011	4502166 NT		8923899 NT	7662307 NT	7662307 NT	1.1	2.1	7.	
	Most Similar (Top) Hit BLAST E Value	1.0E-69 AI80999	8.0E-70	8.0E-70 L77566.	7.0E-70 AI49780	7.0E-70 AI497807	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70 AJ00005	7.0E-70 AB03771	7.0E-70 AB03771	7.0E-70 M74099.	7.0E-70 M74099.	7.0E-70 X59841.1	7.0E-70 X59841.1	7.0E-70 AF15371	7.0E-70	7.0E-70	7.0E-70	7 0F-70		6.0E-70	6.0E-70 M30938.	6.0E-70	5.0E-70	5.0E-70	5.0E-70 BE16603	3.0E-70 BE071790	3.0E-70 BE071790	•
	Expression Signal	232	1.52	2.16	1.93	1.93	1.83	3.57	3.86	5.28	5.28	1.89	2.36	2.36	3.98	3.98	3.72	3.72	3.13	1.56	1.56	1.78	178		1.93	1.36	0.39	1.83	1.83	1.73	0.89	0.89	
	ORF SEQ ID NO:		22065	23954	21547	21548	21660		23807	25124	26126	26120	26980	26981	27131	. 27132	27357	27358	26627	26648	26649	28978	28979		20630	21874	22232	22268	22269		21332	21333	
	Exon SEQ ID NO:	19124	12717	14176	11670	11670	11784	11909	14032	15289	15289	15985	16788	16788	16940	16940	17159	17159	16441	16457	16457	18687	18687		10780	11979	12338	12723	12723	18879	11475	11475	
	Probe SEQ ID NO:	9510	2284	4277	1771	1771	1888	2018	4132	5369	5369	6138	6910	6910	7063	7063	7283	7283	7428	7445	7445	8875	8875		853	2080	2461	2505	2505	9116	1571	1571	

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Table 4
Single Exon Probes Expressed in Heart

		Т	Т	T		Т	1	Т	Т	_	_	12	_	_	_	_	_	٠,	<del>- ;;</del>	<del></del>	-	Ψ.	,	_	-		-		-	
Single Exoli Plobes Expressed in hear	Top Hit Descriptor	602141561F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE: 4302806 5	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5	1y07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR	yo7a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI RAT P29288 3-HYDROXYISOBITYRATE DEHYOROGENASE PRECI IRSOR	qx51h01x1 NC  CGAP Pan1 Homo sapiens cDNA clone IMAGE-2004g13.3"	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA	hz64c12x1 NCI_CGAP_Lu24 Homo septens cDNA done IMAGE:3212758 3'	Homo sapiens chromosome 21 segment HS21C002	248g04.11 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A P03346 GAG POI YPROTEIN	Human nonmuscle myosin heavy chain-B (MVH10) mRNA nartial che	H.saplens gene for schwannomin (CS8)	H.sapiens gene for schwannomin (CS8)	Homo sapiens NALP1 mRNA, complete cds	Human mRNA for NF1 protein Isoform (neurofibromin Isoform), complete cds	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds	Homo saplens cytoplasmic dynein intermediate chain 1 mRNA, complete cds	Homo sapiens sialylitansferase 6 (N-acetylacosaminide albha 2 3-sialylfrancferase) (SIATR)	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha). Anna 4 and 5	Homo saplens calcium-binding transporter mRNA, partial cds	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA	Homo sapiens eukaryotic franslation initiation factor 3, subunit 6 (48kD) (FIF3S6) mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens transglufaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA	zv64c03.r1 Soares testis NHT Homo sabiens cDNA clone IMAGE:757444 F	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5
	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	뒫	F	Z	EST_HUMAN	N N	EST HIMAN	N	N.	F	F	M	N N	 	Ę	F	NT	N	Į.	N _T	N	N-		T HUMAN	HUMAN
	Top Hit Acession No.	3.0E-70 BF685233.1	3.0E-70 BF685233.1	V42161.1	142161.1	2.0E-70 AI246899.1	8923669 NT	7661983 NT	7661983 NT	3E467311.1	2.0E-70 AL163202.2	2.0E-70 AA054010 1				2.0E-70 AF310105.1		2.0E-70 AF123074.1	4.1	11422642 NT		3.1	8923420 NT	8923420 NT	4503520 NT	11430460 NT	11430460 NT	4507476 NT	12	9.1
	Most Similar (Top) Hit BLAST E Vatue	3.0E-70	3.0E-70	2.0E-70 N42161	2.0E-70 N42161	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70 BE46731	2.0E-70	2.0E-70	2.0E-70 M69181.	2.0E-70 X72662.1	2.0E-70 X72662.1	2.0E-70	2.0E-70 D12625.1	2.0E-70	2.0E-70 AF12307	2.0E-70	2.0E-70 M21741.1	2.0E-70	2.0E-70	2.0E-70	. 2.0E-70	2.0E-70	2.0E-70	1.0E-70	1.0E-70 AA44229	1.0E-70 AV73853
-	Expression Signal	3.88	3.88	13.15	13.15	2.01	1.7	1.95	1.95	0.97	2.09	3.62	3.95	8.05	8.05	1.42	1.88	6.83	9.83	1.69	7.67	1.3	3.19	3.19	5.82	2.58	2.58	2.97	2.57	13.73
	ORF SEQ ID NO:	25865	25866	20426	20427	20449	20766	20924	20925	21148	21479	W-1-1	23648	25156	25157	25780	26028	. 26042	26043	24853	26685	27930	28550	28551	29010	25289	25290			28429
	Exon SEQ ID NO:	15751	15751	10608	10608	10622	10922	11079	11079	11292	11609	12156	13870	15304	15304	15673	15904	15915	15915	15134	16498	17685	18296	18296	18716	19114	19114	13267	17492	18182
	Probe SEQ ID NO:	5845	5845	674	674	689	1004	1167	1167	1387	1708	2272	3963	5385	5385	5766	5999	6010	6010	6177	6618	7835	8422	8422	8908	9499	9499	3347	7642	8305

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Single Exon Planes Expressed in Reart	Top Hit Descriptor	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE: ;	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:014045 014045 PHOSPHOTRANSFERASE;	wb52c05x1 NCI_CGAP_GC6 Homo sapiens cDNA done IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.	wb52c05.x1 NCI_CGAP_GC8 Homo septiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.	2p21d11.r1 Stratagene neurospithellum (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL.	zv60h06.r1 Soares_testis_NHT Homo sapiens cONA clone IMAGE:758075 5'	291a06.s1 Soares_fetal_liver_spleen_1NRLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds	QV4-ST0234-181199-037-f05 ST0234 Homo saplens cDNA	W/18h10.x1 NCI_CGAP_Uff Homo sapiens cDNA clone IMAGE:2425315 3'	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA	Human neurofibromatosis protein type 1 mRNA, 3' end of cds	Homo sapiens transcription factor WSTF mRNA, complete cds	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective fissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA	Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA	Homo saplens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds	Homo sapiens hook1 protein (HOOK1), mRNA	Homo saplens hook1 protein (HOOK1), mRNA	Homo sapiens plasminogen (PLG) mRNA	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds	Homo sapiens putative heme-binding protein (SOUL), mRNA
JIB EXON Proc	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	۲	TN	EST_HUMAN	EST_HUMAN	NT	TN	NT	NT	Į.	Z	LN	TN	NT	IN	TN	LN	NT	NT	LN L	TN
	Top Hit Acession No.	9.0E-71 AI143870.1	9.0E-71 A1143870.1	9.0E-71 Al654903.1	9.0E-71 AI654903.1	8.0E-71 AA171451.1					5.0E-71 AW816405.1	5.0E-71 A1829496.1	4502740 NT	5.0E-71 M38106.1	1	5.0E-71 X13467.1	11436514 NT	11438069 NT	11417862 NT	11418039 NT	7592	[1]	4.0E-71 AF157626.1	7705414 NT	7705414 NT	4505880	4.0E-71 AF056322.1	7657602 NT
	Most Similar (Top) Hit BLAST E Value	9.0E-71	9.0E-71	9.0E-71	9.0E-71	8.0E-71	7.0E-71	7.0E-71	7.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71
	Expression Signal	6.04	6.04	1.88	4.65	1.97	7.91	1.52	4.18	3.45	1.38	3.2	2.14	1.59	19.78	2.26	1.9	2	1.84	1.62	1.13	115.63	115.63	0.88	0.88	1.63	3.35	4.99
	ORF SEQ ID NO:	25621	25622	28228	26226		26386	27103	28786		23710	24782	25577		26585		28477	28668					20124					24567
	Exon SEQ ID NO:	15536	15536	16077	16077	17122	16226	16914	18507	12050	13933	15011	15501	16295	16406	17552	18225	18400	18848	19063	10082	10306	10306	12778	12778	12785	14227	14792
	Probe SEQ ID NO:	5621	5621	6192	8811	7245	සස	7037	8643	2163	4030	5144	5586	6434	6548	7702	8348	8528	2906	9411	97	347	347	2850	2820	2857	4330	4913

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Table 4
Single Exon Probes Expressed in Heart

	in	T	Т	Т	T		T	Т	7	Т	7	Т	$\neg$	$\overline{}$	Ť	Ť	Т	Ť	T	T	Ť	Ť	T	_	Т	<del></del>
Top Hit Descriptor	nI45h10.s1 NCI_CGAP_Pr4 Homo sepiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element :	Homo saplens chromosome 21 segment HS21Cons	Human mRNA for KIAA0272 gene, partial ods	Human mRNA for KIAA0272 gene, partial cds	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds.	bb81a06.yf NIH_MGC_10 Homo saplens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P64727 UV EXCISION REPAIR PROTEIN PROTEIN RAD33 HOMO! OG B.	Ve43e09.r1 Soares fetal liver soleen 1NFLS Homo saniens cDNA clans IMA CE 120520 F	oy15e03.s1 Soares_senescent_fibroblasts_NbHSF Homo sepiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element	Homo sapiens neuronal cell death-related protein (I OCS1616) mRNA	Homo saplens disabled-2 dene expns 2 through 15 and complete eds	Homo sablens phosphatidylinositol 4-kinase 230 (ni4K/230) mDNA complete ad-	Homo saplens PMS2L16 mRNA, partial cds	Homo saplens PMS2L16 mRNA partial cds	Homo sapiens hair/venhancer-of-split related with YRPW moff-like (HEVI ) mDNIA	Homo sapiens increanic pyrophosphafase mRNA complete ode	Homo saplens SNARE protein kinase SNAK mRNA complete cas	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA done 02_15 5' similar to Homo sapiens chromosome 19	02_15 Human Epidermal Keratinocyte Subtraction Library-Upregulated Transcripts Homo saplens cDNA	Homo sabiens affractin precirent (ATRN) repose asset 19	Human mRNA for KIAAAAA sone complete ada	Homo saplens GCM5 (nemeral control of amino acid staticals and acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid at a control of acid acid at a control of acid at a control of acid acid at a control of acid at a control of acid at a control of acid at a control of	Homo sapiens CAGI 79 mRNA partial colo	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOMA) mDNA	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
Top Hit Database Source	EST HUMAN	N.	본	NT LN	Ä	Ŋ	EST HUMAN	EST HUMAN	EST HUMAN	F	L	N	NT	NT	N	N	FN.	NT	EST_HUMAN	EST HIMANI	TN TN	LN	L L	Ę	Z-	Ę
Top Hit Acession No.	3.0E-71 AA557683.1	2.0E-71 AL163206.2		2.0E-71 D87462.1	2.0E-71 AF095703.1	2.0E-71 AF095703.1	BE018477.1	T95489.1	1.0E-71 AI077927.1	7706281 NT		72.1	17.1	17.7	7153	AF119665.1	19.1	19.1	1.0E-71 BE122850.1	1 0E-71 BE122860 1	T		11426182	U80753.1	11425430	8922811 NT
Most Similar (Top) Hit BLAST E Value	3.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71 BE0184	2.0E-71 T95489.	1.0E-71	1.0E-71	1.0E-71 AF2058	1.0E-71 AF0128	1.0E-71 AB0170	1.0E-71	1.0E-71	1.0E-71 AF11966	1.0E-71 AF2462	1.0E-71 AF2462	1.0E-71	1 0F-74	1.0E-71	1.0E-71 D28476	1.0E-71			1.0E-71
Expression Signal	3.32	2.52	6.96	96.9	2.56	2.56	2.3	6.22	2.11	1,83	4.01	10.59	123	123	4.85	1.17	4.73	4.73	0.94	0.94	1.87	1.86	4.1	10.62	6.98	4.18
ORF SEQ ID NO:	28218	20968		24958	28114	281.15	28219		20371	20699	20841	21080	21821	21822	22416	23179	23256	23257	23298	23289	23381	24050	26079	26351	26816	26986
Exon SEQ ID NO:	17968	11119	15181	15181	17872	17872	17970	18920	10559	10851	11000	11224	11927	11927	12528	13373	13462	13462	13511	13511	13595	14266	15947	16189	16629	16794
Probe SEQ ID NO:	8077	1210	5259	5259	8022	8022	8079	9181	622	926	1084	1317	2036	2036	2661	3467	3546	3546	3597	3597	3681	4370	6044	6326	6750	6916

Page 271 of 413 Table 4 Single Exon Probes Expressed in Heart

		Т	7	Т	Т	$\neg$	7	-	_	Tip.	Į10				_	<del>-</del>	-7-	<del></del>	-		<u>.</u>	_	<del>- , -</del>			-	
Oligie Lyon Flores Expressed III near	Top Hit Descriptor	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA	Homo sapiens cytochrome c oxidase subunit VII a-related protein gene, complete cde	AV761217 MDS Homo saplens cDNA clone MDSEIA03 5	AV761217 MDS Homo sapiens cDNA clone MDSFIA03 5	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA	Homo sapiens leucy/cystiny/ aminopeptidase (LNPEP) mRNA	Homo sapiens leucy//cystiny/ aminopeptidase (LNPEP), mRNA	Homo sapiens gene for AF-6, complete cds	wk95g03.XI NCI_CGAP_Lu19 Homo saplens cDNA clone IMAGE:2423188 3' shnilar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN :contains Alu repetitive element:	wk95g03.x1 NCI_CGAP_Lu19 Home septens cDNA clone IMAGE:2423188 3' similar to TR.O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. contains Alu repetitive element:	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial profess mBNA	Homo saplens aconitase 2 milochandra (ACO2) micloar nene encolorio mitocondical estatuta (ACO2) micloar nene encolorio mitocondical estatuta encolorio mitocondical estatuta encolorio microandra encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio encolorio en	Home contains a 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the state of the state of the	lose deposis acquirase 2, minorinarial (ACC2), nuclear gene encoding mitocondrial protein, mRNA (oseudonene) PTMAP2=profityment alnha lhuman Commits 402 14	Homo sapiens chromosome 21 segment HS210046	7k63e05.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:3480080 3' similar to SW:KMLC_RABIT_P07313 MYOSIN I IGHT CHAIN KINASE SYELETAL MILES E	QV0-CS0010-150900-398-e11 CS0010 Homo saniens CDNA	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens CDNA	QV0-CS0010-150900-398-e11 CS0010 Homo sepiens CDNA	QV0-CS0010-150900-398-e11 CS0010 Homo saniens CDNA	Homo sapiens alpha-tubulin mRNA, complete cds	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 6'	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to	MR4-BT0598-010000-015-0100-02-4 ND FNO Eliv journains element MSK1 repetitive element;	MR4-BT0598-010600-005-405 BT0598 Home saniers cDNA	QV1-BT0632-280800-342-a10 BT0632 Hamo sapiens cDNA
מוש באחוו ביות	Top Hit Database Source	NT	F	EST HUMAN	EST HUMAN	NT.	N _T	NT	N	EST_HUMAN	EST_HUMAN	Į Į	<u> </u>	<u> </u>	L	N N	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	EST_HUMAN	EST HIMAN	EST HIMAN	EST HUMAN	EST_HUMAN
ี้ วั	Top Hit Acession No.	8922811 NT	1.0E-71 AY007643.1	AV761217.1	1.0E-71 AV761217.1	11418903 NT	11417191 NT	11417191 NT	99.1	9.0E-72 Al857635.1	9.0E-72 AI857635.1	4501866 NT	4501866 NT	A501BGB NT	S41694.1	16.2		Г	07.1	07.1	07.1	Γ	1.1	5.0E-72 AW161274 1	T		5.0E-72 BE926645.1
	Most Similar (Top) Hit BLAST E Value	1.0E-71	1.0E-71	1.0E-71 AV7612	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71 AB0113	9.0E-72	9.0E-72	7.0E-72	7.0E-72	7.05-72		6.0E-72	6.0E-72	5.0E-72 BF3337	5.0E-72 BF3337	5.0E-72 BF3337	5.0E-72 BF3337	5.0E-72	5.0E-72	5.0E-72	5.0E-72	5.0E-72	5.0E-72
	Expression Signal	4.18	6.49	3.39	4.87	3.2	2.33	2.33	4.48	1,15	1.15	5.23	5.23	5.33	2.94	3.72	222	0.88	0.88	2.95	2.95	2.75	1.47	3.55	3.18	3.18	2.43
	S. O		27820			28383		28624		20173	20174	23700	23701	23702			28893	19854	19855	19854	19855		26163	27167	28706	28707	
	_ W		17598	17642	18052				19147	10347	10347	13926	13926	13926	16094	16764	18603	10043	10043	10043	10043	11037	16023	16974	18437	18437	19700
	Probe SEQ ID NO:	6916	7748	7792	8164	8256	8486	8486	9547	401	401	4023	4023	4023	6228	6885	8788	56	22	22	22	1122	9120	7097	8569	8569	9253

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Table 4
Single Exon Probes Expressed in Heart

ORF SEQ   Expression   Top Hit Acession   Top Hit				,	_																<b>-</b> .									
Exan         Most Similar         Most Similar         Most Similar         Top Hit Acession         Top Hit Acession           14602         ID NO:         Signal         1.0F.72         11034844 INT         Top Hit Acession         Top Hit Acession           14602         276         4.0E-72         17034844 INT         Top Hit Acession         Top Hit Acession         Source           17484         27705         1.42         4.0E-72         5729667 INT         FST HUMAN           18628         28917         7.32         4.0E-72         11034844 INT         EST HUMAN           18628         28917         7.32         4.0E-72         11034844 INT         INT           18628         28917         7.32         4.0E-72         11034844 INT         INT           18628         28917         7.32         4.0E-72         11034844 INT         INT           18628         28917         7.32         4.0E-72         110414141         INT           110611         4.0E-72         ALDE-72         INT         INT           11062         2.02895         6.06         3.0E-72         In4306.1         INT           11063         2.2445         2.51         3.0E-72         ALDE-72	and Expressed III realt	Top Hit Descriptor	Homo sapiens hypothetical protein d.11057820 2 (T.) 11057820 2) mRNA	Homo sapiens hect domain and RLD 2 (HEDC2) DNA	Homo sapiens hynothetical profess (FI 120788) (FI 120788)	WZ8803.11 Spares fetal liver coleen 1/NET S. Homo continue CONIA - Line III S. Continue	vd29d09.s1 Soares fetal liver spleen 1NFI S Homo equipme DNA alone 11A CE 235084 5	Homo sanjene WEE4 neme for modelin biness and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market and market an	ah63a06.s1 Scares festis NHT Home seniors cDNA data 434000 3.	Human chondrollin suifate protocolus a vareform VO - miss.	Ummon chandestille a lifet.	Home seniors of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract o	trong capters as an actual previous from CBK1 on chromosome 21q22, segment 3/3	TOR V delta 2-0 appear and a support delta and C alpha fusion gene (alternatively spliced, splice junction) himses appearance of the support of the support delta and C alpha fusion gene (alternatively spliced, splice junction)	Homo capiens hundhefical acatain (CI 14472)	wb31g08 x1 NCL CGAP GC6 Home contract of the little of the contract of	Homo seniens arough factor recently beauty protein 40 (OBB4)	Homo sapiens growth factor recentor-bound protein 10 (ChB 10) gene, exon 5	Homo saplens mRNA for KIA41084 nastring protein in Condition gentle, excell 3	Homo sapiens mRNA for KIAA 1081 brotein partial cyle	Homo sapiens ribosomal protein L3-like (RPI 31 ) mRNA	Homo saplens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory	Homo sapiens mitches recentor subfamily 4 areas U	Homo sabiens S100A12 dene for Calorentifin Court 2 and Libert 1.	Homo sapiens gene for AF-6, camplete cds	aj28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb;X02067 H.sapiens	Baffils nonedials mitative aboneholds.	ai83402 st Soares parathered hince NELIDA II.	Homo sablens varuolar protein endim 44 (seed homelan) (VDC 44) - DNA	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13) mRNA
Exam NO::         CRF SEQ ID NO::         Expression Signal         (Top) Hit Veilue         Top Hit Acess No.           14602 17602 1762 1764 1778 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18628 18638 18638 18638 18634 18651 18651 18651 18651 18651 18652 18651 18654 18651 18654 18651 18654 18651 18654 18651 18654 18651 18654 18651 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 18654 1865 1865 1865 1865 1865 1865 1865 1865	OI LINE OIG	Top Hit Database Source	NT	TN	LN LN	EST HUMAN	EST HUMAN	L IN	EST HUMAN	l L	L L	Į	TA L	1	TN TN	EST HUMAN	NI I	N	Į.	Į.	NT	Ę	LA	<u> </u>	F		NO.	Т		
Exon         ORF SEQ         Expression         (T           NO:         ID NO:         Signal         BL           14602         1.06         1.42           16242         26402         1.42           17484         27705         1.42           17842         27705         1.42           18628         28917         7.32           18628         28917         7.32           18629         2.76         4.2           19185         25249         4.2           10811         4.88         4.2           11053         20895         6.06           11064         22653         2.63           13695         22759         4.28           13695         22643         2.63           14339         2445         2.51           14339         2445         2.51           1552         25643         2.51           1555         25643         2.51           1565         25549         4.35           1665         25769         4.35           1683         26016         3.02           16834         26501         2.32		Top Hit Acession No.	1 ~	5729867	8923669		T81910.1	2				-	02354R		1416196	-	_	-	,	_	4826987		5031892	(98289.1	9.1				357676	11321578 NT
Exon         ORF SEQ         Expression           NO:         ID NO:         Signal           14602         26402         1           16242         26402         1           17484         27705         1           18628         28917         7           18628         28917         7           18628         28917         7           18629         28930         2           10811         22063         2           13695         22759         6           13695         22759         6           13693         23445         2           14339         24129         3           14717         24500         0           15552         25643         4           15651         25759         4           16651         25759         4           16834         26501         2           16834         26501         2           16834         26501         1           19129         25262         1           19180         25266         1           19181         25266         4		Most Similar (Top) Hit BLAST E Value	4.0E-72	4.0E-72	4.0E-72	4.0E-72	4.0E-72	4.0E-72	3.0E-72	3.0E-72	3.0F-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	2.0E-72	2.0E-72	1.0E-72	1.0E-72	1.0E-72
Exan SEQ ID NO: 14602 16242 17484 18628 18737 19185 12965 17483 14339 15552 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15651 15		Expression Signal	1.06	4.	1.42	7.32	2.76	4.2	4.88	90.08	90.9	10.51	263	2.51	3.22	0.94	24	2.4	4.35	4.35	3.02	2.32	1.26	1.3	1.85	4.45	3.74	2.61	3.15	19.78
		ORF SEQ ID NO:			ļ		29030			20894	20895	ŀ		23445	24129	24500	25843	25644	25758	25759	26016	26501	26822	28051	25262	28257	25246	21812	25506	25976
Probe SEQ ID NO: A7716 6380 7633 8815 8815 8815 885 885 885 885 885 885		Exan SEQ ID NO:							10811		11053	12965	13164	13683	14339	14717	15552	15552	15661	15651	15893	16334	16634	17810	19129	18010	19182	11921	15441	15854
		Probe SEQ ID NO:	4716	6380	7633	8815	8929	9603	882	1139	1139	3037	3241	3750	4445	4835	5639	5639	5743	5743	2988	6475	6755	7960	9516	8122	9600	2030	5524	5949

Page 273 of 413 . Table 4 Single Exon Probes Expressed in Heart

DRF SEQ   Expression   Top) Hit   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acessio		<u> </u>				П	Т	7	Т	$\top$	_		$\neg$		_		$\neg$	Т		۳	Ť	····T	٣,	Т	Ψ,	·	_	ï	<u> </u>	<u> </u>	<del>-i</del>	<del></del>	-:-
DRF SEQ   Expression   Top) Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit Acession   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top Hit   Top H	Des Expressed in Heart	Top Hit Descriptor	Homo sanjane mynein haanv antwantiide 42 - 1-1-1-1	RC4-H70578-170300-012-02-H70578-1-2-3-868888 muscle (MYH13), mRNA	RC4-HT0578-170300-012-902 HT0578 HT0578 HT0578-17014	Homo sapiens synabilic plycopropein SC2 (SC2) in DNA	Homo sapiens synaptic disconotein SC2 (SC2) mRNA complete da	MR0-CT0063-071099-002-h11 CT0063 Home content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content	Homo sapiens ribosomal protein   13a (RPI 13A) mRNA	ws55c06x1 NCL_CGAP_Brn25 Homo septies cDNA done IMAGE:2501098 3' similar to TR:Q59050 D59050 HYPOTHETICAL PECTEIN M1455	OX39h08 x1 Space faetie NHT Long continue PNIA	Homo saciens lysochume homolog (1 OCE2464) Thomas aprens Cone ilyAGE:1639743 3	Homo sapiens vacuolar A Thase Isoform VA69 mbNs	bb62a06.vf NIH MGC 9 Homo saniens cDNA clore IMAGE 3020004 61 21 31	CYTOPLASMIC 2 (HUMAN); db://dx/2495 Mouse cytoskeletal gamme-entin mBN A commission inch.	Homo saplens interleukin 12 recentor, heta 1 (il 19881), monta	Homo sapiens interleukin 12 recentor, beta 1 / II 19RR11 mRNA	Homo saplens DNA for Human P2XM complete cds	Homo saplens thyroid autoantigen 70kD (Ku antigen) (Goop 1) mBNA	Homo sapiens hypothetical protein FL 120309 (FI. 120300) mRNA	Homo saplens chromosome 21 segment HS21Cnn6	Homo sapiens chromosome 21 segment HS21C082	Homo sapiens chromosome 21 segment HS21C018	QV0-HT0494-020300-137-d03 HT0494 Homo saniens cDNA	Homo sapiens HELG protein (FAW4A1) mRNA	Homo sapiens heme-binding protein (HEBP) mRNA	Homo sapians heme-binding profein (HERP) mRMA	Homo saplens BASS ( RASS ) mEMA mental calc	RC3-NN0066-270400-011-004 NNIONES Home complete PNIA	Human beta dobin region on chromosome 44	Homo sapiens caspase 8, apontosis-related custoine protected (CASDO) DNA	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA	
ORF SEQ         Expression Signed         (Top) Hit Top Hit Acess In IDNO:         Value Signed         Most Similar In Institution         Top Hit Acess In Institution         No.         Value PLAST E No.         No.         Value PLAST E No.         No.         Value PLAST Institution         No.	gie Exon Pro		Ę	lt			F	EST HUMAN	FA FA	EST HUMAN	EST HUMAN	NT	NT.		EST_HUMAN	N	F	F	N	N	N	N F	NT	EST_HUMAN	TN	LN PA	₽ F	FN	T HUMAN	ı			
Mos ORF SEQ Expression (Tild No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No. Signal No.		Top Hit Acession No.		BE1754	BE175434.1	AF222742.1	AF222742.1	AW374968.1	11424099		Al024877.1				BE019900.1	11526037	11526037	AB002059.1	11418189	8923290		AL163282.2	4L163218.2	3E166574.1	11422159	11435913	11435913	97.1	381.1	-	1	TN 659539	
ORF SEQ Express Sign D NO: Sign Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: Sign D NO: S		Most Similar (Top) Hit BLAST E Value	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	9.0E-73	9.0E-73	8.0E-73	8.0E-73	8.0E-73	8.0E-73		8.0E-73	8.0E-73	8.0E-73	8.0E-73	8.0E-73	7.0E-73	7.0E-73	7.0E-73	6.0E-73	6.0E-73	4.0E-73	3.0E-73	3.0E-73	2.0E-73	2.0E-73 /	2.0E-73	2.0E-73	2.0E-73	
		Expression Signal	19.78	3.82	3.82	90.9	90.9	1.23	23.9	1.03	3.06	4.6	2		15.88	2.22	2.22	2.12	2.69	0.78	1.06	1.62	2.37	3.36	2.05	0.99	0.99	1.75	1.48	1.1	3.48	0.96	
		ORF SEQ ID NO:				27594	27595	21213		20782	21163	25986	26785		27459	27682	27683	25282	25235	20875	22983			26274	24832	21595	21596	20610			22869	23221	
- 0   1   1   1   1   1   1   1   1   1		· Exon SEQ ID NO:	15854	16360	16360	17383	_ i		18197		11304	15864	16595		17254	17465	17465	19081	19217	11033	13184	14743	10126	16121	15138	11715	11715	10760	11798	12135	13069	13420	
Probe SEQ ID NO: NO: 17532 17532 17532 17532 17532 17532 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 17385 173		Probe SEQ ID NO:	5949	6501	6501	7532	7532	1443	8320	1022	1399	5959	6715		7385	7614	7614	9446	9654	1118	3261	4863	152	6255	5215	1818	1818	88	1902	2251	3144	3503	

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Table 4
Single Exon Probes Expressed in Heart

1	-					
ORF SEQ Expression ID NO:	Signal Signal		Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	0.0	96.0	2.0E-73	TR 669539 NT	Ŋ	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
	<u> </u>	7.6	2.0E-73	AB04681	본	Homo sapiens mRNA for KIAA1591 protein, partial cds
	1	1.35	2.0E-73	11431471 NT	¥	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
	1.	1.35	2.0E-73	11431471 NT	F	Homo saplens interleukin 4 receptor (IL4R), mRNA
	1.	1.34	2.0E-73	4504168 NT	F	Homo sapiens glufathione synthetase (GSS) mRNA
	2	45	2.0E-73	11496980 NT	F	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
28086 2	2	2.45	2.0E-73	11496980 NT	F	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
28272	4	4.14	2.0E-73	11431598 NT	IN	Homo sepiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
	6	3.79	2.0E-73	4557612 NT	N.	Homo sapiens galactosyteeramidase (Krebbe disease) (GALC), mRNA
	۳ ا	3.79	2.0E-73	4557612 NT	N.	Homo saplens galactos/iceramidase (Krabbe disease) (GAI C) mRNA
28562 1	7	1.78	2.0E-73	2.0E-73 AB028982.1	LN LN	Homo saplens mRNA for KIAA1059 protein, partial cds
1	1	1.72	2.0E-73	2.0E-73 AW898081.1	EST HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
	1	1.57	1.0E-73	1.0E-73 AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5
22207 0		0.93	1.0E-73		NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
27534	,	36	1.0E-73.AI147427	1	EST HIMAN	4961b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element
28140 2	2	2.67	1.0E-73 BE38547	BE385477.1	EST HUMAN	601276071F1 NIH MGC 20 Homo seniens cDNA clone IMA GE-2847405 F
20485 1	1	1.39	8.0E-74	4557428	4557428 NT	Homo sepiens CD39-like 4 (CD39L4) mRNA
		1.84	8.0E-74 S83194.1	583194.1		Ca2+/calmodulin-dependent protein kinase IV kinase isoform frats, brain, mRNA 3429 nfl
	•	1.84	8.0E-74 S83194.1		FZ	Ca2+/calmodulin-dependent protein kinase IV kinase Isoform [rats. brain, mRNA, 3429 nr]
		3.01	7.0E-74 AJ00168	3.1	NT	Homo sapiens NKG2D gene, exan 10
		669	7.0E-74 AL16324		NT	Homo sapiens chromosome 21 segment HS21C046
		7	7.0E-74		EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
25234		2.81	7.0E-74 L	7.0E-74 BE266305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
		2.58	6.0E-74 AF10990	1.7		Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
		1.03	6.0E-74 AW2631	77.1	EST HUMAN	xn78g07.x1 Soares NFL T GBC S1 Homo sabiens cDNA clone IMAGE-27nns36 31
	6	9.36	6.0E-74 E	0.1	EST_HUMAN	601283521F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3605453 5'
	6	96.6	6.0E-74	6.0E-74 BE388260.1 E	Г	601283521F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3605453 5
	+	1.39	6.0E-74	6.0E-74 AW014039.1	EST_HUMAN	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE-27ng3653
	`	1.39	6.0E-74		EST_HUMAN	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:27093653
23352 2	7	283	6.0E-74 E	6.0E-74 BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'

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Table 4
Single Exon Probes Expressed in Heart

		_													_	_				A11.	H . F									
	Top Hit Descriptor	hr64e11.x1 NCI CCAP Kid11 Home services only a less 1840 Consession	Homo saplens actin filament associated archin / A EAD) Days	df 7509 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica Homa cariotta - Data - Line St. 2009 v1 Morton Estal Cochica - Data - Line St. 2009 v1 Morton Estal Cochica - Data - Line St. 2009 v1 Morton Estal Cochica - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data - Data -	PM0-CT0289-27109-001-bn7 CT0280 Uses COINT CT0280 Uses CT0380 Uses CT0380-27109-001-001-001-001-001-001-001-001-001-	Homo sapiens phosphaticklinosital oliven clean (April) para	H. Sapiens mRNA for TDCR46 metein	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,	Bin variable products Homo saplens Interlaukin A recomfee (II AB)	Homo sabiens injerialikin 4 recentor (II AD)	Homo sapiens KIAA0716 dene moduri (ILAR), mrtiVA	Homo seplens hundhelical protein El 143232/El 143253	H.sablens mRNA for HIP-I	H.sapiens mRNA for HID-I	Homo sapiens DNA for amyloid medities amyloid medities and the sapiens and the sapiens and the sapiens and the sapiens and the sapiens are sapients and the sapiens are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the sapients are sapients and the 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dene product (KIAA0569) mBNA	Homo sapiens mRNA for transmetrana recentor profesion	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenasd3-ketoacyl-Coenzyme A thiolass/enoyl-Coenzyme A	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketcacyl-Coenzyme A thiolass/enoyl-Coenzyme A hydrotese (titli metional	EST13131 Thymus tumor III Homo sanlens cDNA 5' and similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar to similar 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,_	Top Hit Database Source	EST HUMAN	Į.	EST HUMAN	EST HUMAN	Į.	Ę	Ę	L	Ę	Į.	L	NT	LN.	N	1N	Į.	TN	1	NT.	NT	N	N	. LV	N	NT.	N-			T_HUMAN
	Top Hit Acession No.	BE048846.1	11056013 NT	5.0E-74 AW020986.1	5.0E-74 AW362756.1	11425417	5.0E-74 X89670.1	4507866INT	11431471 NT	11431471 NT	7662263 NT	11345483 NT	Y09420.1	Y09420.1	387675.1	AB028942.1	4.0E-74 AB026898.1	2	508192	4506192 NT	4.0E-74 AB032994.1		1	2	2	7662183 NT		4504326 NT	4504326 NT	3.0E-74 AA300378.1
	Most Similar (Top) Hit BLAST E Value	6.0E-74	6.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74 Y09420.1	5.0E-74 Y09420.1	4.0E-74 D87675.1	4.0E-74 AB02894;	4.0E-74 /	4.0E-74 AB026808	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74 AL 163210.	4.0E-74 AL 163247	4.0E-74	4.0E-74 Z17227.1	4.0E-74	4.0E-74	3.0E-74 A
	Expression Signal	2.63	2.49	258	5.19	2.15	10.48	6.74	1.85	1.85	3.73	2.69	1.88	1.88	1.89	4.95	2.44	2.44	4.34	4.34	1.21	0.99	4.44	0.83	1.31	1.57	0.82	3.76	3.76	5.03
	ORF SEQ ID NO:	23353				25045	25526	25552	25594	25595	26152	26758	28252	28253	20063	20611	21692	21693	21808	21809	21870	22149	22772	23204	23655	24142	24192	24644	24645	
	Exon SEQ ID NO:	13566			12534		15456	15479	15516			16564	18006	18006	10243	10761	11814	11814	11918	11918	11975	12257	12979	13389	13880	14351	14405	14880	14880	16854
	Probe SEQ ID NO:	3652	5294	887	2669	5320	5539	5563	5602	5602	6120	6684	8117	8117	278	834	1919	1919	2027	2027	2085	2377	3052	3483	3973	4457	4512	5006	5006	6977

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Single Exon Probes Expressed in Heart

	T	Т	T	T	T	Т	Т	Т	Т	Т	T	T	Т	T	Т	Τ"	Ť	T	T	T	Ť	Т	Ť	Ŧ	Ť	Ť	T	T	T
Top Hit Descriptor	Homo sapiens chromosome 21 segment HS210068	RC2-BT0642-270300-019-f06 BT0642 Homo sepiens cDNA	hz73h08x1 NCI_CGAP_Lu24 Homo saplens cDNA done IMAGE:3213663 3' similar to WP:B0511.12 CE17351 :	Homo sapiens DCRR1 mRNA, partial cds	601070088F1 NIH MGC 12 Homo saplens cDNA clone IMAGE:345626n 5	601070088F1 NIH MGC 12 Homo sapiens cDNA clone IMAGE:3456260 5	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds	Homo sapiens hypothetical protein FLJ10783 (FLJ10783) mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens glutafrione S-transferase fheta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) denes, complete cds	Homo sablens DNA cytosine-5 methytransferase 3R (DNM/T3R) mBNA complete 24.	Homo sablens chromosome 21 segment HS24Cnn2	wk38a08.x1 NCI_CGAP_Pr22 Homo septens cDNA done IMAGE:2417654 3' similar to gb:M14123_cds4_RETROVIRUS-RELATED POL POL YPROTEIN (HUMAN)	aj28c06.s1 Scares_testis_NHT Homo sapiens cDNA chee 1391626 3' similar to TR:Q15377 Q15377 YCHROMOSOME RNA RECOGNITION MOTIF PROTEIN:	MRO-SN0040-080600-006-q06 SN0040 Homo saniens cDNA	602186616T1 NIH_MGC 49 Homo sapiens cDNA done IMAGE 4298738 3'	#31o12.x1 NC _CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20.1 KD PROTEIN	QV1-BT0632-210200-079-e02 BT0632 Homo sepiens cDNA	yx90h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE-2eones st	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA	601303866F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE 3638344 5	Homo sapiens eukaryotic translation initiation factor 3. subunit 8 (110km) (FIF3SR) mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1). mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds	Homo saplens HTRA serine protease (PRSS11) gene, complete cds
Top Hit Database Source	NT	EST_HUMAN	EST HUMAN	<u>k</u>	EST HUMAN	EST HUMAN	I'N	F	N.	F	N.		LZ.	Į.	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	N	F	NT	, LN	LN	ĽΝ
Top Hit Acession No.	1.0E-74 AL163268.2	1.0E-74 BE083080.1	1.0E-74 BE467769.1		5.1	1.0E-74 BE549105.1	1.0E-74 AF214562.1	11420549 NT	11417856 NT	11417856 NT	1.0E-74 AB002059.1	1.0E-74 AF240788.1	4F176228.1	8.0E-75 AL163202.2	6.0E-75 AI817415.1	AA789285.1	3E841305.1	3F690254.1	٠.	4.0E-75 BE081333.1		4.0E-75 AW897230.1	3E409464.1	5579457 NT	11417946 NT	11417946 NT	39505	1.1	5
Most Similar (Top) Hit BLAST E Value	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	8.0E-75 AF17622	8.0E-75	6.0E-75	6.0E-75 AA78928	5.0E-75 BE84130	5.0E-75 BF690254	5.0E-75 A1638623	4.0E-75	4.0E-75 N36757.1	4.0E-75	4.0E-75 BE40946	4.0E-75	4.0E-75	4.0E-75	4.0E-75	3.0E-75 /	3.0E-75 AF157623
Expression Signal	4.56	6.0	6.0	1.19	1.83	1.83	3.92	1.31	1.6	2.83	4.14	1.36	4.07	1.67	0.88	0.86	1.04	1.22	3.1	1.05	1.23	1.5	4.65	4.29	1.56	1.56	8.72	2.91	2.25
ORF SEQ ID NO:	23584		23845	24754		26766	27182		. 29108		21968				22055		24746	27520	27969	19903		21498	22540	25806	26084	26085	28214	20754	20754
Exon SEQ ID NO:		13881	14070	14980		16574		17838			12066	19261	12475	19059	12157	14995	14970	17313	17726	10088	10395	11629	12747	15698	15953	15953	17963	10909	10909
Probe SEQ ID NO:	3887	3974	4170	5112	6694	6694	7112	7988	9024	9106	9249	9720	2607	9406	2273	5128	5102	7395	7876	107	451	1728	2818	5792	6052	6052	8072	986	987

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Table 4
Single Exon Probes Expressed in Heart

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Single Extension Tropes Expressed in hear	. Top Hit Descriptor	Homo sapiens mRNA for KIAA0581 protein, partial cds	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA	Homo sapiens chromosome 21 segment HS21C001	Homo saplens mRNA for KIAA0581 protein, partial cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Homo saplens DNA for amyloid precursor protein, complete cds	Homo sapiens KIAA0971 protein (KIAA0971), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevislae) homolog A (HIRA), mRNA	Homo sapiens HIR (histone cell cycle regulation defective. S. cerevicios) homologo A (una A.	Homo sapiens KIAA0623 gene product (KIAA0623) mRNA	Homo saplens KIAA0623 gene product (KIAA0623) mRNA	Homo saplens Oncodene TIM (TIM) mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo saplens snail 1 (drosophila homolod), zinc finger protein (SNAI1), mRNA	AV734680 cdA Homo sapiens cDNA clone cdABED02 5	qo91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE	xg60d02.xf NCI_CGAP_Ut4 Homo sepiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.t1 PTR7 repetitive element :	H.sapiens ERCC2 gene, exons 1 & 2 (partial)	257h03.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S RIBOSOMAL PROTEIN S17 (HUMAN):	601900294F1 NIH MGC 19 Home seniens CDNA clone IMAGE-4420878 E	601900294F1 NIH MGC 19 Homo sepiens cDNA clone IMAGE-4129678 5	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5	wb30b10.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2307163 3' similar to TR:075235 075235   TRAP1;
gie Exuil Fio	Top Hit Database Source	ΙN	TN	NT	NT	. TN	NT	NT	TN	NT	TN	TN	L	NT	IN	NT	NT	EST HUMAN	EST_HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	3.0E-75 AB011153.1	4507334 NT	4759153 NT	3.0E-75 AL163201.2	3.0E-75 AB011153.1	M72393.1	M72393.1	D87675.1	7662421 NT	11526319 NT	TN 61526319	7662209 NT	7662209 NT	4885632 NT	4885832 NT	11420804 NT	2.0E-75 AV734680.1	2.0E-75 Al311783.1	1.0E-75 AW168135.1	X52221.1	4A399270.1	1.0E-75 BF313645.1	1.0E-75 BF313645.1	√A664377.1	1.0E-75 AF223391.1	1.0E-75 BE894192.1	9.0E-76 A1652648.1
	Most Similar (Top) Hit BLAST E Value	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75 M72393	3.0E-75 M72393.	3.0E-75 D87675.	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	2.0E-75	2.0E-75	1.0E-75	1.0E-75 X52221.1	1.0E-75 AA39927	1.0E-75	1.0E-75	1.0E-75 AA66437	1.0E-75	1.0E-75	9.0E-76
	Expression Signal	1.98	1.05	3.66	1.19	1.33	1.01	1.01	1.42	96.0	1.53	3.1	3.83	3.83	2.92	2.92	123	1.5	1.73	5.09	3.17	4.13	3.73	3.73	3.99	2.6	1.86	1.45
	ORF SEQ ID NO:	21569			22711	. 22877	23030			24015	26183	26184			26522	26523	27259		27152	22037	22644		27499	27500		28573	24892	19825
	Exan SEQ ID NO:		11955		12916				13979	14233	16041	16041		16100	16353	16353	17070	15400	16959	12139	12843	16781	17290	17290	18137	18315	15100	10026
	Probe SEQ ID NO:	1795	2065	2373	2988	3152	3306	3306	4077	4336	6058	6058	6234	6234	6494	6494	7193	5480	7082	2255	2916	6903	7423	7423	8257	8441	9299	38

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ed in Heart	Top Hit Descriptor	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:075235 075235 TRAP1;	zl85b07.st Scares fetal liver spleen 1NFLS S1 Homo saniens cDNA clone IMAGE 447544 at	Heavy subunit mRNA, complete cds	H factor 1 (complement) (HF1) mRNA	H factor 1 (complement) (HF1) mRNA	mediator (Sur2), mRNA	LIM domain kinase 1 (LIMK1), mRNA	serine/threonine kinase 2 (STK2), mRNA	baculoviral IAP repeat-containing 6 (BIRC6), mRNA	calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyrnyata dehydrogenasa complex 2 cos	ex, branched chain keto acid dehydrogenase complex) (DLD) mRNA	cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	ymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA	Homo sapiens sepianterin reductase (7.8-dihydrobicoterin: NADP+ oxidoreductase) (SPR) mRNA	Homo sapiens sepiapterin reductase (7.8-dihydrobiopterin:NADP+ oxidoredinctase) (SPR) mRNA	VIH MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5	VIH_MGC_14 Homo saplens cDNA clone IMAGE:3506029 5'	for HMG-1, complete cds	for HMG-1, complete cds	for HMG-1, complete cds	Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5	Human fetal brain (TFujiwara) Homo saplens cDNA clone GEN-178G01 5'	b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 31	b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'	sukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA	sukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA	80100-033-A03 ST0300 Homo saplens cDNA	80100-033-A03 ST0300 Homo sapiens oDNA	ormalized Infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
Single Exon Probes Expressed in Heart	Top Hit Descriptor	b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar a	07.s1 Soares fetal liver spleen 1NFLS S1 Hamo saciens cDNA clone IMAGE.	Human ferritin Heavy subunit mRNA, complete cds	Homo sepiens H factor 1 (complement) (HF1) mRNA	Homo sapiens H factor 1 (complement) (HF1) mRNA	Homo sapiens mediator (Sur2), mRNA	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA	Homo sapiens serine/threonine kinase 2 (STK2), mRNA	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA	Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA	sapiens dihydrolipoamide dehydrogenase (E3 component of pynwate dehydrogen	glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo saplens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sepiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cycl (CBFA2T1) mRNA	sapiens sepiapterin reductase (7.8-dihydrobiopterin NADP+ oxidoreductase) (SP	sapiens sepiapterin reductase (7.8-dihydrobiopterin:NADP+ oxidoreductase) (SP	601312019F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3658757 5	601142253F1 NIH_MGC_14 Homo saplens cDNA clone IMAGE:3506029 5	Human mRNA for HMG-1, complete cds	Human mRNA for HMG-1, complete cds	Human mRNA for HMG-1, complete cds	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5	3W1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:30	UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'	Homo sapiens eukaryotic franslation elongation factor 1 beta 2 (EEF1B2) mRNA	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA	RC5-ST0300-180100-033-A03 ST0300 Homo saplens cDNA	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens oDNA	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zod04 3'
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e Exon P	Top Hit Database Source	EST HUMAN	EST HUMAN	LN LN	F	<u> </u>	11	1	±	  -	H		П	NT	П	E	E	上	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	_	T	EST_HUMAN	EST_HUMAN	EST_HUMAN
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	Most Similar (Top) Hit BLAST E Value	9.0E-76 AI65264	9.0E-76 AA70241	9.0E-76 M12937.	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76		7.0E-76	7.0E-76	7.0E-76	7.0E-76	7.0E-76	7.0E-76	6.0E-76	6.0E-76	5.0E-76 D63874.	5.0E-76 D63874.	5.0E-76 D63874.1	4.0E-76 D81625.	4.0E-76 D81625.	3.0E-76 B	3.0E-76	3.0E-76	3.0E-76	3.0E-76 BF37568	3.0E-76 BF37568	3.0E-76 Z41314.1
	Expression Signal	1.45	1.16	23.8	1.69	1.69	1.06	5.38	1.3	6.44	1.44	_	4.12	2.64	7.08	1.1	4.3	4.3	19.65	2.69	3.69	3.69	3.69	5.6	5.6	1.78	1.78	2.78	2.78	4.18	4.18	9.13
	ORF SEQ ID NO:	19826		27770	20695	20696	22603	25760	26443	28198			20527	22975	22982	23017	23951	23952		28154	21673	21674	21675	27834	27835	20359	20360	21345	21346	23099	23100	29104
	Exan SEQ ID NO:	10026	12244	17547	10848	10848	12807	15652	16282	17948	19207		10689	13177	13183	13215	14174	14174	11122	17910	11795	11795	11795	17609	17609	10549	10549	11485	11485	13300	1330	15084
	Probe SEQ ID NO:	38	2364	7697	923	923	2880	5744	6421	8057	9636		769	3254	3260	3293	4275	4275	1214	8761	1899	1899	1899	7759	7759	613	613	1581	1581	3382	3382	5204

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens andiostatin hinding protein 1 mDNA	W20a10.1 Soares melanocute 2NHM Home conjunction and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a 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Homo sapiens GM2 gandlocide activator protein (CR24) - 1014	Homo saplens GM2 gangloside activator protein (CM2A)	ZS60h11.sf Stratanene schizo brein S11 Home series - Date 1	OLFACTORY RECEPTOR-LIKE PROTEIN FR	zw64e02.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SI IRI INIT PREC IDSORD.	zw64e02.s1 Soares_testis_NHT Homo saplens SDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18984 INTECEDIA BETA 6 SI INIT FOLLOWING STATES IN THE SECOND BETA 6 SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT FOLLOWING STATES SI INIT	Human mRNA for possible madein TDBDII Complete 23	QV3-OT0028-220300-132-511 OT0028 Home conjunctions	Homo sapiens EGF-like repeats and discoidin Lille domains 3 (EDII 3) DNA	Homo sapiens mRNA for KIAA1081 mortal rac	Homo sapiens TPCR86 protein (HSTPCR8RP) PNIA	Homo sapiens similar to ribosomal protein S26 (H. carican) (1 CCS2252)	Homo Sapiens HIRA interacting protein 4 (dna Lillica) (HIRDIDA) - DNIA	Human mRNA for HMG-1 complete ode	Human mRNA for HMG-1, complete cds	601589896F1 NIH MGC 7 Homo saniens cDNA close MAA CE 2042282 El	601512435F1 NIH MGC 71 Homo seniens cDNA clone IMAGE: 3043737 E	601866926F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4109503 5'
21 - 100 - 216	Top Hit Database Source	Ę	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT -	¥	L	LV.	Į.	¥	¥	Z	EST HUMAN	SWISSPROT	EST HUMAN	EST HIMAN	LN LN	T HUMAN		NT	F	Ę	Ę	F	Z.	EST HUMAN		П
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	Most Similar (Top) Hit BLAST E Value	3.0E-76	3.0E-76 N42671	3.0E-76	3.0E-76	3.0E-76	3.0E-76 AW967	3.0E-76	2.0E-76	2.0E-76	2.0E-76 D84295.	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76 AA2539	2.0E-76 P23266	2.0E-76	2.0E-76	2.0E-76 D84295.	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	1.0E-76 D63874.	1.0E-76 D63874.	1.0E-76 BE79653	9.0E-77	8.0E-77 E
	Expression Signal	7.85	1.92	3.2	1.32	1.32	. 2.13	3.75	1.22	3.66	3.66	2.17	1.07	1.03	1.53	1.53	1.43	2.83	2.01	2.01	0.94	6.33	1.25	4.74	1.79	3.28	2.78	2.18	2.18	5.29	3.98	1.65
	ORF SEQ ID NO:	25861	26806	27667	27684	27685	25062	24895	20065	20112	20113		20320	20778	21281	21282	21658	22536	22979	22980	20065	24527	24710	25432	26554	27988	28416	23881	23882	25093	26119	24101
	Exon SEQ ID NO:	15748	16616	17453	17466	17466	19537	19745	10245	10298	10298	10397	10513	10932	11423	11423	11782	12740	13180	13180	10245	14747	14938	15374	16377	17748	18172	14100	14100	15266	15984	14315
	Probe SEQ ID NO:	5842	6737	7602	7615	7615	9014	9120	280	339	339	453	575	1014	1518	1518	1886	2811	3257	3257	4043	4867	2068	5453	6518	7898	8293	4200	4200	5345	6137	4421

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Table 4
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA	Ze62e02 rt Soares reithe NohAHP Home continue CDN/4 - Inc. 1144 OF Continue CDN/4	ze62e02.r1 Soares refina N2b4HR Home canions cDNA closs INA CE 220 FT	ye69f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains	219/1001 st Sogres facilie NHT Home amines and states assessed	Homo sepiens bolymerase (RNA) II (DNA directed) white II 7 (2015) (100)	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25KD) (POLRZE) mRNA	Homo sepiens interferon (alnha hete and one of virginity) (Coll R2E) mRNA	EST369823 MAGE resequences MAGE Long conjunction of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the Conference of the 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reneats and discoidin Like domains 3 (EDILS), mixiva	DKF26434G1728 r1 434 (synonym: Hoosa Union conjugate a (EULS), IIIRNA	Homo saplens 3-hydroxylsobuhryl-Coepayas A hydrolese (LIBCU) - Bala	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH) PNA	Homo sapiens sorting nexth 5 (SNX5) mRNA	Homo saplens sorting nexth 5 (SNXS), mRNA	Human mRNA for KIAA0299 gene, partial cds	Human mRNA for KIAA0299 gene, partial cds	Homo saplens SET domain and mariner transmisses frielow room (SETMAD).	Homo sapiens SET domain and mariner transposes finder con (SET 1/10)	PM3-MT0078-080800-005-003 MT0078 Home content of the ST I MAK) IMKNA	AV764617 MDS Home canians a DNA close MDS DT Co. 1	RC3-BND053-170200-041-brd BND059 Home Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control of the Cartesian Control	Homo sepiens CVP17 gene 5' and	Homo saniens CG-70 protein (1 OCE1624) TENA	Homo sapiens mRNA for Kla4445 mothin and in 24.	Homo sepiens mRNA for KIAA1415 protein, partial cds
Top Hit Database Source	FZ	EST HUMAN	EST HUMAN	ENT HIMANI	EST HUMAN	NT	N	Į.	EST HUMAN	EST HUMAN	N	LN	TN	N.	F	EST HUMAN	LN LN	N	F	TN	NT	N.	N-	N L	EST HUMAN	EST HUMAN	EST HUMAN	N-	Ę	NT	¥
Top Hit Acession No.	4506230 NT	11	AA019770.1	8.0E-77 R00245 1	AA625755.1	4505944 NT	4505944 NT	4504600 NT	170	6.0E-77 AI204066.1	AF041015.1	4557250 NT	4503160 NT	5031660 NT	5031660 NT	ľ	11428849 NT	11428849 NT	11421928 NT	11421928 NT	17.1	17.1	5730038 NT	E730038 NT	7.1	7.1	12.1		7706315	2.0E-77 AB037836.1	
Most Similar (Top) Hit BLAST E Value	8.0E-77	8.0E-77 AA0197	8.0E-77 AA0197	8.0E-77	7.0E-77 AA6257	7.0E-77	7.0E-77	6.0E-77	6.0E-77 AW957	6.0E-77	5.0E-77 AF0410	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77 AL0439	5.0E-77	6.0E-77	5.0E-77	5.0E-77	. 5.0E-77 AB00229	5.0E-77 AB0022	3.0E-77	3.0E-77	3.0E-77 BF35991	2.0E-77 AV76461	2.0E-77 AW9977	2.0E-77 L41825.	2.0E-77	2.0E-77	2.0E-77 A
Expression Signal	2.46	2.12	2.12	7.25	3.28	2.1	2.1	4.29	6.0	17.64	1.78	1.16	76.0	2.02	2.02	2.05	1.39	1.39	2.55	2.55	1.96	1.98	1.12	1.12	3.31	1.71	1.73	0.84	2.64	2.02	2.02
ORF SEQ ID NO:	25095	28861	28862	25232	21659	22136	22137	20043	20882	21287	20973	21101	22492	24280	24281	24514	26947	26948	27543	27544	28080	28081	21705	21706	28377	21093	21185	21830	21842	22312	22313
Exon SEQ ID NO:	15268	18578	18578	19289	11783	12240	12240	10227	11040	11429	11124	11243	12598	14493	14493	14733	16752	16752	17338	17338	17840	17840	11824	11824	18129	11237	11320	11935	11946	12724	12724
Probe SEQ ID NO:	5347	8691	8691	1776	1887	2360	2360	262	1125	1524	1216	1337	2736	4605	4605	4853	6873	6873	7519	7519	066/	88	1929	1929	8249	1330	1414	2044	2056	2549	2549

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Single Exon Probes Expressed in Heart

		-	_	-	_	_	_	_	_	_		<b>,</b>				_									****					<u>15.</u> 6				
, 110	Top Hit Descriptor	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28	Human von Willebrand factor gene, exon 20	Homo sapiens elastin (supravalvular aortic stenosis. Williams-Barren syndroma) /El NVDNA	Homo sapiens hu-GloAT-P mRNA for alucuranyliransferase, complete cds.	Homo sapiens hu-GlcAT-P mRNA for glucuron/transferase, complete cds	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA	RC2-ET0023-080500-012-e05 ET0023 Homo sabiens cDNA	RC2-E10023-080500-012-e05 ET0023 Homo saplens cDNA	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'	Homo sapiens GDNF family receptor alpha 1 (GFR41) mRNA	Home saplens hypothetical protein FLJ11316 (FLJ1316) mRNA	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6	CE22121;	Human collagenase type IV (CLG4) gene, exon 6	Homo sapien's Best's macular dystrophy related protein mRNA, partial ode	Homo saplens transforming growth factor, beta-induced, 68kD (TGFR)), mRNA	EST365190 MAGE resequences, MAGB Homo saniens cDNA	Human lysosomal alpha-mannosidase (manB) gene exon 7	601648061F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE 3931A87 5	Novel human gene mapping to chomosome 22	wr97b12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW:WAP_PIG	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA complete cds	Homo saplens syncytin (LOC30816), mRNA	Homo saplens phosphatidylinosital 4-kinase catalylic alpha polynemida (DIVACA) DNA	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polyneptide (PIKACA) mBNA	Homo saplens hypothetical C2H2 zinc finaer protein FI 1925/04 (FI 1925/04) mBNA	Homo sapiens hypothetical C2H2 zinc finger protein FI (22504 (FI (22504) mBN))	Homo sapiens s-CaBP1 (CABP1) mRNA. complete cds	Human transforming growth factor-beta precursor gene exons 4-5 (and injust mature matida)	Homo sapiens gene for AF-6, complete cds	Homo sapiens eRF1 gene, complete cds
	Top Hit Database Source	L	IN	LN	N.	LN	LN LN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	N.	L		EST_HUMAN	NT .	INT	NT	EST HUMAN	NT	EST_HUMAN	N _T	EST HUMAN	N F	Z Z	¥	¥	Ę			LN L	NT	NT
	Top Hit Acession No.	1.0E-77 AF086944.1	1.0E-77 AF086944.1	M25844.1	5881412 NT	1.0E-77 AB029396.1	1.0E-77 AB029396.1	9.0E-78 AW753302.1	AW947061.1	4W947061.1	AU118789.1	4U118789.1	11432710 NT	11422486 NT		4W673424.1		5.0E-78 AF038536.1	11416585 NT	120.1		5.0E-78 BE960836.1	11.1	4.0E-78 AI985094.1	05.1	7656876 NT	4505806 NT	4505806 NT	11560151 NT	11560151 NT	4.0E-78 AF169148.1	1	99.1	11.1
	Most Similar (Top) Hit BLAST E Value	1.0E-77	1.0E-77	1.0E-77 M25844	1.0E-77	1.0E-77	1.0E-77	9.0E-78	8.0E-78 AW947	8.0E-78 AW947	6.0E-78 AU1187	6.0E-78 AU1187	6.0E-78	5.0E-78	1	5.0E-78 AW673	5.0E-78	5.0E-78	5.0E-78	5.0E-78 AW953	5.0E-78 U60889.1	5.0E-78	4.0E-78 AL3558	4.0E-78	4.0E-78 AF1074	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78 X05844	4.0E-78 AB0113	3.0E-78 AF09590
	Expression Signal	1.93	1.93	1.56	11.39	1.22	1.22	2.53	2.97	2.97	1.83	1.83	2.51	1.1	,	4.1	3.81	2.39	9.35	2.17	6.5	3.75	1.6	1.53	2.21	1.39	1.27	1.27	1.94	1.94	1.97	3	2.85	1.6
	ORF SEQ ID NO:	25607	25608	25698	26089	28093			25907	25908		19882		19996	70000	18222	23066	25048	25396	26262	27318	27319	21265	21393	22053	23899	24340	24341	28058	28059	28822	28944	25239	19944
	Exon SEQ ID NO:	15525	15525	15597	15957	17852	17852	17863	15786	15786	10064	10064	15855	10182	70007	12389	13259	15243	15343	16110	17125	17126	11406	11533	12154	14125	14550	14550	17817	17817	18538	18656	19224	10129
	Probe SEQ ID NO:	5610	5610	5688	6197	8002	8002	8013	2880	2880	8	8	2950	211	7,700	C107	333	5323	5422	6244	7248	7249	1502	1629	2270	4227	4664	4664	7967	7967	8721	8844	9664	155

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Single Exon Probes Expressed in Heart

Single Extra Figures Expressed in real	Top Hit Database Source	NT Homo saplens eRF1 gene, complete cds	Homo saplens nuclear antigen Sp100 (SP100) mRNA	34 NT Homo sapiens synaptojanin 1 (SYNJ1), mRNA	EST_HUMAN CM0-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA	EST_HUMAN QV0-HT0367-150200-114-g09 HT0367 Homo saplens cDNA	NT Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20	EST_HUMAN EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end	EST_HUMAN UI-HF-BK0-saj-g-10-0-UI-1 NIH_MGC_36 Homp saplens cDNA clone IMAGE:3054139 5	EST_HUMAN UI-HF-BK0-aaj-9-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA done IMAGE:3054139 5	EST_HUMAN 602186529F1 NIH_MGC_49 Home sapiens dDNA clone IMAGE:4298599 5	EST_HUMAN AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5	EST HUMAN Pt2.1_16_B07.r tumor2 Homo septiens cDNA 3'				T_HUMAN	04 NT Homo sapiens GAP-like protein (LOC51306), mRNA	NT Human serine/threonine kinase MNB (mnb) mRNA, complete cds				EST_HUMAN RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA	NT Homo sapiens mRNA for activator of S phase Kinase, complete cds		NT Homo sapiens casein kinase II alpha subunit mRNA, complete cds	NT Homo sapiens casein kinase II alpha subunit mRNA, complete cds	NT Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete ods	NT Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds	NT Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds			
Healt		gene, complete cds	r antigen Sp100 (SP10	ojanin 1 (SYNJ1), mRI	3-065-c07 HT0180 Hol	114-g09 HT0367 Hot	collagen alpha 5 chair	cells VI Homo sapiens	JULY NIH MGC 36	J-UI.r1 NIH MGC 36	GC_49 Homo sapiens	o sapiens cDNA clone	r2 Homo sapiens cDN	r2 Homo sapiens cDN	P_Brn25 Homo sapler	KINASE;	tal liver spleen 1NFLS	ke protein (LOC51306	ne kinase MNB (mnb)	nsity lipoprotein-related	to lymphocyte activation	YY (PYY), mRNA	H014-C12 BN0074 Hor	for activator of S phas	in-conjugating enzyme	kinase II alpha subuni	kinase II alpha subuni	iger protein 216 splice	iger protein 216 splice	Pregulated IKK activat	ssor of white apricot h	ssor of white apricot h	a-glutamyltransferase
ul pesseidx⊒ se		Homo saplens eRF1 g	Homo sapiens nuclea	Homo sapiens synapt	CM0-HT0180-041099	QV0-HT0367-150200	Homo sapiens type IV	EST182583 Jurkat T-	UI-HF-BK0-aaj-g-10-0	UI-HF-BK0-aaj-g-10-0	602186529F1 NIH M	AV714177 DCB Hom	Pt2.1_16_B07.r tumo	Pt2.1_16_B07.r tumos	qisohosx1 NCI_CGA	CE06325 PROTEIN !	za48f12.s1 Soares fel	Homo sapiens GAP-II	Human serine/threoning	Homo sapiens low der	Homo sapiens similar	Homo sapiens peptide	RC2-BN0074-090300	Homo sapiens mRNA	Homo sapiens ubiquit	Homo sapiens casein	Homo sapiens casein	Homo sapiens zinc fin	Homo sapiens zinc fin	Homo sapiens TRAF6	Homo sapiens suppre	Homo sapiens suppre	Homo sapiens gamma
ופ באטוו רוטם	Top Hit Database Source	TN	N	NT	EST_HUMAN	EST_HUMAN	k	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	۲	NT.	Z			П	דא	5	Ę		닐	Z				
3110	Top Hit Acession No.	3.0E-78 AF095901.1	4507164 NT	4507334 NT	3.0E-78 BE144758.1	3.0E-78 BE156318.1			Г		1.1	7.1	2.0E-78 AI557509.1	2.0E-78 AI557509.1		-	2.0E-78 N66951.1	11417304 NT	1.0E-78 U52373.1	11430460 NT	11435903 NT	11525891 NT	7.1	1.1	5454145 NT			9.0E-79 AF062346.1	9.0E-79 AF062346.1	9.0E-79 AY008273.1	11423827 NT	11423827 NT	11417877 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78	2.0E-78 U04489.1	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78 AV71417	2.0E-78	2.0E-78		2.0E-78	2.0E-78	1.0E-78	1.0E-78	1.0E-78	1.0E-78	9.0E-79	9.0E-79 BE00083	9.0E-79 AB02807(	9.0E-79	9.0E-79 J02853.1	9.0E-79 J02853.1	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79
	Expression Signal	1.6	16.0	0.93	5.56	5.52	2.22	1.68	1.46	1.46	3.88	2.73	1.84	1.84		4.5	3.28	2.9	1.68	5.14	1.26	4.48	2.48	12.03	2.18	4.99	4.99	1.31	1.31	1.82	2.82	2.82	1.49
	ORF SEQ ID NO:	19945		23439		28478			26435		26584	26761	76897	26992				24943		25350	25327	24274	24431	25078	25844	27315	27316			28547	28906		25213
	Exon SEQ ID NO:	10129	13103	13657	17752	18226	13010	13841	16274	16274	16405	16567	16799	16799		18303	18340	15170	16622	18924	18986	14488	14643	15255	15733	17120	17120	17803	17803	18293	18616	18616	19347
	Probe SEQ ID NO:	165	3178	4015	7902	8349	3083	3932	6412	6412	6547	6687	6921	6921		8429	8467	5247	6743	9189	9284	4600	4758	5335	5827	7243	7243	7953	7953	8419	8802	8802	9854

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	[	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	Ť	T	T	Ϊ	T	T	T	T	Ť	T	Ť	T	Ť	T	-Mary
Omgo Lyon I open Lypessed III Healt	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C010	Human mRNA for KIAA0045 gene, complete cds	Human mRNA for KIAA0045 gene, complete cds	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3	294e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBLINIT	Homo sapiens chromosome 21 segment HS21C082	Homo saplens hypothetical protein FLJ10283 (FLJ10283) mRNA	601874522F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE-4101245 5'	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo saplens cell-line tsA201a chloride ion current inducer protein I/Cin) gene complete cds	Human zinc finger protein ZNF131 mRNA, partial cds	Homo sapiens MSTP016 (MST016) mRNA, complete cds	Homo saplens mRNA for KIAA0892 protein, partial cds	Homo sapiens netrin 1 (NTN1), mRNA	Homo sapiens netrin 1 (NTN1), mRNA	Homo sapiens mRNA for KIAA0620 protein, partial cds	Homo sapiens mRNA for KIAA0620 protein, partial cds	601159415F2 NIH MGC 53 Homo sapiens cDNA clone IMAGE:3511107 5'	Homo sapiens BCI 2-like 2 (BCI 2I.2) mRNA	th18h07.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:21186853'	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)	Homo sapiens hepatocellular carcinoma associated antigen 88 (HCA88) mRNA, complete cds	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds	Homo saplens mRNA for Fas-associated factor, FAF1 (Faf1 gene)	Homo sapiens chromosome 21 segment HS210006	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6) transcript variant 4 mRNA	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4 mRNA	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA	H4(D10S170)=putative cytoskeletal protein ihuman, thyroid, mRNA, 3011 nti	H4(D10S170)-putative cytoskeletal protein fluman, thyroid, mRNA, 3011 nri
און וווסעדו מול	Top Hit Database Source	N	N	NT	NT	EST_HUMAN	EST HUMAN	F	TN	EST HUMAN	N	NT.	N	NT	LN	LN	N	NT	IN	EST_HUMAN	4757841 NT	EST_HUMAN	NT	NT	TN	NT	NT	NT	IN.	FN.	N	M	NT	NT
5	Top Hit Acession No.	AL163210.2	D28476.1	4-	8567387 NT	7.0E-79 BE619648.1	6.0E-79 AA699829.1		2325	4.0E-79 BF210869.1	3.0E-79 AF114488.1	3.0E-79 AF232708.1	_	3.0E-79 AF110322.1	3.0E-79 AB020699.1	11426770 NT	11426770 NT		3.0E-79 AB014520.1	2.0E-79 BE379926.1	4757841	AI523747.1	4585863 NT	4585863 NT				3.1	5.2	7382479 NT	7382479 NT	11427428 NT		
	Most Similar (Top) Hit BLAST E Value	8.0E-79 AL16321	8.0E-79 D28476.	8.0E-79 D28476.	8.0E-79	7.0E-79	6.0E-79	5.0E-79	4.0E-79	4.0E-79	3.0E-79	3.0E-79	3.0E-79 U09410.	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79 AB01452	3.0E-79	2.0E-79	2.0E-79	2.0E-79 AI523747	2.0E-79	2.0E-79	2.0E-79 AJ271408	2.0E-79	2.0E-79	2.0E-79	2.0E-79 AL16320	2.0E-79	2.0E-79	2.0E-79	2.0E-79 S72869.1	2.0E-79 S72869.1
	Expression Signal	1.2	0.94	0.94	4.4	6.85	1.29	4.15	1.12	1.33	1.4	2.68	1.36	4.52	1.71	3.47	3.47	3.28	3.28	1.05	1.14	1.43	14.14	14.14	0.99	1.54	0.86	1.17	96'0	1.83	1.83	2.6	1.44	1.44
	ORF SEQ ID NO:	23382	24069	24070	24889			28891		24590	20091	20733	22778	25012	25486	25507	25508	26091	26092	20367	20685		21888	21889	21931	22049	23542	23755	24265	26270	26271	27029	27896	27897
	Exon SEQ ID NO:	13596	14287	14287	15097	13138	18827	18601	13064	14823	10272	10885	12987			15442	15442	15960	15960	10555	10836	10937	11990	1388	12034	12149	13749	13976	14478	16117	16117	16834	17658	17658
	Probe SEQ ID NO:	3682	4391	4391	9107	3214	9040	8786	3139	4946	310	362	3060	5291	5506	5525	5525	6200	6200	618	912	1019	2304	2303	2146	2265	3838	4074	4590	6251	6251	9269	7808	7808

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Single Exon Probes Expressed in Heart

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Onigio Evoli i ioneo Expressed III neall	Top Hit Descriptor	RC4-BT0310-110300-015-f10 BT0310 Homo sepiens cDNA	RC4-BT0310-110300-015-f10 BT0310 Homo septems cDNA	Homo sapiens KIAA0879 protein (KIAA0879), mRNA	Homo sapiens mRNA for KIAA0833 profein, partial cds	Homo sapiens cadherin EGF LAG seven-bass G-thoe recentor 1 (CFI SR1) mRNA	MR0-NN0087-250600-017-b10 NN0087 Homo saniens citiNA	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA	at23e05.s1 Soares testis NHT Homo sapiens cDNA clone 1343648.31	at23e05.s1 Soares testis NHT Home sapiens cDNA clone 1343648 s	601581652F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3936061 5'	Homo saplens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA	Homo saplens Y chromosome spermatracenesis candidate protein (PBNA)	Homo sapiens KIAA0724 gene product (KIAA0724) Theory Production (No. 1) pour or a sapiens KIAA0724 gene product (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home production (KIAA0724) Home p	Homo sapiens KIAA0724 gene product (KIAA0724) mRNA	Homo sapiens trible functional domain (PTPRE Internation) (TRIO)	Homo sapiens triple functional domain (PTPRF interaction) (TRIO) mRNA	#58402.x1 NCL_CGAP_Brrz3 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD St IRI INIT PRECTIREORD.	Homo sapiens NRD convertase mRNA, complete cds	Homo sapiens mRNA for KIAA1155 protein, partial cds	Homo sapiens mRNA for KIAA1155 protein, partial cds	Homo sapiens malate dehydrogenase 2. NAD (mitochondrial) (MDH2) mRNA	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)	Homo saplens tubby like protein 3 (TULP3), mRNA	Homo sapiens G protein-coupled receptor 51 (GPR51) mRNA	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA	Homo saplens chromosome 21 segment HS21C101	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gans, axon 21	Homo saplens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
באטון וייטאן פול	Top Hit Database Source	EST HUMAN	EST HUMAN	NT	IN.	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	IN	M	N LN	Į.	F F	F	N	EST_HUMAN	NT	IN	LN	NT	N	TN	TN	N	TN	NT	NT
5	Top Hit Acession No.	2.0E-79 BE064386.1	2.0E-79 BE064386.1	7662357 NT	2.0E-79 AB020640.1	11418322 NT	1.0E-79 BF363071.1	1.0E-79 BF087405.1	9.0E-80 AA725848.1	9.0E-80 AA725848.1	9.0E-80 BE798603.1	11433924 NT	11433924 NT		11422647 NT	11422647 NT	6005921 NT	6005921 NT	1422197.1		Ξ.	۲.	11421462 NT	6.0E-80 AJ404468.1	11436736 NT	11526464 NT	11526464 NT	.2		11427366 NT
-	Most Similar (Top) Hit BLAST E Value	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	1.0E-79	1.0E-79	9.0E-80	9.0E-80	9.0E-80	9.0E-80	9.0E-80	8.0E-80 U94387.1	8.0E-80	8.0E-80	8.0E-80	8.0E-80	6.0E-80 AI422197	6.0E-80 U64898.1	6.0E-80 AB03298	6.0E-80 AB032981	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80 AL163301	6.0E-80 U20211.1	6.0E-80
	Expression Signal	4.22	4.22	2.6	4.23	1.96	2.78	2.74	3.79	3.79	1.28	11.05	11.05	0.95	2.83	2.83	1.19	1.19	2.34	2.05	1.09	1.09	4.01	2.56	3.84	3.07	3.07	1.74	1.68	2.91
	ORF SEQ ID NO:	28516	28517	24888	25341	25307			22828	52829	27824	28735	28736		26512	26513	27482	27483	20657	21386	23865	23866	25532	25712	25791	27191	27192	27281	27748	28437
	Exon SEQ ID NO:	18267	18267		18907	19050	19456	18704	13033	13033	17601	18464	18464	13466	16343	16343	17276	17276	10808	11528	14088	14088	15461	15610	15683	17000	1700	17091	17522	18188
	Probe SEQ ID NO:	8391	8391	8078	9161	9391	5971	8894	3107	3107	7751	8597	8597	3551	6485	6485	7409	7409	882	1624	4188	4188	5545	5702	2776	7123	7123	7214	7672	8311

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	Top Hit Descriptor		tf58d02.x1 NCI_CGAP_Bm23 Homo saplens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR :	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	ilfotransferase, expn 1 2 3 4 5	otransporter (SGLT2 gene)	Homo sapiens proteasome (prosome, macropain) 26S subunit, nor-ATPase, 3 (PSMD3) mRNA	se (MNBH) mRNA, complete cds	se (MNBH) mRNA, complete cds		\$21C083	nolete cds	partial cds	(H3FJ) mRNA	annosyltransferase complete orls	lannos/itansferase complete orls	3210068	Krt2-6a). mRNA	ne s4000045F03	121C010	omo sapiens cDNA	mo sapiens cDNA	0023e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to	et	sapiens cDNA clone IMAGE:38060 5'	no sapiens cDNA clone RET487	DKFZp434D1323_r1 434 (synonym: https3) Homo saplens cDNA clone DKFZp434D1323 5'	in (90 kDa) (GTC90), mRNA	z/70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315	RESSED PROTEIN.;	521C103	
Onigia Lyon Frones Expressed III near		Homo sapiens Cyt19 mRNA, complete cds	#58d02.x1 NGI_CGAP_Bm23 Homo sapil Q16795 NADH-UBIQUINONE OXIDORE	Homo sapiens glutathione S-transferase the genes, complete cds	Homo sapiens CST gene for cerebroside sulfotransferase, expn 1, 2, 3, 4, 5	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)	Homo sapiens proteasome (prosome, mac	Homo saplens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	H.sapiens ncx1 gene (exon 12)	Homo saplens chromosome 21 segment HS21C083	Human ((3)mbt protein homolog mRNA, complete cds	Homo sapiens mRNA for KIAA1434 protein, partial cds	Homo saplens H3 histone family. member J (H3FJ) mBNA	Homo sapiens HMT-1 mRNA for beta-1.4 mannosyltransferase, complete cds	Homo sapiens HMT-1 mRNA for beta-14 mannosyltransferase, complete cds	Homo saplens chromosome 21 segment HS21C068	Mus musculus keratin complex 2, gene 6a (Krt2-6a). mRNA	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03	Homo sapiens chromosome 21 segment HS21C010	PM0-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA	QV4-BN0263-040600-241-910 BN0263 Homo sapiens cDNA	0023912.x1 Soares_NSF_F8_9W_OT_PA	1K:035/90 035/90 PIG-L.;	yg65a08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5'	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7	DKFZp434D1323_r1 434 (synonym: https3	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA	ZI7012.r1 Soares_testis_NHT Homo sapie	GISTSTS ANDROGEN-DEPENDENT EXPRESSED PROTEIN.	Homo sapiens chromosome 21 segment HS21C103 Homo sapiens chromosome 21 unknown mRNA	
פום רישונים	Top Hit Database Source	NT	EST_HUMAN	ĮN	NT	NT	NT	NT	NT	TN	NT	-N	N	N	N	NT	NT	F	EST_HUMAN	NT	Г	EST_HUMAN		OMAN	UMAN	UMAN	EST_HUMAN	NT		ESI HUMAN		
5	Top Hit Acession No.	6.0E-80 AF226730.1	A1422197.1	6.0E-80 AF240786.1	6.0E-80 AB029900.1	6.0E-80 AJ133127.1	4506228 NT	5.0E-80 AF108830.1	4F108830.1	X91647.1	5.0E-80 AL163283.2		5.1	4504292 NT	5.0E-80 AB019038.1			0203	-25915.1	3.0E-80 AL163210.2		3.0E-80 BE817465.1	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1091675.1	335321.1	1444821.1	2.0E-80 AL043116.2 EST_H	11421930		1	1.0E-80 AF231920.1	1
	Most Similar (Top) Hit BLAST E Value	6.0E-80	6.0E-80 A1422197	6.0E-80	6.0E-80	6.0E-80	. 5.0E-80	5.0E-80	5.0E-80 AF10883(	5.0E-80	5.0E-80	5.0E-80	5.0E-80 AB03785	5.0E-80	5.0E-80	5.0E-80	. 5.0E-80 /	5.0E-80	4.0E-80 F25915.1	3.0E-80	3.0E-80 t	3.0E-80 E	20 70 0	3.0E-80 AI091675.	2.0E-80 F	2.0E-80 /	2.0E-80/	2.0E-80	00 10 0	4 0E-80 AH383302	1.0E-80/	
	Expression Signal	50.71	1.98	1.62	4.55	2.25	1.11	1.26	1.26	4.77	2.28	0.92	3.98	1.13	1.07	1.07	1.74	1.48	7.48	4.71	1.43	4.97	0	2.05	6.39	1.91	9.9	1.58	900	1 200	1.12	
	ORF SEQ ID NO:	78694	20657				20319	20592	20593			22091	22152	22518	23636	23637	24531	26938	27441		24287		77130	14007	21527	21593	21791	26115	28372	2000	20551	
	Exen SEQ ID NO:	18425	10808	19562	19037	19686	10511	10745	10745	11084	11345	12192	12260	12626	13861	13861	14752	16745	17237	10181	14498	14701	46470	0/401	11656	11713	11901	15979	181.02	1020	10712	
	Probe SEQ ID NO:	8555	9047	9172	9371	9847	573	817	817	1172	1440	2311	2380	2764	3953	3953	4872	9989	7333	210	4610	4818	255	3	1/2/	1816	808	6132	8243	337	782	

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	Top Hit Descriptor	EST372729 MAGE resequences, MAGF Homo sapiens cDNA	2445h09.r1 Soares_pregnant_uterus_NbHPU Homo saplens cDNA clone IMAGE:485825 5' similar to PR:S52437 S52437 CDP-diaevidiocerol synthese - fruit fly	1245c04.v1 NCI CGAP Bm52 Homo saniens cDNA clone MAGE-2201528 F	Human aconitate hydratase (ACO2) gene, exon 3	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA	Homo sapiens arm-repeat protein NPRAP/heuroiungin (CTNND2) mRNA partial cris	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA	601645051F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE:3930228 5	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'	601577339F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3838280 5'	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA	MR0-CT0006-250599-019 CT0006 Homo saplens cDNA	EST372729 MAGE resequences, MAGF Horno saplens cDNA	601867714F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4110459 5	Homo saplens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA	Homo sapiens HSPC288 mRNA, partial cds	Homo sepiens HSPC288 mRNA, pertial cds	Human ORFB4 gene, partial cds	Human CRFB4 gene, partial cds	Human CRFB4 gene, partial cds	Homo sapiens mRNA for KIAA1327 protein, partial cds	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2	mRNA	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'	nf69e11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:925196 3'
2.6	Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	N	FN	Ę	N	N	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	TN	N	Z.	Z	N.	LN		NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	1.0E-81 AW960658.1	AA040370.1		U87928.1	11432966 NT	11432966 NT	U52351.1	U52351.1	1.0E-81 BF674641.1	11432966 NT	BE958278.1	BE958278.1	1.0E-81 BE564367.1	1.0E-81 BE744545.1		1.0E-81 AW897550.1	1.0E-81 AW844986.1	1.0E-81 AW844986.1	1.0E-81 AW960658.1	1.0E-81 BF204253.1	11418138 NT	6.1	AF161406.1	1			8.0E-82 AB037748.1		6715601 NT	8923432 NT	7.1	0.1	2.1
	Most Similar (Top) Hit BLAST E Value	1.0E-81	1.0E-81 AA0403	1.0E-81	1.0E-81 U87928.	1.0E-81	1.0E-81	1.0E-81 U52351.	1.0E-81 U52351.	1.0E-81	1.0E-81	1.0E-81 BE95827	1.0E-81 BE95827	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	8.0E-82	8.0E-82 AF16140	8.0E-82 U08988.	8.0E-82 U08988.	8.0E-82 U08988.	8.0E-82		8.0E-82	8.0E-82	7.0E-82 BF03532	7.0E-82	5.0E-82 AA51551
	Expression Signal	2	3.07	7.85	9.03	4.01	4.01	3.54	3.54	3:15	6.4	2.62	2.62	4.81	2.93	2.93	1.46	1.96	1.96	2.42	1.96	3.62	1.87	1.26	1.66	2.17	1.11	1.12		1.24	0.81	1.27	1.82	0.81
	ORF SEQ ID NO:	23304	24091	24222	29103	24982	24983	25449	25450	25750	26606	27702	27703	27799	27909	27910	28091	28568	28569	23304	28915	25325	19789	19789	20044	20566	20845	21244		21400	23825		22495	23713
	Exen SEQ ID NO:	13516	14308	14439	15083		15206	15388		_			$\sqcup$		_		_		_}	_ [			8666	8666	10228	10726	10795	11380			14050	11339	12601	13937
	Probe SEQ ID NO:	3602	4414	4546	5203	5284	5284	5468	5468	5737	6567	7831	7831	7726	7819	7819	8	8438	8438	8694	8810	9278	12	ģ	383	797	88	1475	0	1636	9	1434	2739	4034

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Top Hit Descriptor	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	wp75e09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' sImilar to TR:O75276	Homo sapiens presenilin-1 gene, exons 1 and 2	Home sanians amount hats (AA)	RC2-BN0120-010400-013-002 BN0130 Decal sor protein (protease nextra-il, Alzheimer disease) (APP), mRNA	Homo sapiens transforming growth factor beta-activated kinasa-hinding motein 4 (TABA) — Data	Home contract and Literature (LAB1), MINNA	1 John Sapriers anythin bein (A4) precursor protein (protease nextin-li, Alzheimer disease) (APP), mRNA 1923-15 st Spares tevirs NIUT Lowers	RC6-PT0001-190400-24-802-B02-B02-B02-B02-B03-B02-B03-B03-B03-B03-B03-B03-B03-B03-B03-B03	Homo sablens chromosome 21 carment HS21 Chos	RC1-BN0005-260700-018-004 BN0005 Home saniens CDNA	Homo saplens ademyate rivilace antivetine antiversation ( tit. 11. )	Homo sapiens neurofronbic forming kings: 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 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YPEPTINE NAMETY CALACTORALISM TO ALLO TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE 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OF THE STATE OF THE	Homo sapiens ankvin-like with transmembrane domains 4 (ANICTMA) TONA	Homo sapiens mRNA for KIAA1077 protein partial cyls	Homo sapiens mRNA for KIAA1077 protein, partial cds	Homo sapiens mRNA for KIAA0999 protein, partial cds	Homo sapiens mRNA for KIAA0999 protein, partial cds	DKFZp434M117 r1 434 (synonym; htes3) Homo saniens cDNA clone DKFZp434M17 Ei	Homo sapiens DNA for amyloid precursor protein, complete cda	Homo sapiens glutamate receptor, ionofronic, keinene 1 (PRIK1) m.D.NA	Homo sapiens mRNA for KIAA1096 mortial cds	Homo sapiens mRNA for KIAA1096 motern nartiel cds	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and	replication ractor of subunit 2 (RFC2) gene, complete cds. Homo earlians trings control of the complete cds.	Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF5) mRNA Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
Top Hit Database Source	N-	EST HUMAN	IN	L	EST HUMAN	TN	TIV	EST HIMAN	EST HIMAN	NT	EST HUMAN	IN	IN		<b>EST HUMAN</b>	LN.	LN	TN	NT	TN	EST_HUMAN	NT	NT.	LN	NT	LN		
Top Hit Acession No.	AF081484.1	Al937300.1	4.0E-82 AF029701.2	4502166 NT	12	5174702 NT	4502166 NT	3.0E-82 AA725848.1	3.0E-82 AW875073.1	3.0E-82 AL163285.2	3.0E-82 BE813232.1	4501922 NT	5453811 INT		3.0E-82 AA135979.1	11425206 NT				16.1	30.1	1	4504116 NT	19.1	19.1	15.	4507580	4507580 NT
Most Similar (Top) Hit BLAST E Value	4.0E-82 AF081	4.0E-82 A19373	4.0E-82	3.0E-82	3.0E-82 BE005	3.0E-82	3.05-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82		3.0E-82	3.0E-82	3.0E-82	3.0E-82 /	2.0E-82 /	2.0E-82 /	2.0E-82 AL0463	2.0E-82 D87675.	2.0E-82	2.0E-82	2.0E-82 AB0290	2.0E-82 A F0455	20E-82	2.0E-82
Expression Signal	6.51	6.47	6.19	13.75	2.19	4.44	3.22	13.76	5.47	2.03	1.82	0.9	2.06		0.91	2.84	3.79	3.79	1.92	1.92	1.75	1.14	1.14	0.98	0.98	3.18	1.66	1.66
ORF SEQ ID NO:	21412	29054		20061	20446	20539	20629		21098		21630	21744			24501	26807	27728	27729	20326	20327	21428	23466	23815	24143	24144	24441	24653	24654
Exon SEQ ID NO:	11551	18761	19130	10242	10620	10700	10779	10963	11240	11355	11755	11855	13158		14718	16617	17504	17504	1920	10520	11562	13684	4 6 6 6 6 7	14352	14352	14653	14887	14887
Probe SEQ ID NO:	1647	8954	9519	276	289	270	852	1045	1333	1450	1859	1961	3234		4836	6738	7854	7654	285	282	1880	3772	4140	4458	4458	4768	5013	5013

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		Т	Т	1	Т	_	Т	$\neg$		Т	Т	_	Т	_	-	_	-	_	-r	_	-	<del></del>	<del>- , ·</del>	·~	·	<del>-</del>		<del>-: ;</del>		<u>-</u> -	
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens mRNA for KIAA0727 profein partial cds	Homo sapiens FAM4A1 splice variant a FAM4A11 mRNA complete add	Homo sapiens slit (Drosophila) homolog 3 (SI 173) mRNA	Human endogenous retrovirus-K. LTR U5 and gar gene	Human endogenous retrovirus-K. LTR U5 and gan gene	Homo sapiens CAGF9 mRNA, partial cds	Homo sapiens CAGF9 mRNA, partial cds	2031d10.s1 Soares parathyroid fumor NhHPA Homo sanions cDNA class NAA CE 202000 21	201g09.rt Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMACE 2002U3 3	Homo sapiens SRY (sex determining region Y-hox 10 (SC) 10 m MANA	Homo saplens melanoma differentiation associated protein-5 (MDAS) mBNA	601510859F1 NIH MGC 71 Homo saniens of NA clone IMAGE 2012207 g	RC4-BT0310-110300-015-f10 BT0310 Homp sapiens cDNA	Homo sapiens mRNA for KIAA0538 protein partial cds	UI-H-BW1-aga-f-03-0-UI.s1 NCI CGAP Sub7 Homo seniens c DNA clone IMAGE 3084052 21	Homo sapiens chromosome 21 segment HS21C009	Homo saplens chromosome 21 segment HS210046	802150403F1 NIH MGC 81 Homo saniens china Ilina Circa Ilina Caraga Ri	601273346F1 NIH MGC 20 Homo sapiens cDNA clope IMAGE 364/362 E	ZB48f12.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clans NAA CE 205922 2	no12h01.s1 NCI_CGAP_Phe1 Homo saplens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element:	7p37e07.x1 NCI_CGAP_Pr2B Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR.Q9Y3I6 Q9Y3I6	Human platelet Givcoprotein IIb (GPIIb) gene evons 2.30	H31h03.x1 Soures, NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2833525 3' similar to	OV. SELD TREIN F4447 I RIPOTHELICAL PROTEIN HI0034.;	2/59cn5 e1 Spares fetal liver enformation of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of t	Homo sapiens hypothetical protein FI J10379 (FI J10379) m.DNA	Homo saplens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,	Homo sapiens hyperion gene exons 1-50	Homo sapiens met proto-cncogene (hepatocyte growth factor receptor) (MET), mRNA
Jie Exon Pro	Top Hit Database Source	Z	Į.	N	LN FN	NT	TN	N	EST HUMAN	'l-'	1	N F	EST HUMAN	EST HUMAN	N	EST HUMAN		N	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	HOT HIMAN	NT	FOT LIBRAN	EST HIMAN	EST HIMAN		Ę	L	
	Top Hit Acession No.	AB018270.1		11321570	Y08032		2.0E-82 U80736.1	_		AA011278.1	11418097 NT	11545921 NT	6.1	1	1	Γ					_	5.1	-	-		6.0E-83 AW816405.1	T	0241	AR07866 NIT		1422024
	Most Similar (Top) Hit BLAST E Value	2.0E-82 AB0182	2.0E-82	2.0E-82	2.0E-82	2.0E-82 Y08032	2.0E-82	2.0E-82 U80736	2.0E-82 N94950.	2.0E-82 AA0112	2.0E-82	1.0E-82	1.0E-82 BE88510	1.0E-82 BE06438	1.0E-82	1.0E-82	1.0E-82	1.0E-82	9.0E-83	8.0E-83 BE38397	8.0E-83 N66951.	7.0E-83 AA58465	7.0E-83 BF22181	6.0E-83 M33320	8.HG	6.0E-83/	6.0E-83/	6.0E-83	6.0E-83	6.0E-83 AJ01077	6.0E-83
	Expression Signal	2.37	4.98	223	1.2	1.2	6.98	6.98	2.23	2.57	1.44	1.45	6.0	1.91	0.83	1.38	2.57	1.76	L'4	1.88	1.96	1.64	5.49	1.34	7.	1.09	0.94	0.95	1.72	2.13	1.79
	ORF SEQ ID NO:	25108	25762			27913					·	20321							27124	21165	21422			20169	21515	22709	22751		24928	25679	26452
	Exon SEQ ID NO:	15278	15654	16713	17671	17871	18493	18493	18868	19205	19395	10515	11100	11171	11172	17732	18016	18250	16934	11297	12647	12764	14596	10343	11647	12912	12969	13431	15160	15579	16291
	Probe SEQ ID NO:	5358	5746	6834	7821	7821	8628	8628	2005	9632	8923	211	1190	1264	1265	7882	8128	8373	7057	1392	1656	2836	4710	397	1747	2984	3031	3515	5236	5669	6430

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Top Hit Descriptor	Homo saplens myomesin (M-protein) 2 (165kD) (MYOM2) mRNA	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.t2 THR repetitive element :	Homo sapiens glutafhlone S-transferase theta 2 (GSTT2) and glutathlone S-transferase theta 1 (GSTT1) genes. complete cds	Human succinate dehadrogenase iran-protein externel A-ARB)	Homo sapiens 26S protessome renulatory subtunit (SI IC2) mDNA commissionals	Novel human dene mapping to chomosome X	Homo saplens catalase (CAT) mRNA	Homo sapiens catalase (CAT) mRNA	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D11) gene axm 11	Homo septiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquilin-conjugating enzyme EZD 3 (UBE2D3) genes, complete cds.	6015/1580F1 NIH MGC 74 Home semiens of NA Alance MAA CE COASCIONER	EST79542 Placenta I Homo sapiens cDNA similar to similar to endocencia control control	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.t2 THR repetitive element:	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 O92614 MYFI ORI AST หางความ	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614	2948/12.s1 Soares felal liver spleen 1NFI S Homo conference CNNA class 1144 OF concess of	RC6-ET0046-280600-013-H12 ET0046 Homo saniens cDNA	Homo sapiens sal (Drosophia)-like 1 (SALI 1) mRNA	Homo sapiens chromosome 21 segment HS210002	Homo sapiens hematopoletic progenitor cell antinen CD34 preminers (CD34) mBNA	Homo sapiens ankyrin repeat-containing protein ASB-2 (I OCS1676) mRNA	Homo sapiens ankyrin repeat-containing protein ASB-2 (1 OCS1676) mRNA	Homo saplens myosin, heavy polypeptide 4. skeletal muscle (MYH4) mRNA	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYHA) mRNA	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA. partial cds	Raffus norvegicus densin-180 mRNA, complete cds	Homo sapiens protein kinase CK2 catalytic subunit alpha gene exon 1	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
Top Hit Database Source	Ę	EST_HUMAN	Þ	¥	Į.	¥	Ā	N _T	N		EST HUMAN		EST HUMAN	EST HUMAN	NAM III TSE	EST HUMAN	EST HUMAN	N-1	Ę	F	Ę	F	Ę	Þ	N FN	N	NT	NT
Top Hit Acession No.	4505314 NT	AA486105.1	AF240786.1	5.0E-83 U17883.1	5.0E-83 AF006305.1		57013	4557013 NT	5.0E-83 AF083827.1							+	1.76	11430834 NT	2.2	9.1	7706398 NT	7706398 NT	11024711 NT	11024711 NT	33.1		2.0E-83 AF011920.1	
Most Similar (Top) Hit BLAST E Value	6.0E-83	6.0E-83 AA4861	6.0E-83 AF2407	5.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0E-83	4.0E-83	4.0E-83	3.0E-83	3.0E-83	2.0E-83	2.0E-83	2.0E-83 N66951.	2.0E-83 BE8286	2.0E-83	2.0E-83 AL1632(	2.0E-83 AF20287	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83 /	2.0E-83 U66707.	2.0E-83 /	2.0E-83 /
Expression Signal	6.77	6.32	3.11	4.14	2.1	0.92	10.99	10.99	0.86	1.47	96.0	4.5	1.82	1.9	9.	2.23	1.11	1.82	1	4.47	8.13	8.13	23.35	23.35	5.9	1.52	2.56	2.56
ORF SEQ ID NO:	27644								24739	20373				21529	21530	21654	22542			23915	24230	24231	25109	25110	26419	26736	26911	26912
Exon SEQ ID NO:	17430	18630	18834	10856	12649	13500	14885	14885	14964	10561	13385	10904	12612	11658	11658	11779	12750	13155	13621	14140	14446	14446	15279	15279	16258	16539	16718	16718
Probe SEQ ID	7579	8817	9050	931	2004	3586	5011	2011	5094	624	3469	981	2750	1759	1759	1883	2821	3234	3708	4241	4553	4553	2320	6329	9336	9659	6839	6839

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	wa76c04.x1 Soarse_NFL_T_GBC_S1 Homo sapiens dDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR:	Homo sepiens myosin light chain klnase (soform 2 (MLCK) mRNA, complete cds	Human 2,4-dienoyl-CoA reductase gene, exans 3 and 4	Homo sepiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens mRNA for KIAA1130 protein, partial cds	Homo sapiens Bach1 protein homolog mRNA, partial cds	Homo capiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens percentriolar material 1 (PCM1) mRNA	Novel human mRNA containing Zinc finger C2H2 type domains	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds	wu20d05.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN):	CM1-BT0795-190600-272-b08 BT0795 Homo saniens cDNA	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA	Homo sapiens myelin transcription factor 1-like (MYT1-1) mRNA complete cds	H.sapiens DNA for endogenous retroviral like element	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5	601887684F1 NIH_MGC_17 Homo saplens cDNA done IMAGE:4121727 5	qm87c09.x1 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1895728 3'	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756C2211:	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:09UGS3 09UGS3 D.I756023 1	Homo sapiens intersectin short (soform (ITSN) mRNA complete cds	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	(1 VITIAL) IIIIVIA Homo caniane community community 5 (CE)DNA	norms septents compenent companent 5 (CS), mKNA am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
	Top Hit Database Source	EST_HUMAN	Ŋ	Į.	E	Ę	뉟	IN.	N	F	F	Ę	F		Z	NT NT	EST HUMAN	EST HUMAN	EST HUMAN	NT	N F	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Ę	TIN	L L	EST_HUMAN
	Top Hit Acession No.	4.0E-84 A1685321.1	4.0E-84 AF069601.2	4.0E-84 U94982.1	11386168 NT	11386168 NT	4.0E-84 AF059650.1	11421326 NT	4.0E-84 AB032956.1	3.0E-84 AF026200.1	4758081 NT	5453855 NT	3.0E-84 AL096880.1	, 000000 A		3.0E-84 AF014459.1	3.0E-84 Al983801.1	7.1		2.0E-84 AF036943.1		2.0E-84 BF308518.1	2.0E-84 BF308518.1	2.0E-84 AI298674.1	2.0E-84 BF448000.1	2.0E-84 BF448000.1	9.1	4507052 NIT	11427631 NT	1.0E-84 AA984379.1
	Most Similar (Top) Hit BLAST E Value	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	100	3.05-04	3.0E-84	3.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	1.0E-84	1 0F-84	1.0E-84	1.0E-84
	Expression Signal	4.03	1.76	1.27	1.31	1.31	2.35	12.15	6.56	1.36	0.89	1.15	3.03	0.7	9 ;	4.11	7.8	5.89	5.89	9.55	0.93	1.11	1.11	1.67	1.89	1.89	1.53	5.2	0.99	1.92
	ORF SEQ ID NO:	21151	24529					26543	28413	20094	20891	21690	21745	73054		23389		21845	21846	22640	22659	24364	24365		25334	25335	20090	20290		21026
	Exon SEQ ID NO:	11294	14749		Ш					10275			11856	43459		13002	18133	11948	11948	12840	12859	14568	14568	16575	19003	19003	10271	10478	10636	11178
	Probe SEQ ID NO:	1389	4869	5060	5416	5416	5791	6507	8290	313	1137	1917	1962	9540	2100	3000	8253	2058	2058	2913	2932	4682	4682	6695	9308	9308	309	537	703	1271

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	601308006F1 NIH MGC 44 Homo sanions aDNA alass 144 CF 200805 F1	Homo sapiens betrientrinlar material 4 (DONA4) - DONA4	INVI2808.ST NCI CGAP SST Homo saniens cinna chara MACE 2228478 21	Homo sablens 959 kb confid between AMI 1 and CRR1 on changing 24 and	DKFZp434N0323 r1 434 (synonym: hies3) Home samiens c DNA down DKEZ-494N0303 r1 434 (synonym: hies3) Home samiens c DNA down DKEZ-494N0300 r1	DKFZp434N0323 r1 434 (synonym htes3) Home septems CDNA clark DK-72-40 strange ri	Homo sapiens 959 kb contig between AMI 1 and CRR1 on chromosome 24,225.	uterine water channel≕28 kda erythrocyte integral membrane protein homolog lhuman, uterus, mRNA, 1340 nri	Novel human dene manning to chomosome 13	Novel human dene manning to chamcsome 43	Novel human dene manning to chamasama 13	Homo saplens bolymerasa (TNA directed) white (DOLA) DNA	Homo sapiens NGFLA binding popiein 1 (FRG4 hinding profess 4) NAAB41	Homo sablens nuclear transport factor 2 (historian de (historian de (historian de de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de historian de 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protein Skip mRNA, complete cds	Human plasminogen gene, exon 7	Human plasminogen gene, exon 7	Homo sapiens DKFZp434P211 protein (DKFZP434P211) mRNA	Homo saplens chromosome 21 segment HS21Cngn	Homo sapiens heat shock transcription factor 2 binding profession (Lie Ender)	Homo saplens chromosome 21 segment HS21Chea	Homo sapiens DKFZo434P211 protein (DKFZD434D241) BNIA	Homo sapiens ribosomal brotein 197 mRNA complete and	Homo sapiens MSTP030 mRNA complete orls	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polymentide 10 (RNA helicals)
gle Exon Pro	Top Hit Database Source	EST HUMAN	NT	EST HUMAN	IN	EST HUMAN	EST HUMAN	NT.		IN	LN PA	LZ.	Ę	NT.	Į.	L	Į.	N _T	Z V	LZ.	NT	FZ	N	TN	- L	N	F	N	F	LN LN	NT	Ļ
LIIO	Top Hit Acession No.	BE392137.1	11427197 INT	1.0E-84 AA720851.1	1.0E-84 AJ229041.1	1.0E-84 AL043314.2	1.0E-84 AL043314.2	Γ	1.0E-84 S73482.1	84.1	84.1	84.1	8393994	11430846 NT	5031984 NT	4507848 NT	4507848 NT	11417812 NT	11418185 NT	39.2	-	1	1	.1	7657020 NT	9.0E-85 AL163280.2	5901979 NT	8.2	7657020 NT	-	0.1	11438573 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84 AL0497	1.0E-84 AL0497	1.0E-84 AL0497	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	9.0E-85 AL1632(	9.0E-85 U51432	9.0E-85 U51432.	9.0E-85 M33282	9.0E-85 M33282	9.0E-85	9.0E-85	9.0E-85	9.0E-85 AL16326	9.0E-85	7.0E-85 L05094.	7.0E-85 AF1132	6.0E-85
	Expression Signal	3.13	1.08	2.14	5.59	3.82	3.82	4.29	1.52	1.49	1.49	1.96	3.12	1.8	2.45	1.85	1.85	2.98	9.6	1.17	2.3	2.3	1.07	1.07	4.93	0.94	1.14	1.01	1.27	3.24	5.81	2.56
	ORF SEQ ID NO:	21790	21964		23998	24275		23998	25773	26143		26236		26490		24884	24885		25330		20816	20817	21322	21323	21417	23832	24449	24491	21417	20877		28819
	Exon SEQ ID NO:	11900	12063		14216	14489	14489	14216	15665	16007	16007	16086	16276	16324	17365	15091	15091	18925	18998	10875	10974	10974	11465	11465	11554	14058	14862	14707	11554	11035	18718	18535
	Probe SEQ ID NO:	2008	2176	3691	4319	4601	4601	4823	5757	6113	6113	6220	6414	9483 883	7495	7639	7639	9190	9538	951	1057	1057	1360 500	1290	1831	4158	4778	4825	9819	1720	8970	8718

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Table 4
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	Homo sapiens DEAD/H (Asp-Glu-Alp-Asp/His) hox notoneofide 40 (DNA bolisses)	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo sapiens T-tvoe calcium channel aichest subumit Abshod Laineásann (2000-1044).	602084730F1 NIH MGC 83 Home saviers ANA Alma MAACE-Andore FI	602084730F1 NIH MGC 83 Homo sepiens CONA clane IMAGE-7248007 5	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA	HSDHEGC03 Stratagene cDNA library Hirman heart cattled 2000 Home consistent and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a constant and a 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member 2 (OB4202), EDNA	Hamo sapiens KIAA0793 gene product (KIAA0793) mRNA	Homo sapiens KIAA0783 gene product (KIAA0793) mRNA	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)	Homo sapiens DENN mRNA, complete cds	Homo sapiens phospholipase C, epsilon (PLCE), mRNA	Homo sapiens EGF-like repeats and discoidin Like domains 3 (FDII 3) mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1) mRNA	Homo saniens KIAA0020 nrotein Mev2 interneting and the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the saniens of the 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Top Hit Database Source	Į,	IN	NT	NT	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	N I	EST HUMAN	EST HUMAN	N N	N	NT	N	IN	N-	IN	N	NT	NT	N	L	N-L	N	NT	N	 	Ę
Top Hit Acession No.	11438573 NT	5.0E-85 AL163284.2	5.0E-85 AF224669.1	5.0E-85 AF211189.1	4.0E-85 BF677910.1	BF677910.1	4.0E-85 BE079263.1	4.0E-85 Z18867.1	3.0E-85 AF096157.1	T97495.1	3.0E-85 BE267189.1	11024695 NT	11024695 NT	3.0E-85 AB046783.1	7363442 NT	TN 605309	7662309 NT	1,1404468.1		11430889 NT	5031660 NT	11418177 NT	7657266 NT	AF248540.1	5174775	5174775 NT		7657468	4505880 NT
Most Similar (Top) Hit BLAST E Value	6.0E-85	5.0E-85	5.0E-85	5.0E-85	4.0E-85	4.0E-85 BF67791	4.0E-85	4.0E-85	3.0E-85	3.0E-85 T97495.1	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85 AJ404468	3.0E-85	3.0E-85	3.0E-85	3.0E-85	2.0E-85		2.0E-85	2.0E-85	2.0E-85 U10525.1	2.0E-85	2.0E-85
Expression Signal	2.56	1.21	1.9	2.45	1.66	1.66	1.68	1.97	1.15	3.37	0.94	1.73	1.73	8.66	0.94	6.94	6.94	7.04	1.61	4.06	2.28	2.66	0.87	1.85	7.1	7.1	212	4.24	5.42
ORF SEQ ID NO:	28820	22066	28598		25751	25752			21035	21509	23894	24475	24476	24523	24540	25739	25740	,	26663	27256	28901		20719	20786	21164	21165	21972		23913
Exan SEQ ID NO:	18535	12168	18335	15094	15646	15646	17867	19549	11185	11642	14117	14689	14689	14744	14764	15636	15636	16025	16474	17067	18610	19298	10871	10942	11305	11305	12070	11222	14138
Probe SEQ ID NO:	8718	2285	8462	9886	5738	5738	8017	9237	1277	1741	4219	4805	4805	4864	4883	62/5	6229	6152	6594	7180	8796	9788	947	1024	1400	1400	2183	2793	4239

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Table 4
Single Exon Probes Expressed in Heart

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Probe SEQ ID S NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4822	14705	24489	1.3	2.0E-85	2.0E-85 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7341	17209	27408	1.29	2.0E-85	2.0E-85 AI760820.1	EST_HUMAN	wi67h08.x1 NCI_CGAP_Kld12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 repetitive element ;
2241	12125		2.44	1.0E-85	1.0E-85 BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA done IMAGE:3945818 6
2344	12224	22121	8.09	1.0E-85	2.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2344	12224	22122	8.09	1.0E-85	2.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7632	17483	27704	2.06	1.0E-85			601109738F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3350553 5'
8296	18175	28419	2.56	1.0E-85	1.0E-85 AA778785.1	EST_HUMAN	245f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4532453'
8296	18175	28420	2.56	1.0E-85	1.0E-85 AA778785.1	EST_HUMAN	2/45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4532453′
8365	18242	28492	2.28	1.0E-85	1.0E-85 BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clane IMAGE:4126440 5'
8365	18242	28493	2.28	1.0E-85	1.0E-85 BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
9194	19082	25283	2.7	1.0E-85	1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9448	19082	25283	3.43	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1410	11315		7.66	9.0E-86	9.0E-86 BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5
220	10190	20001	1.3	7.0E-86	7662247 NT	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
921	10845	20691	1.33	7.0E-86	1.1	EST_HUMAN	aj88f08.s1 Scares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
921	10845	20692	1.33	7.0E-86	AA86080	EST_HUMAN	aj88f08.s1 Scares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6164	15121	24865	6.91	7.0E-86	_	NT	Homo sapiens Taxt (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
7078	16955	27148	2.91	7.0E-86	L38557.1	NT	Homo sapiens galactocerebrosidase (GALC) gene, exon 15
7593	17444		1.63	7.0E-86	5453997 NT	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
7624	17475	27696	2.35	7.0E-86	11526307 NT	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
8329	18206	28455	2.15	7.0E-86	1	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
8329	18206		2.15	7.0E-86	1	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
1272	11179	21027	9.33	6.0E-86	4505492 NT	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
204	10175		1.48	4.0E-86	3.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
2299	15586		10.18	4.0E-86	4.0E-86 BE295843.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
8567	10175	19993	1.9	4.0E-86	4.0E-86 BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo saplens cDNA clone IMAGE:3458830 5'
5435	15355	25411	6.02	3.0E-86	3.0E-86 AW340946.1	EST_HUMAN	xz92h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
7868	17718	27963	3.31	3.0E-86	3.0E-86 BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7868	17718	27964	3.31	3.0E-86	3.0E-86 BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5
8734	17883	28125	9.01	3.0E-86	3.0E-86 AI659240.1	EST_HUMAN	tu18b02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251371 3'
9163	19560		2.02	3.0E-86	3.0E-86 BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
266	10231	20046	1.33	2.0E-86	2.0E-86 AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5 end
408	10354		1.67	2.0E-86	2.0E-86 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21 C003

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Г	т	_	Т	1	Т	$\overline{}$	Т	Т	Т	Т	7			丁	_	Т	1	Т	Ť	Ť	<u></u>				1	٦	Ï	7	٦	T	7	
	Top Hit Descriptor	yz19a08.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:283478 5	Human endogenous refrovirus, complete genome	Homo sapiens mRNA for KIAA1277 protein, partial cds	EST378215 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds	hd87g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3	Homo sapiens cAMP-specific phosphodiesterase 84 (PDE8A) mRNA, partial cos	H.sapiens mRNA encoding phospholipase c	H.sapiens mRNA encoding phospholipase c	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)	(BBOX), mRNA	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA	Homo sapiens fibulin 5 (FBLN5) mRNA	Human gamma-glutamyl transpeptidase mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS210009	Homo sapiens hypothetical protein (LOC51318), mRNA	Homo sapiens hypothetical protein (LOC51318), mRNA	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens FK506-binding protein FKB23 isoform mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C084	qb77c09.xt Soares_fetal_heart_NbHH19W Homo saplens cDNA clone IMAGE:1706128 3' similar to SW:K1C1_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;
Single LAULI TODGS	Top Hit Database Source	T_HUMAN			T_HUMAN			T HUMAN	Ŋ	NT	NT	Þ		NT	NT	NT	NT	NT	FN	TN	NT	TN	NT IN	Ę	NT	Į.	N	NT	NT	TN	NT	EST_HUMAN
Sills	Top Hit Acession No.		9635487 NT	1	2.0E-86 AW966142.1	2.0E-86 AF156776.1	2.0E-86 AF156776.1	-	7.			11437135 NT		11437135 NT	11422084 NT	11545846 NT	11545846 NT	4759051 NT	11418189 NT	2.0E-86 AB011399.1	11417883 NT	4826855	5453649 NT	20492.1	4L163209.2	1.0E-86 AL163209.2	7706161 NT	7706161	AL 163300.2	1.0E-86 AF100751.1 NT	1.0E-86 AL163284.2	9.0E-87 AI150703.1
	Most Similar (Top) Hit BLAST E Value	2.0E-86 N58977.1	2.0E-86	2.0E-86 AB033103.	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86 A	2.0E-86 Z16411.1	2.0E-86 Z16411.1	2.0E-86		2.0E-88	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	1.0F-86	1.0E-86	1.0E-86 [L20492.1	1.0E-86	1.0E-86				1.0E-86		
	Expression Signal	2.18	2.37	1.12	1.43	2.16	2.16	2.42	2.8	1.53	1.53	222		2.22		2.69	2.69	1.83	2.4	1.81		3.1		2.42	1.32				5.76	1.11	2.15	1.47
	ORF SEQ ID NO:	20929	21930	22011	23087		23386			25571		27057		27058					25250		25139	21343									25378	
	Exon SEQ ID NO:	11085	12032	12107	13288	13599	13599	13862	14565	15495	15495	l	L	16864	1_	_	L	18156	19187	1	19520	l	1	1	\		1	1_	L		15328	1
	Probe SEQ ID NO:	1173	2144	2222	3369	3686	3686	3954	4679	5580	2580	6087		6987	7372	7969	7969	8276	9096	9772	9955	1570	3125	3197	3256	3256	3864	3864	4167	4832	8882	5287
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Single Exon Probes Expressed in Heart

Probe Exon SEQ ID SEQ ID NO: NO: 6403 16264 6403 16264 6403 16264 471 10414 2250 12134	S. Θ	Express: Signs	Most Similar (Top) Hit BLAST E Value 9.0E-87 8.0E-87 7.0E-87 7.0E-87	o. 4757721 4757721 1.1	Top Hit Database Source NT NT EST_HUMAN	Top Hit Descriptor  Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA O.cuniculus mRNA for elongation factor 1 alpha 7h85702.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
12134 17644 17644 18144 13398		2.74 2.67 2.67 3.38 3.38 10.88 0.87	7.0E-87 7.0E-87 7.0E-87 7.0E-87 7.0E-87 6.0E-87	2 2 2 657213	EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT NT	The STOCK INC. COAP. COTO Troing septens count done INAGE:3322779 3' The STOCK INC. COAP. COTO Homo septens cond live Coap.  IL3-HT0619-060700-198-D10 HT0619 Homo septens cond.  DKFZp434N0323_r1 434 (synonym: htes3) Homo septens cond. clone DKFZp434N0323 6'  DKFZp434N0323_r1 434 (synonym: htes3) Homo septens cond. clone DKFZp434N0323 6'  Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A  Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A  Homo septens hormonally upregulated neu tumor-associated kinese (HLNK) mRNA
15774 17997 11056 11056 11068 11068 11316		3,52 1,69 1,63 1,054 0,86 0,92	6.0E-87, 6.0E-87, 5.0E-87, 4.0E-87, 4.0E-87, 4.0E-87, 4.0E-87,	6.0E-87 AB029004.1 NT 6.0E-87 AA382811.1 ES 5.0E-87 AA382811.1 ES 4.0E-87 AL163210.2 NT 4.0E-87 AB037835.1 NT 4.0E-87 R78133.1 ES 4.0E-87 R78133.1 ES	NT EST_HUMAN EST_HUMAN NT NT EST_HUMAN	Homo sapiens mRNA for KIAA1081 protein, partial cds  Homo sapiens similar to SET translocation (myelcid leukemia-associated) (H. sapiens) (LOC63102), mRNA EST96094 Testis I Homo sapiens cDNA 5' end EST96094 Testis I Homo sapiens cDNA 5' end Homo sapiens chromosome 21 segment HS21C010 Homo sapiens mRNA for KIAA1414 protein, partial cds y80f10.r1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element, Homo sapiens mRNA for KIAA0456 protein, partial cds
12252 12252 13336 15264 15595	22142 22143 23140 25090 25696	1.07 1.07 2.19 6.47 4.36	4.0E-87 4.0E-87 4.0E-87 4.0E-87 8.0E-87	7706299 7706299 5174574 84.1	NT NT SWISSPROT EST HUMAN	Homo sapiens CGI-60 protein (LOC51626), mRNA Homo sapiens CGI-60 protein (LOC51626), mRNA Homo sapiens CGI-80 protein (LOC51626), mRNA Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4   (MLLT4) mRNA ETS-REIATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2) TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Bayfor-HGSC project=TCBA Homo sapiens   CONA clone TCBAP4051
18378 18798 19246 12611 13629 14708	29091 22502 22502 23414 24492	4.35 2.13 14.77 0.89 0.89	4.0E-87   4.0E-87 4.0E-87 2.0E-87   2.0E-87	7339 7812 5420	T HUMAN	Human von Willebrand factor pseudogene corresponding to exons 23 through 34 Human von Willebrand factor pseudogene corresponding to exons 23 through 34 Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA AU116935 HEMBA1 Homo sapiens cDNA done HEMBA1000307 5 CM0-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA

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Table 4
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3.0E-88 4501912 NT	3.0E-88 N66951.1 EST_HUMAN	3.0E-88 4508020 N	3.0E-88 4508020 NT	3.0E-88 11545800 NT	4.0E-88 /66194/NI	4.0E-88 7661947 NT	4.0E-88 7661947 NT	4.0E-88 4502694 NT	4.0E-88 11416585 NT	4.0E-88 BF091229.1 EST_HUMAN	4.0E-88 BF091229.1   EST_HUMAN	5.0E-88 AL163284.2 NT	5.0E-88 H10932.1   EST_HUMAN	5.0E-88 AF114488.1 NT	5.0E-88 AF114488.1 NT	5.0E-88 A 1693217.1 EST HUMAN		3.0E-00 At 114400.1	5.0E-88 AF114488.1 NT	5.0E-88 AF114488.1 NT	J.UE-00/AF (14400.1	5.0E-88 AF114488.1 NT	EST_HUMAN		7661887 NT	6.0E-88 AF003528.1 NT			ExpressionTop HitTop Hit AcessionTop Hit AcessionTop Hit AcessionSignalBLASTENo.Source
3 OF-88 4501012 NT	3.0E-88 4501912 NT 3.0E-88 4501912 NT	3.0E-88 Neo951.1 ESI_HUMAN 3.0E-88 4501912 NT 3.0E-88 4501012 NT	3.0E-88 N66951.1 EST_HUMAN 3.0E-88 4501912 NT 3.0E-88 4511012 NT	3.0E-88   4508020   NT 3.0E-88   N66951.1   EST_HUMAN 3.0E-88   4501912   NT 3.0E-88   4511012   NT	3.0E-88	3.0E-88 11545800 NT 3.0E-88 NG6951.1 EST_HUMAN 3.0E-88 NG6951.1 EST_HUMAN 3.0E-88 A501912 NT	4.0E-88     7661947 NT       3.0E-88     11545800 NT       3.0E-88     4508020 NT       3.0E-88 N66951.1     EST_HUMAN       3.0E-88     4501912 NT       3.0E-88     4501912 NT	4.0E-88     7661947 NT       4.0E-88     7661947 NT       3.0E-88     11545800 NT       3.0E-88     4508020 NT       3.0E-88 N66951.1     EST_HUMAN       3.0E-88     4501912 NT       3.0E-88     4501912 NT	4.0E-88	4.0E-88 11416585 NT 4.0E-88 7681947 NT 4.0E-88 7681947 NT 3.0E-88 11545800 NT 3.0E-88 4508020 NT 3.0E-88 4508020 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT	4.0E-88 BF091229.1 EST_HUMAN 4.0E-88 11416585 NT 4.0E-88 7661947 NT 3.0E-88 11545800 NT 3.0E-88 4508020 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 4501912 NT 3.0E-88 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      EST HUMAN           5.0E-88         AF114488.1         NT           6.0E-88         AF114488.1         NT           6.0E-88         AF114488.1         NT           6.0E-88         H10932.1         EST_HUMAN           4.0E-88         BF091229.1         EST_HUMAN           4.0E-88         T681947         NT           4.0E-88         T681947         NT           4.0E-88         T681947         NT           3.0E-88         T681947         NT           3.0E-88         4508020         NT           3.0E-88         4501912         NT           3.0E-88         4501912         NT           3.0E-88         4501912         NT	6.0E-88 AF003528.1 NT 5.0E-88 N89399.1 EST HUMAN 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 5.0E-88 AF144488.1 NT 6.0E-88 AF144488.1 NT 6.0E-88 AF144488.1 NT 6.0E-88 AF144488.1 NT 6.0E-88 AF163284.2 NT 6.0E-88 AF163284.2 NT 6.0E-88 AF163284.2 NT 6.0E-88 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1.21     3.0E-88     4501912 NT       3.17     3.0E-88     11429300 NT       4.09     3.0E-88     11429567 NT       3.84     3.0E-88     9966888 NT	1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429567 NT 3.84 3.0E-88 9966889 NT	4.31 3.0E-88 ND69501.1 ESI_HUMAN 1.21 3.0E-88 4501912 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429507 NT 3.84 3.0E-88 9966888 NT	4.31       3.0E-88   N66951.1       EST_HUMAN         1.21       3.0E-88       4501912   NT         1.21       3.0E-88       4501912   NT         3.17       3.0E-88       11429300   NT         4.09       3.0E-88       11429567   NT         3.84       3.0E-88       9966888   NT	4.77     3.0E-88     4508020 NT       4.31     3.0E-88 N66951.1     EST_HUMAN       1.21     3.0E-88     4501912 NT       3.17     3.0E-88     4501912 NT       4.09     3.0E-88     11429300 NT       4.09     3.0E-88     11429567 NT       3.84     3.0E-88     9966888 NT	4.77 3.0E-88 4508020 N1 4.31 3.0E-88 N66951.1 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4508020 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT	264 5.0E-88 H10932.1 EST_HUMAN 1.64 4.0E-88 RC91229.1 EST_HUMAN 1.63 4.0E-88 RC91229.1 EST_HUMAN 1.93 4.0E-88 T1416565 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 N66951.1 EST_HUMAN 4.77 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 3.0E-88 T601912 NT 3.0E-88 T601912 NT 3.0E-88 T601912 NT 3.0E-88 T601912 NT	2.64 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.84 5.0E-88 AL163284.2 NT 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 T091229.1 EST_HUMAN 1.93 4.0E-88 T091229.1 EST_HUMAN 2.1 4.0E-88 T081947 NT 2.1 4.0E-88 T081947 NT 2.1 4.0E-88 T081947 NT 2.1 3.0E-88 T081947 NT 4.31 3.0E-88 T081912 NT 1.21 3.0E-88 T4508020 NT 1.21 3.0E-88 T4508020 NT 1.21 3.0E-88 T4508020 NT 1.21 3.0E-88 T4508020 NT 1.21 3.0E-88 T1429300 NT 1.21 3.0E-88 T1429300 NT 1.21 3.0E-88 T1429300 NT 3.17 3.0E-88 T1429300 NT 3.17 3.0E-88 T1429300 NT 3.17 3.0E-88 T1429300 NT 3.17 3.0E-88 T1429300 NT 3.17 3.0E-88 T1429300 NT 3.184 3.0E-88 T1429300 NT	0.61 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.84 5.0E-88 H163284.2 NT 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 F1091229.1 EST_HUMAN 1.93 4.0E-88 T1416565 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 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5.0E-88 A1693217.1 EST_HUMAN 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 H10932.1 EST_HUMAN 1.84 5.0E-88 H10932.1 EST_HUMAN 1.84 4.0E-88 BF091229.1 EST_HUMAN 1.83 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 14501912 NT 1.21 3.0E-88 14501912 NT 1.21 3.0E-88 14501912 NT 1.21 3.0E-88 14501912 NT 1.21 3.0E-88 11429300 NT 4.09 3.0E-88 11429507 NT	2.31 5.0E-88 AI693217.1 EST_HUMAN 0.61 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.84 5.0E-88 H10932.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 T6091947 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 11545800 NT 2.1 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT 3.384 3.0E-88 9966898 NT	2.31 5.0E-88 AF114488.1 NT  2.31 5.0E-88 AI693217.1 EST_HUMAN  0.091 5.0E-88 AF114488.1 NT  2.64 5.0E-88 AF114488.1 NT  1.64 4.0E-88 BF091229.1 EST_HUMAN  1.64 4.0E-88 BF091229.1 EST_HUMAN  1.63 4.0E-88 BF091229.1 EST_HUMAN  1.93 4.0E-88 BF091229.1 EST_HUMAN  2.84 4.0E-88 BF091229.1 EST_HUMAN  2.95 3.0E-88 T061947 NT  2.1 4.0E-88 T061947 NT  2.1 3.0E-88 T061947 NT  4.77 3.0E-88 T061947 NT  4.31 3.0E-88 T061912 NT  1.21 3.0E-88 T061912 NT  4.31 3.0E-88 T061912 NT  4.31 3.0E-88 T061912 NT  4.31 3.0E-88 T061912 NT  3.17 3.0E-88 T1429301 NT  4.09 3.0E-88 T1429301 NT  3.17 3.0E-88 T1429301 NT  3.18 3.0E-88 T1429301 NT	0.94 5.0E-88 AF/14488.1 INT 0.94 5.0E-88 AF/14488.1 INT 2.31 5.0E-88 AF/14488.1 INT 0.61 5.0E-88 AF/14488.1 INT 0.61 5.0E-88 AF/14488.1 INT 0.67 5.0E-88 AF/14488.1 INT 2.64 5.0E-88 H10832.1 EST_HUMAN 1.63 5.0E-88 H10832.1 EST_HUMAN 1.63 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 T1416586 INT 2.1 4.0E-88 T16590 INT 2.1 4.0E-88 T16590 INT 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 EST_HUMAN 1.21 3.0E-88 H606951.1 IT H429300 INT 1.21 3.0E-88 11429300 INT 1.21 3.0E-88 11429300 INT 1.21 3.0E-88 11429507 INT 1.21 3.0E-88 11429507 INT	0.94 5.0E-88 AF114488.1 NT  2.31 5.0E-88 AI693217.1 EST_HUMAN  0.91 5.0E-88 AI693217.1 EST_HUMAN  0.91 5.0E-88 AF114488.1 NT  2.64 5.0E-88 AF114488.1 NT  1.84 6.0E-88 H10932.1 EST_HUMAN  1.84 6.0E-88 BF091229.1 EST_HUMAN  1.64 4.0E-88 BF091229.1 EST_HUMAN  1.93 4.0E-88 BF091229.1 EST_HUMAN  1.93 4.0E-88 T601942 NT  2.1 4.0E-88 7661947 NT  2.1 4.0E-88 7661947 NT  2.1 3.0E-88 A501912 NT  4.77 3.0E-88 A501912 NT  1.21 3.0E-88 A501912 NT  4.0B-88 A501912 NT  4.0B-88 A501912 NT  3.17 3.0E-88 A501912 NT  4.0B-88 A501912 NT  3.17 3.0E-88 A501912 NT  4.0B-88 A501912 NT  3.17 3.0E-88 A501912 NT  3.17 3.0E-88 A501912 NT  3.17 3.0E-88 A501912 NT  3.17 3.0E-88 A501912 NT  3.17 3.0E-88 A501912 NT	0.92       5.0E-88 AF114488.1       NT         0.94       5.0E-88 AF114488.1       NT         0.94       5.0E-88 AF114488.1       NT         0.91       5.0E-88 AF114488.1       NT         0.97       5.0E-88 AF114488.1       NT         2.64       5.0E-88 AF114488.1       NT         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.63       4.0E-88 BF091229.1       EST_HUMAN         2.84       4.0E-88 BF091229.1       EST_HUMAN         2.94       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 T661947 NT       T         4.0E-88 T661947 NT       4.0E-88 T661947 NT       T         4.0F-88 T661947 NT       4.0E-88 T661947 NT       T         4.3       3.0E-88 T661947 NT       T         4.3       3.0E-88 T661947 NT       T         4.3       3.0E-88 T661947 NT       T         4.3       3.0E-88 T661947 NT       T         4.0B-88 T661912 NT	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.63 4.0E-88 T061947 NT 2.1 4.0E-88 T061947 NT 2.1 3.0E-88 T061947 NT 4.77 3.0E-88 T061947 NT 4.77 3.0E-88 T061947 NT 1.21 3.0E-88 T061912 NT 1.21 3.0E-88 T061912 NT 1.23 3.0E-88 T061912 NT 1.24 3.0E-88 T061912 NT 1.25 3.0E-88 T061912 NT 1.27 3.0E-88 T061912 NT 1.28 3.0E-88 T061912 NT 1.29 3.0E-88 T061912 NT 1.29 3.0E-88 T061912 NT 1.21 3.0E-88 T061912 NT 1.21 3.0E-88 T061912 NT 1.21 3.0E-88 T061912 NT 1.22 3.0E-88 T061918 NT	3 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3.0E-88 NG6951.1 EST_HUMAN  1.22 3.0E-88 NG6951.1 EST_HUMAN  1.23 3.0E-88 NG6951.1 EST_HUMAN  1.24 3.0E-88 NG6951.1 EST_HUMAN  1.25 3.0E-88 NG6951.1 EST_HUMAN  1.26 3.0E-88 NG6951.1 EST_HUMAN  1.27 3.0E-88 NG6951.1 EST_HUMAN  1.28 3.0E-88 NG6951.1 EST_HUMAN  1.29 3.0E-88 NG6951.1 EST_HUMAN  1.21 3.0E-88 NG6951.1 EST_HUMAN  1.21 3.0E-88 NG6951.1 EST_HUMAN  1.22 3.0E-88 NG6951.1 EST_HUMAN  1.23 3.0E-88 NG6951.1 EST_HUMAN  1.24 3.0E-88 NG6951.1 EST_HUMAN  1.25 3.0E-88 NG69588 NT	3.69 6.0E-88 AF003528.1 NT  1.19 5.0E-88 N89399.1 EST HUMAN  0.92 5.0E-88 AF114488.1 NT  0.94 5.0E-88 AF114488.1 NT  0.94 5.0E-88 AF114488.1 NT  0.97 5.0E-88 AF114488.1 NT  0.87 5.0E-88 AF114488.1 NT  1.84 5.0E-88 AF114488.1 NT  2.64 5.0E-88 AF114488.1 NT  1.84 5.0E-88 AF114488.1 NT  2.64 5.0E-88 AF11468.1 NT  2.64 5.0E-88 AF116328.2 NT  1.64 4.0E-88 BF091229.1 EST HUMAN  1.63 4.0E-88 AF16328.1 EST HUMAN  1.63 4.0E-88 AF16328.1 EST HUMAN  1.63 4.0E-88 AF16328.1 EST HUMAN  2.1 4.0E-88 AF16328.1 EST HUMAN  2.1 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11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 3.31 3.0E-88 11429300 NT 3.31 3.0E-88 11429300 NT 3.31 3.0E-88 11429300 NT 3.32 3.0E-88 11429907 NT	2.31 5.0E-88 Al693217.1 EST_HUMAN 0.87 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 F7091229.1 EST_HUMAN 2.1 4.0E-88 F7091229.1 EST_HUMAN 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 2.1 3.0E-88 7661942 NT 1.21 3.0E-88 7661942 NT 1.21 3.0E-88 7661942 NT 1.21 3.0E-88 7661942 NT 1.21 3.0E-88 7661942 NT 1.21 3.0E-88 7661942 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 1.21 3.0E-88 11429300 NT 3.39 3.0E-88 11429567 NT 3.39 3.0E-88 11429667 NT	2.31 5.0E-88 Al693217.1 EST_HUMAN 0.91 5.0E-88 AF114488.1 NT 2.64 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.84 6.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 N66951.1 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AF114488.1       NT         1.64       4.0E-88 BF091229.1       EST HUMAN         1.64       4.0E-88 BF091229.1       EST HUMAN         1.64       4.0E-88 BF091229.1       EST HUMAN         2.1       4.0E-88 BF091229.1       EST HUMAN         2.1       4.0E-88 T061947 NT       T061947 NT         2.1       4.0E-88 T061947 NT       T061947 NT         3.0E-88 NG0951.1       EST HUMAN         1.21       3.0E-88 A501912 NT         4.31       3.0E-88 A501912 NT         3.17       3.0E-88 A501912 NT         4.09       3.0E-88 B066888 NT         3.39       3.0E-88 B066888 NT         3.39       3.0E-88 B066888 NT	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 AF163284.2 NT 0.93 3.0E-88 T061947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 T661947 NT 1.21 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T1429300 NT  1.21 3.0E-88 T1429300 NT  1.21 3.0E-88 T1429300 NT  4.09 3.0E-88 T1429300 NT  1.21 3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  4.09 3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT  3.0E-88 T1429300 NT	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 N89399.1 EST_HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.95 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 AF163284.2 NT 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 3.0E-88 T661947 NT 1.21 3.0E-88 T661947 NT 1.21 3.0E-88 T661912 NT 1.21 3.0E-88 T11429300 NT 1.21 3.0E-88 T11429300 NT 1.21 3.0E-88 T11429300 NT 1.21 3.0E-88 T11429300 NT 1.21 3.0E-88 T11429300 NT 1.21 3.0E-88 T11429300 NT 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3.39     3.0E-88     11420697     NT	4.77 3.0E-88	0.93     3.0E-88     11545800 NT       4.77     3.0E-88     4508020 NT       4.31     3.0E-88 N66951.1     EST_HUMAN       1.21     3.0E-88     4501912 NT       1.21     3.0E-88     11429300 NT       4.09     3.0E-88     11429300 NT       3.84     3.0E-88     9966888 NT       3.39     3.0E-88     11420697 NT	2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11645800 NT 4.77 3.0E-88 4508020 NT 4.31 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429567 NT 3.84 3.0E-88 11420697 NT	2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11645800 NT 4.77 3.0E-88 4508020 NT 4.31 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429567 NT 3.84 3.0E-88 11420697 NT	2.84 4.0E-88 4502694 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11545800 NT 4.77 3.0E-88 4508020 NT 4.31 3.0E-88 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AF114488.1       NT         1.64       4.0E-88 BF091229.1       EST HUMAN         1.64       4.0E-88 BF091229.1       EST HUMAN         1.64       4.0E-88 BF091229.1       EST HUMAN         2.1       4.0E-88 BF091229.1       EST HUMAN         2.1       4.0E-88 T061947 NT       T061947 NT         2.1       4.0E-88 T061947 NT       T061947 NT         3.0E-88 NG0951.1       EST HUMAN         1.21       3.0E-88 A501912 NT         4.31       3.0E-88 A501912 NT         3.17       3.0E-88 A501912 NT         4.09       3.0E-88 B066888 NT         3.39       3.0E-88 B066888 NT         3.39       3.0E-88 B066888 NT	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 AF163284.2 NT 0.93 3.0E-88 T061947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 T661947 NT 1.21 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T1429300 NT 3.0E-88 T1429300 NT 3.0E-88 T1429300 NT 3.0E-88 T1429300 NT 3.0E-88 T1429300 NT 3.0E-88 T1429300 NT 3.0E-88 T1429300 NT 3.0E-88 T1429300 NT	1.19 5.0E-88 7661887 NT  3 5.0E-88 N89399.1 EST HUMAN  0.92 5.0E-88 AF114488.1 NT  0.94 5.0E-88 AF114488.1 NT  2.31 5.0E-88 AF114488.1 NT  2.091 5.0E-88 AF114488.1 NT  2.092 5.0E-88 AF114488.1 NT  2.093 5.0E-88 AF114488.1 NT  1.64 4.0E-88 BF091229.1 EST HUMAN  1.93 4.0E-88 BF091229.1 EST HUMAN  1.93 4.0E-88 BF091229.1 EST HUMAN  1.93 4.0E-88 BF091229.1 EST HUMAN  2.1 4.0E-88 F091229.1 EST HUMAN  2.1 4.0E-88 F091229.1 EST HUMAN  2.1 4.0E-88 F091229.1 EST HUMAN  2.1 3.0E-88 T061947 NT  4.0E-88 T661947 NT  2.1 3.0E-88 T661942 NT  1.21 3.0E-88 H1429300 NT  4.09 3.0E-88 T1429300 NT  4.09 3.0E-88 T1429300 NT  3.17 3.0E-88 T1429300 NT  4.09 3.0E-88 T1429300 NT  3.39 3.0E-88 T1429300 NT  3.39 3.0E-88 T1429300 NT  3.39 3.0E-88 T1429300 NT	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 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4501912 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429367 NT 3.34 3.0E-88 11420607 NT	4.77 3.0E-88 11545800 NT 4.31 3.0E-88 4508020 NT 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT 3.84 3.0E-88 9966889 NT 3.39 3.0E-88 11420697 NT	2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11645800 NT 4.77 3.0E-88 4508020 NT 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT 3.34 3.0E-88 11429667 NT	2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11645800 NT 4.77 3.0E-88 4508020 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT 3.39 3.0E-88 11429667 NT	2.84	1.93 4.0E-88 11416565 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11645800 NT 4.77 3.0E-88 450820 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 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   3.0E-88 INGG951.1     EST_HUMAN       1.21     3.0E-88     4501912 INT       3.17     3.0E-88     11429300 INT       4.09     3.0E-88     11429567 INT	2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11545800 NT 4.77 3.0E-88 4508020 NT 1.21 3.0E-88 N66951.1 EST HUMAN 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 3.17 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT	2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11545800 NT 4.77 3.0E-88 4508020 NT 4.31 3.0E-88 N66951.1 EST HUMAN 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT	2.84 4.0E-88 4502694 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11545800 NT 4.77 3.0E-88 4508020 NT 4.31 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT	1.93 4.0E-88 11416565 NT 2.84 4.0E-88 4502694 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11545800 NT 4.77 3.0E-88 4508020 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 4501912 NT 1.21 3.0E-88 11429300 NT 4.09 3.0E-88 11429300 NT	1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 11416565 NT 2.84 4.0E-88 4502694 NT 2.1 4.0E-88 7661947 NT 2.1 4.0E-88 7661947 NT 0.93 3.0E-88 11545800 NT 4.77 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 11428300 NT 1.21 3.0E-88 11428300 NT 1.21 3.0E-88 11428300 NT 4.09 3.0E-88 11428300 NT	1.64	1.64	264 5.0E-88 H10932.1 EST_HUMAN 1.64 4.0E-88 RC91229.1 EST_HUMAN 1.63 4.0E-88 RC91229.1 EST_HUMAN 1.93 4.0E-88 T1416565 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 NG6951.1 EST_HUMAN 4.77 3.0E-88 NG6951.1 EST_HUMAN 1.21 3.0E-88 NG6951.1 EST_HUMAN 1.21 3.0E-88 NG6951.1 EST_HUMAN 1.21 3.0E-88 NG6951.1 EST_HUMAN 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 T601912 NT 1.21 3.0E-88 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5.0E-88 AF114488.1       NT         0.97       5.0E-88 AF114488.1       NT         2.64       5.0E-88 AF114488.1       NT         1.84       5.0E-88 AF114488.1       NT         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.63       4.0E-88 BF091229.1       EST_HUMAN         2.84       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 T661947 NT       T661947 NT         4.77       3.0E-88 T661947 NT       EST_HUMAN         4.77       3.0E-88 T66995 NT       EST_HUMAN         4.31       3.0E-88 T66995 NT       EST_HUMAN         4.31       3.0E-88 T66995 NT       EST_HUMAN         4.31       3.0E-88 T66995 NT       EST_HUMAN         4.09       3.0E-88 T1426900 NT       T1429300 NT         4.09       3.0E-88 T1426900 NT       T1429300 NT	3 5.0E-88 N89399.1 EST HUMAN  0.92 5.0E-88 AF114488.1 NT  0.94 5.0E-88 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3.0E-88 A501912 NT 1.21 3.0E-88 A501912 NT 1.21 3.0E-88 A501912 NT 1.21 3.0E-88 A501912 NT	0.94 5.0E-88 AF114488.1 INT 0.94 5.0E-88 AF114488.1 INT 2.31 5.0E-88 AI693217.1 EST_HUMAN 0.91 5.0E-88 AF114488.1 INT 0.87 5.0E-88 AF114488.1 INT 2.64 5.0E-88 AF114488.1 INT 1.84 5.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 2.1 4.0E-88 T661947 INT 2.1 4.0E-88 T661947 INT 2.1 3.0E-88 A508020 INT 4.31 3.0E-88 A508020 INT 1.21 3.0E-88 A501912 INT 1.21 3.0E-88 A501912 INT 1.21 3.0E-88 A501912 INT 1.21 3.0E-88 A501912 INT 1.21 3.0E-88 A501912 INT 1.21 3.0E-88 A501912 INT	0.94 5.0E-88 AF114488.1 NT  2.31 5.0E-88 AI693217.1 EST_HUMAN  0.91 5.0E-88 AI693217.1 EST_HUMAN  0.87 5.0E-88 AF114488.1 NT  2.64 5.0E-88 AI163284.2 NT  1.64 4.0E-88 BIF091229.1 EST_HUMAN  1.63 4.0E-88 BIF091229.1 EST_HUMAN  1.63 4.0E-88 BIF091229.1 EST_HUMAN  1.93 4.0E-88 BIF091229.1 EST_HUMAN  1.93 4.0E-88 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     EST_HUMAN         3.0E-88 T61947 NT       4.0E-88 T61912 NT         4.77       3.0E-88 T61912 NT       EST_HUMAN         4.31       3.0E-88 T61912 NT       EST_HUMAN         1.21       3.0E-88 T61912 NT       EST_HUMAN         3.17       3.0E-88 T61912 NT       EST_HUMAN	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 HT0932.1 EST HUMAN 1.84 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 T091229.1 EST HUMAN 2.4 4.0E-88 T091229.1 EST HUMAN 2.7 3.0E-88 T091229.1 EST HUMAN 2.1 4.0E-88 T091229.1 EST HUMAN 2.1 4.0E-88 T091229.1 EST HUMAN 2.1 3.0E-88 T091947 NT 4.77 3.0E-88 T091947 NT 1.21 3.0E-88 T091912 NT 1.21 3.0E-88 T091912 NT 1.21 3.0E-88 T091912 NT 1.21 3.0E-88 T091912 NT	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 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A501912 NT	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 AF003528.1 NT 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 1.84 5.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 T091229.1 EST_HUMAN 1.93 4.0E-88 T091229.1 EST_HUMAN 1.93 4.0E-88 A502694 NT 2.1 4.0E-88 T091229.1 EST_HUMAN 1.93 3.0E-88 T091912 NT 4.77 3.0E-88 T091912 NT 1.21 3.0E-88 T1429300 NT 1.21 3.0E-88 T1429300 NT 1.21 3.0E-88 T1429300 NT 1.21 3.0E-88 T1429300 NT 1.21 3.0E-88 T1429300 NT	3.69 6.0E-88 AF003528.1 NT  1.19 5.0E-88 N89399.1 EST HUMAN  0.92 5.0E-88 AF144488.1 NT  0.94 5.0E-88 AF144488.1 NT  0.94 5.0E-88 AF144488.1 NT  0.97 5.0E-88 AF144488.1 NT  0.87 5.0E-88 AF144488.1 NT  2.64 5.0E-88 AF144488.1 NT  1.84 5.0E-88 AF14488.1 NT  2.64 5.0E-88 AF14488.1 NT  2.64 5.0E-88 BF091229.1 EST HUMAN  1.64 4.0E-88 BF091229.1 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T165181 NT  2.1 3.0E-88 T165181 NT  1.21 3.0E-88 H509121 NT	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 1.64 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 AF163284.2 NT 2.1 4.0E-88 T061947 NT 2.1 4.0E-88 T061947 NT 2.1 3.0E-88 A501912 NT 1.21 3.0E-88 A501912 NT 1.21 3.0E-88 A501912 NT	3.69 6.0E-88 AF003528.1 NT  1.19 5.0E-88 N82399.1 EST HUMAN  0.92 5.0E-88 AF114488.1 NT  0.94 5.0E-88 AF114488.1 NT  0.91 5.0E-88 AF114488.1 NT  0.91 5.0E-88 AF114488.1 NT  0.91 5.0E-88 AF114488.1 NT  0.91 5.0E-88 BF091229.1 EST HUMAN  1.64 4.0E-88 BF091229.1 EST HUMAN  1.63 4.0E-88 AF16528.1 EST HUMAN  1.63 4.0E-88 AF16528.1 EST HUMAN  1.63 4.0E-88 AF16528.1 EST HUMAN  1.64 4.0E-88 AF16528.1 EST HUMAN  1.63 4.0E-88 T165129.1 EST HUMAN 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3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN	2.31 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.84 5.0E-88 H10932.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 T1416585 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 4.0E-88 T661947 NT 2.1 3.0E-88 NG6951.1 EST_HUMAN 4.77 3.0E-88 NG6951.1 EST_HUMAN 1.21 3.0E-88 NG6951.1 EST_HUMAN 1.21 3.0E-88 NG6951.1 EST_HUMAN	2.31 5.0E-88 Al693217.1 EST_HUMAN 0.91 5.0E-88 AF114488.1 NT 2.64 5.0E-88 H10932.1 EST_HUMAN 1.84 5.0E-88 H10932.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.63 4.0E-88 T091229.1 EST_HUMAN 1.93 4.0E-88 T091229.1 EST_HUMAN 2.84 4.0E-88 T091229.1 EST_HUMAN 2.94 4.0E-88 T091229.1 EST_HUMAN 2.1 4.0E-88 T091912 NT 2.1 4.0E-88 T091912 NT 4.77 3.0E-88 N66951.1 EST_HUMAN 4.77 3.0E-88 N66951.1 EST_HUMAN 1.21 3.0E-88 N66951.1 EST_HUMAN	2.31 5.0E-88 AI693217.1 EST_HUMAN 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EST_HUMAN	0.94 5.0E-88 AF114488.1 NT  2.31 5.0E-88 AI693217.1 EST_HUMAN  0.91 6.0E-88 AF114488.1 NT  2.64 5.0E-88 AF114488.1 NT  2.64 5.0E-88 H10932.1 EST_HUMAN  1.84 6.0E-88 H10932.1 EST_HUMAN  1.64 4.0E-88 BF091229.1 EST_HUMAN  1.64 4.0E-88 BF091229.1 EST_HUMAN  1.64 4.0E-88 BF091229.1 EST_HUMAN  1.63 4.0E-88 T691929.1 EST_HUMAN  2.84 4.0E-88 T691929.NT  2.94 4.0E-88 T661947 NT  2.1 4.0E-88 T661947 NT  2.1 3.0E-88 N66951.1 EST_HUMAN  4.77 3.0E-88 N66951.1 EST_HUMAN  1.21 3.0E-88 N66951.1 EST_HUMAN	0.92       5.0E-88 AF114488.1       NT         0.94       5.0E-88 AF114488.1       NT         0.94       5.0E-88 AF114488.1       NT         0.91       5.0E-88 AF114488.1       NT         0.87       5.0E-88 AF114488.1       NT         2.64       5.0E-88 H10932.1       EST_HUMAN         1.84       5.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         2.84       4.0E-88 T061929.1       EST_HUMAN         2.1       4.0E-88 T061947       NT         2.1       4.0E-88 T061947       NT         2.1       4.0E-88 T061947       NT         2.1       4.0E-88 T061947       NT         3.0E-88 NG6951.1       EST_HUMAN         4.31       3.0E-88 NG6951.1       EST_HUMAN         4.31       3.0E-88 NG6951.1       EST_HUMAN	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 1.84 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 T6091229.1 EST HUMAN 2.84 4.0E-88 T6091229.1 EST HUMAN 2.94 4.0E-88 T6091229.1 EST HUMAN 2.95 3.0E-88 AF16580 NT 2.1 4.0E-88 T609127 NT 2.1 3.0E-88 AF16580 NT 2.1 3.0E-88 R60951.1 EST HUMAN 4.77 3.0E-88 R60951.1 EST HUMAN 4.77 3.0E-88 R60951.1 EST HUMAN 4.77 3.0E-88 R60951.1 EST HUMAN 4.77 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N66951.1 EST_HUMAN	3.69 6.0E-88 AF003528.1 NT  1.19 5.0E-88 N89399.1 EST HUMAN  0.92 5.0E-88 AF114488.1 NT  0.94 5.0E-88 AF114488.1 NT  0.94 5.0E-88 AF114488.1 NT  0.97 5.0E-88 AF114488.1 NT  0.87 5.0E-88 AF114488.1 NT  1.84 5.0E-88 HT0932.1 EST HUMAN  1.84 5.0E-88 HT0932.1 EST HUMAN  1.84 4.0E-88 BF091229.1 EST HUMAN  1.84 4.0E-88 BF091229.1 EST HUMAN  1.84 4.0E-88 BF091229.1 EST HUMAN  1.83 4.0E-88 T661947 NT  2.1 4.0E-88 T661947 NT  2.1 4.0E-88 T661947 NT  2.1 4.0E-88 T661947 NT  4.77 3.0E-88 N66951.1 EST HUMAN  4.31 3.0E-88 N66951.1 EST HUMAN  4.31 3.0E-88 N66951.1 EST HUMAN  4.31 3.0E-88 N66951.1 EST HUMAN	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 AF003528.1 NT 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 1.64 4.0E-88 BF091229.1 EST HUMAN 1.63 4.0E-88 BF091229.1 EST HUMAN 1.63 4.0E-88 BF091229.1 EST HUMAN 1.63 4.0E-88 AF16588 NT 2.1 4.0E-88 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T661947 NT  4.31 3.0E-88 T661947 NT  4.31 3.0E-88 T661947 N	0.92       5.0E-88 AF114488.1       NT         0.94       5.0E-88 AF114488.1       NT         0.94       5.0E-88 AF114488.1       NT         0.91       5.0E-88 AF114488.1       NT         0.87       5.0E-88 AF114488.1       NT         2.64       5.0E-88 AF114488.1       NT         1.84       5.0E-88 AF1143284.2       NT         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.64       4.0E-88 BF091229.1       EST_HUMAN         1.69       4.0E-88 BF091229.1       EST_HUMAN         2.84       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 AL163284.2       NT         2.84       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 BF091229.1       EST_HUMAN         2.1       4.0E-88 AL163284.2       NT         2.3       4.0E-88 AL16328.1       7661947 NT         2.1       4.0E-88 AL163600 NT       4.0E-88 AL163600 NT         3.0E-88 AL1645800 NT       4.0E-88 AL1645800 NT         4.31       3.0E-88 AL1645800 NT       EST_HUMAN	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 2.64 5.0E-88 HT0932.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.63 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 BF091229.1 EST HUMAN 2.84 4.0E-88 BF091229.1 EST HUMAN 2.95 3.0E-88 T061947 NT 2.1 4.0E-88 T061947 NT 2.1 3.0E-88 T061947 NT 4.77 3.0E-88 T061947 NT 4.77 3.0E-88 T061947 NT 4.77 3.0E-88 T061950 NT 4.31 3.0E-88 T061950 NT 4.31 3.0E-88 T061950 NT 4.31 3.0E-88 T061951 T061940 NT 4.31 3.0E-88 T061951 T061940 NT 4.31 3.0E-88 T061951 T061940 NT 4.31 3.0E-88 T061951 T061940 NT 4.31 3.0E-88 T061951 T061940 NT	3 5.0E-88 N89399.1 EST HUMAN 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 0.87 5.0E-88 AF114488.1 NT 1.84 5.0E-88 HT0932.1 EST HUMAN 1.64 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4.77 3.0E-88 N66951.1 EST HUMAN  4.77 3.0E-88 R60920 NT  4.31 3.0E-88 R60951.1 EST HUMAN	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 F003528.1 NT 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 1.84 5.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.64 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 BF091229.1 EST_HUMAN 1.93 4.0E-88 AF09129.1 EST_HUMAN 1.93 4.0E-88 AF09129.1 EST_HUMAN 1.93 4.0E-88 AF09129.1 EST_HUMAN 2.1 4.0E-88 AF09129.1 EST_HUMAN 4.0E-88 AF091229.1 EST_HUMAN 1.93 4.0E-88 AF09129.1 EST_HUMAN 2.1 4.0E-88 AF09129.1 EST_HUMAN 2.1 4.0E-88 AF09129.1 EST_HUMAN 3.0E-88 AF09129.1 IT F09129.1 .69 6.0E-88 AF003528.1 NT  1.19 5.0E-88 N89399.1 EST HUMAN  0.92 5.0E-88 AF144488.1 NT  0.94 5.0E-88 AF144488.1 NT  0.97 5.0E-88 AF144488.1 NT  0.87 5.0E-88 AF144488.1 NT  0.87 5.0E-88 AF14488.1 NT  1.84 5.0E-88 AF14488.1 NT  2.64 5.0E-88 AF163284.2 NT  1.64 4.0E-88 BF091229.1 EST HUMAN  1.63 4.0E-88 BF091229.1 EST HUMAN  1.64 4.0E-88 BF091229.1 EST HUMAN  1.63 4.0E-88 T691229.1 EST HUMAN  2.84 4.0E-88 T691229.1 EST HUMAN  1.93 4.0E-88 T691229.1 EST HUMAN  2.84 4.0E-88 T691229.1 EST HUMAN  2.84 4.0E-88 T691929.1 EST HUMAN  3.0E-88 T691929 NT  2.1 4.0E-88 T691929 NT  2.3 3.0E-88 T69192 NT  4.31 3.0E-88 R60951.1 EST HUMAN  4.31 3.0E-88 R60951.1 EST HUMAN	3.69 6.0E-88 AF003528.1 NT 1.19 5.0E-88 AF003528.1 NT 0.92 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.94 5.0E-88 AF114488.1 NT 0.91 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 0.97 5.0E-88 AF114488.1 NT 1.84 5.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.64 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 BF091229.1 EST HUMAN 1.93 4.0E-88 AF16588 NT 2.1 4.0E-88 AF08090 NT 2.1 4.0E-88 AF08090 NT 4.77 3.0E-88 AF08090 NT 4.77 3.0E-88 BF09551.1 EST HUMAN 4.77 3.0E-88 AF08090 NT 4.31 3.0E-88 BF09551.1 EST HUMAN	

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Top Hit Descriptor Source Source	1.41 3.0E-88 AF034374.1 NT mRNA, complete cds	2.12 3.0E-88 11526262 NT Homo sapiens v-ets avian erythrobiastosis virus E28 oncogene related (ERG), mRNA	4.78 3.0E-88 11417974 NT Homo sapiens transcobalamin II; macrocytic enemia (TCN2), mRNA	1.42 2.0E-88 7305198 NT Homo sapiens Calsenilin, presentlin-binding protein, EF hand transcription factor (CSEN), mRNA	TN	AF24621	1666 NT	T_HUMAN	4.98 1.0E-88 AW 139565.1 EST_HUMAN   UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2718750 3'	7.1 NT	17.59 1.0E-88 AB007877.1 NT Homo sapiens KIAA0417 mRNA, complete cds	4.06 1.0E-88 AA488981.1 EST HIMAN CE00851:	1.0E-88 AL043314.2 EST HUMAN	2.27 1.0E-88 AA991479.1 EST HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN):	6.2 NT	4.12 9.0E-89 11421238 NT Homo sapiens transgelin 2 (TAGLN2), mRNA	T_HUMAN	1.35 7.0E-89 7657213 NT Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	7.0E-89 7657213 NT	57390 NT	7.0E-89 AL045748.1 EST_HUMAN	7.0E-89 X99832.1 NT	7.0E-89 X99832.1 NT	7.0E-89 11420754 NT	TN	1.42 7.0E-89 X62048.1 NT H.sapiens Wee1 hu gene	1.17 7.0E-89 AB020630.1 NT Homo saplens mRNA for KIAA0823 protein, partial cds	1.17 7.0E-89 AB020630.1 NT Homo sapiens mRNA for KIAA0823 protein, partial cds	7.0E-89 U87927.	6.0E-89 5803114 NT	1.12 6.0E-89 4506124 NT Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
																		8.0E-89												7.0E-89		
	Expression Signal	1.41	2.12	4.78	1.42	0.93	4.19	1.93	4.98	4.98	17.59	17.59	4.06	2.95	2.27	2.98	4.12	1.41	1.35	1.35	2.94	5.14	1.35	1.35	1.78	1.42	1.42	1.17	1.17	3.07	1.07	1.12
	ORF SEQ ID NO:	26836	26626		20780	21372		24007	25597	25598	26033	26034	26282		28135		28447	22459	20194		24457					28097		28107	28108			21954
	Exan SEQ ID NO:	16648		18988		11512			15518	15518	15909	15909	16128	i	17891	19117	18198	12568	10371			_			$\perp$	17856		17862	17862	_ [		12053
	Probe SEQ ID NO:	6929	7427	9286	1020	1607	1716	4328	5604	5604	6004	6004	6263	7524	8742	9502	8321	2705	426	426	4785	4847	5334	5334	6428	8008	8008	8012	8012	9920	1006	2166

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Single Exon Probes Expressed in Heart	SEQ Expression (Top) Hit Acession (Top) Hit Acession (Signal BLAST E No. Signal Value		22155 1.97 6.0E-89 4507788 NT Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA	0.84 6.0E-89 7661817 NT	AB007866.2 NT	24212 3.5 6.0E-89 AB007866.2 NT Homo sapiens mRNA for KIAA0406 protein, partial cds	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic faukemia Baylor-HGSC project=TCBA Homo sapiens 5.0E-89 BE244323.1 EST_HUMAN clone TCBAP0383	TCBAPZE0383 Pediatric pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Homo sapiens constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant co	1.33 4.0E-89 BE762749.1	1.61 3.0E-89 AW976181.1 EST_HUMAN	26215 1.92 3.0E-89 AV705749.1 EST_HUMAN   AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5'	1.46 2.0E-89 7706670 NT	1.46 2.0E-89 7706670 NT	0.91 2.0E-89 7706670 NT	0.91 2.0E-89 7706670 NT	20272 0.83 2.0E-89 AB037763.1 NT Homo sapiens mRNA for KIAA1342 protein, partial cds	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 22569 2.0E-89 Al222095.1 EST_HUMAN GAMMA-GLUTAM/YLTRANSPEPTIDASE 1 PRECURSOR (HUMAN):contains Alu repetitive element:	1.45 2.0E-89 AF089897.1 NT	2.0E-89 X58742.1 NT	6.18 2.0E-89 X58742.1 NT	1.14 2.0E-89 AJ007378.1 NT	2.5	1.6 2.0E-89 U03985.1 NT	26557 4.93 2.0E-89 U81004.1 NT Human GT24 (GT24) mRNA, partial cds	26699 3.73 2.0E-89 11428801 NT Homo sepiens solute carrier family 24 (sodium/potassium/caldum exchanger), member 2 (SLC24A2), mRNA	28851 2.63 2.0E-89 11434411 NT Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA	.2.0E-89 11433673 NT	2.24 2.0E-89 U10692.1 NT
	Exon ORF SEQ NO: ID NO:	12263	12263	13396	14430	14430	14881	14881	16336	12775	19241	10348	10348	10348	10348	10461	12780		13963	13963	14292	15288	15455	16379	16510	18568	18666	18762
	Probe SEQ ID NO:	2383	2383	3480	4537	4537	5007	5007	6477	2847	9688	121	121	402	402	519	2852	4053	4061	4061	4396	5368	5538	6520	6630	8680	8854	8955

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Single Exon Probes Expressed in Heart

		- m	7.5	_	_	_	_	_			_	_	_		_	<u> </u>		ine.		-	1111	estra-	_	~1100					artis.	Libera . albi
Single Lybressed III near	Top Hit Descriptor	hr81d09-x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN :	hr81d09x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTFIN ·	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	7e36f08.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284583.31	7e36f08 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	ai63d08.sr Soares testis NHT Homo saniens cDNA clone 1275503.3	601655837R1 NIH MGC 66 Homo sapiens cDNA class MAAGE-385834 3	601655837R1 NIH, MGC 66 Homo saplens cDNA clane IMAGE:3855824 3'	W86e04.s1 Soares fetal liver spleen 1NFLS Homo septiens cDNA clone IMAGE:212190 3' similar to SP:C1TC HUMAN P11586 C-1-TETRAHYDROFOI ATE SYNTHASE CYTOR ASMIC.	y86e04.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-C1TC HI IMAN P11588 C1. TETTA LIVER CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTENT AT EXAMPLES OF CONTE	H. sapiens ECE-1 dene (exon 6)	H.saplens ECE-1 gene (exon 6)	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sapiens HsGCN1 mRNA, partial cds	Homo sapiens HsGCN1 mRNA, partial cds	Hamo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo sapiens tnositol 1,4,5-triphosphate receptor, type 3 (TTPR3) mRNA	Hamo sapiens TCL6 gene, exon 1-10b	Human gamma-aminobutyric acid transaminase mRNA, partial cds	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds	Homo sapiens pregnancy-zone protein (PZP) mRNA	2982g10.s1 Soares fetal liver spleen 1NFLS S1 Homo saniens china Inda CE 481447 2	2/82g10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE-481442 2	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762P1616 5'
שום ביעטוו ג וה	Top Hit Database Source	EST HUMAN	EST HUMAN	ΝΤ	LN L	L L	Į.	EST_HUMAN	EST_HUMAN	L L	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HIMAN	NT	TN	NT	LN L	ΙN	TN	NT	NT	NT	NT	IN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession . No.	1.0E-89 BF196052.1	1.0E-89 BF196052.1	AL163246,2	9.0E-90 AL163246.2	8.0E-90 AL163246.2	8.0E-90 AL163246.2	BE670561.1	8.0E-90 BE670561.1	7.0E-90 AF223391.1		BE962525,2	7.0E-90 BE962525.2	468849.1	168849 1			TN 8922398	8922398 NT	1	1	4504794 NT	4504794 NT		5.0E-90 U80226.1		4506354 NT	5.0E-90 AA705222.1		5.0E-90 AL135549.1
	Most Similar (Top) Hit BLAST E Value	1.0E-89	1.0E-89	9.0E-90 AL1632	9.0E-90	8.0E-90	8.0E-90	8.0E-90	8.0E-90	7.0E-90	7.0E-90	7.0E-90	7.0E-90	7.0E-90 H68849.	7.0E-90)H68849	6.0E-90 X91926.	6.0E-90 X91926.	6.0E-90	6.0E-90	6.0E-90 U77700.	6.0E-90 U77700.	6.0E-90	6.0E-90	5.0E-90 AB03534	5.0E-90 I	5.0E-90 /	5.0E-90	5.0E-90	6.0E-90	5.0E-90/
	Expression Signal	6.12	6.12	1.16	1.16	1.62	2.93	5.28	5.28	2.65	1.91	1.88	1.88	1.98	1.98	1.14	1.14	7.33	7.33	3.54	3.54	3.25	3.25	10.5	1.55	2.19	3.08	1.07	1.07	0.98
	ORF SEQ ID NO:	28960	28961						21073			27250	27251	27927	27928	22749	22750	23809	23810	25646	25647	26918	26910		20931	22273	24124	24186	24187	24251
	Exan SEQ ID NO:	18672	18672	16668	16668	10965	10965	12690	12690	10746	16785	17060	17060	17683	17683	12957	12957	14034	14034	15554	15554	16725	16725	10123	11087	12382	14334	14400	14400	14463
	Probe SEQ ID NO:	8860	8860	6789	62/9	1047	1048	1308	1308	818	2069	7183	7183	7833	7833	3029	3029	4134	4134	6641	5641	6846	6846	<del>5</del>	11/5	7208 7208	<del>호</del>	4507	4507	4571

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Single Exon Probes Expressed in Heart	Xon ORF SEQ     Expression ID NO:     Signal     Another Signal     Top Hit Acession No.     Top Hit Acession Signal     Top Hit Acession Database Source     Top Hit Descriptor	5353 25409 2.52 5.0E-90 216411.1 NT H.sapiens mRNA encoding phospholipase c	5.0E-90 Z16411.1 NT	26302 2.26 5.0E-90 AF113708.1 NT	26303 2.26 5.0E-90 AF113708.1 NT	26489 7.93 5.0E-90 4557258 NT	26899 4.66 5.0E-90 11345483 NT	27646 1.24 5.0E-90 11419429 NT	28060 15.41 5.0E-90 11433721 NT	2.16 5.0E-90 AB01139	2.37 5.0E-90 A1523366.1 EST HUMAN	20083 1.85 4.0E-90 AF231920.1 NT	20084 1.85 4.0E-90 AF231920.1 NT	20829 2.94 4.0E-90 4505316 NT	21432 9.22 4.0E-90 X99033.1 NT	24235 4.07 4.0E-90 D87675.1 NT	24372 1.97 4.0E-90 AB033070.1 NT	24385 1.9 4.0E-90 M95967.1 NT	29004 103.62 3.0E-90 BE563833.1 EST HUMAN	19995 4.28 2.0E-90 BE537913.1 EST_HUMAN	20913 3.65 2.0E-90 5031748 NT	20914 3.65 2.0E-90 5031748 NT	23465 2.81 2.0E-90 A138213.1 EST HIMAN	24264 1.13 2.0E-90/AB006627.1 NT	24488 8.33 2.0E-90 5729855 NT	25519 4.34 2.0E-90 AW 672686.1 EST HUMAN	27708 2.9 2.0E-90 11427320 NT	27709 2.9 2.0E-90 11427320 NT	27796 1.56 2.0E-90 AU1189
										100	6																		
	SEQ ID NO:						16704	17432	17818	19306	19299	10263			_	_			18709	$\Box$		11069	13683	14476	14703	15451	17489	17489	17572
	Probe SEQ ID NO:	5433	5523	6283	6283	6464	6825	7581	7968	9744	9789	299	239	1070	1663	4557	4691	4713	8901	207	1156	1156	3771	4588	4820	5534	7638	7638	7722

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Table 4
Single Exon Probes Expressed in Heart

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onigne Exon Flobes Expressed III Real	Top Hit Descriptor	AU118985 HEMBA1 Homo saniene ADNA Alama LIELIDA400.1775 FI	Homo sapiens myosin, heavy polyneoritide 4. skeletal miscle (AVNA). — DNA	Homo saniane amulaid beta (AA) area mean in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th	Homo sapiens chromosome 21 inchesion protein (protease nextr-II, Alzheimer disease) (APP), mRNA	Homo sabiens chromosome 21 information PNA	Homo sapiens mRNA for T-box transcription factor (TBX20 conc.)	Homo sapiens mRNA for T-box transcription factor (TPV20 20015), partial	Homo saplens ALR-like profein mRNA partial rate.	Homo saplens ALR-like profein mRNA partial cds	Homo sapiens Krubnel-like factor 7 (Inhimitons) (KI E2) mDNA	Homo saplens profein phosphatase 24 RR damma cultumit and	Homo saplens profesion phesophetace 2.4 BB committee with the saplens profesion between the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee 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committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the committee of the	60/159563F2 NIH MGC 53 Home explana Chik All MACE 252/159	Homo sapiens similar to SAI 1 / cel / Presentally life // OCE24621	Homo sabians chromosome 8 area reading from 2 (2000) 101 (1)	Homo saniens mRNA for KIAAA002 matrix	Homo saplens mRNA for KIAA0903 protein, partial cas	Homo saplens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, atternative exons 9	Homo sapiens mRNA for KIA A Ress matrices	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6)	MKNA	Home septents prenendin A-thribited guanine nucleotide-exchange protein 2 (BIG2), mRNA	Houring Sapiens Sivicy Isonorm (SNCA) gene, complete cds, alternatively spliced	riomo sapiens CGI-15 protein (LOC51006), mRNA	Hours septens Cut-19 protein (LOCS1008), mRNA	Homo capteris DNA for 11	HIMMONS384 I have Une Complete cds	Rafflis noncold is the months and the Home sapiens cun a sapiens cun a sapiens cun a sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens 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sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens sapiens s	Homo sanjans makorin him finant maketing A Augusta.	290b04.s1 Soares fetal liver spleen 1NEI S St Long Control 1	AU143539 Y79AA1 Homo saplens cDNA clone Y79AA1002087 5
פום בעמון בנמי	Top Hit Database Source	EST HUMAN	NT	<u> </u>	L	L	NT	NT	NT	N	LN	IN	NT	EST HUMAN	4.	NT.	LZ	NT	LN LN	LN								T HI IMANI	Т		T HUMAN	П
	Top Hit Acession No.	2.0E-90 AU118985.1	11024711 NT	4502166 NT	18	4F231920.1	4J237589.1	4J237589.1	AF264750.1	750.1	4507828	12	54.1	384.1	11420514	6005720 NT	12	710.1	1.0E-90 AF167340 1	T		11420/38 NI	AF163864 4	2400	11422108	1,0E-90 AB002059 1		T	-	11419234		39.1
	Most Similar (Top) Hit BLAST E Value	2.0E-90	2.0E-90	1.0E-90	1.0E-90 AF231	1.0E-90 AF231	1.0E-90 AJ2378	1.0E-90 AJ237	1.0E-90 AF264	1.0E-90 AF264	1.0E-90	1.0E-90 AF096	1.0E-90 AF096	1.0E-90 I	1.0E-90	1.0E-90	1.0E-90 AB020	1.0E-90 AB020	1.0E-90	1.0E-90/	20 10	10F.		1 0F-90	1 0F-80	1.0E-90 A	1.0E-90 A	8.0E-91 D12234.1	7.0E-91 AF0537	7.0E-91	5.0E-91 AA7027	5.0E-91 A
	Expression Signal	1.56	49.27	3.39	121	1.04	2.03	2.03	7.71	7.71	2.45	3.47	3.47	4.02	4.98	8.4	1.18	1.18	<del>-</del>	2.2	20 0	3.78	120	1.72	1.72	1.89	89.	5.48	0.88	2.05	1.47	1.05
	ORF SEQ ID NO:	27797	28159	20060	20148	20148	20435			20473			21045		21631	22545	23473	23474	24005	25464	26558	27/189		27444	27445	25225	25226	23780	21199	26907	23151	24092
	Exon SEQ ID NO:	17572	17914	10241	12639	12639	10613	10613	10645	10645	11010	11192	11192	11548	11756	12752	13689	13689	14223	15401	16380	16998	17224	17240	17240	19268	19268	14001	11333	16714	13346	14309
	Probe SEQ ID NO:	7722	8765	275	370	371	089	88	713	713	1094	1284	1284	1644	1860	2823	3777	3777	4326	5481	6524	7121	7356	7371	7371	9732	9732	4101	1428	6835	3429	4415
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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4415	14309	24093	1.05	5.0E-91	5.0E-91 AU143539.1	EST HUMAN	AU143539 Y79AA1 Homo seriens cDNA clone Y794A1000ne7 5'
4703			0.82	5.0E-91		NT	Homo sapiens chromosome 22 open reading frame 5 (C220RES) mBNA
4703			0.82	5.0E-91		NT	Homo saplens chromosome 22 open reading frame 5 (C22OREs) within
7087	16964	27157	1.34	5.0E-91	5.0E-91 AV649878.1	EST HUMAN.	AV649878 GLC Hamo sabiens cDNA clone Cl CRYENS 3'
7087			1.34	5.0E-91		EST HUMAN	AV649878 GLC Horno sapiens cDNA clone GL CBYF08 3'
3166		22895	1.3	4.0E-91	4.0E-91 AF156776.1	FN	Homo sapiens lysophosphatidic acid acviransferase-delta (I PAAT delta) mRNA
3166			1.3	4.0E-91		N.	Homo sapiens lysophosphatidic acid acytransferase-delta (I PAAT-delta) mRNA complete cus
8301	18180	28427	3.13	4.0E-91	4.0E-91 AL163284.2	N	Homo saplens chromosome 21 segment HS21C084
9239	18954	25314	1.67	4.0E-91	4.0E-91 M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #836205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gap polyprotein
9239	18954	25360	1.67	4 0F-91		FST HIMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to
1601	11506		5.12	3.0E-91	11430193	TN	Homo sapiens solute cerrier families, onice machineses
1601	11506	21367	5.12	3.0E-91		LN	Homo sapiens solute certier famility anion contracts.
2624	12492	22382	66.0	3.0E-91	AF169555.1	NT	Homo sabiens beta-ureidononionase (R) 194) gans awa R
2624		22383	0.99	3.0E-91	3.0E-91 AF169555.1	NT	Homo sapiens beta-ureidopropionase (BLIP1) gene even 8
3297		23020	1.77	3.0E-91		NT	Homo sapiens chromosome 21 segment HS21C083
3416		23136	2.96	3.0E-91		N-	Homo sapiens mRNA for KIAA1278 protein martial cds
3416		23137	2.96	3.0E-91	3.0E-91 AB033104.1	M	Homo sapiens mRNA for KIAA1278 protein, partial cds
3720	_1	23418	0.83	3.0E-91	10.1	N	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4487	_	24168	4.02	3.0E-91		FX	Human Ku (p70/p80) subunit mRNA, complete cds
4905		24560	1.2	3.0E-91	5.2	NT	Homo sapiens chromosome 21 segment HS21C085
4905		24561	1.2	3.0E-91	3.0E-91 AL163285.2	N	Homo sapiens chromosome 21 segment HS21C085
5488	_]	25470	1.45	3.0E-91	11434964 NT		Homo sapiens epididymal secretory protein (19,5kD) (HE1), mRNA
2807	15712		2.39	3.0E-91	4502740 NT		Hamo saplens cyclin-dependent kinase 6 (CDK6) mRNA
5967	15872	25996	4.11	3.0E-91	11497611 NT		Homo sapiens gamma-aminobutyric acid (GABA) B receptor. 1 (GABBR1) franscrint variant 2, mDNA
5967		25997	4.11	3.0E-91	11497611 NT		Homo sapiens gamme-aminobutvric acid (GARA) R recentry 1 (GARBA) transaction to the same aminobutvric acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) R recentry 1 (GARBA) transaction to the same acid (GARA) transaction to the same acid (GARA) transaction to the same acid (GARA) transaction to the same acid (GARA) transaction to the same acid (GARA) transaction to the same acid (GARA) transaction transaction transaction to the same acid (GARA) transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction transaction tra
6502	_	26535	4.4	3.0E-91	3.0E-91 U86959.1	N P	Human L-type calcium channel beta-1 subunit (CACNII 84) gans expers 40 and 44
6502	[	26536	4.4	3.0E-91		LN	Human L-type calcium channel beta-1 subunit (CACNI B1) nene exons 10 and 11
7083	16970	27163	3.31	3.0E-91			Human mRNA for very low density lipoprotein receptor, complete cds
9480	19104	25286	1.45	3.0E-91	3.0E-91 AF240786 1	L _N	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
					1		one madine forms

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	Top Hit Descriptor	Homo sapiens ARP2 (actin-related protein 2, veast) homolog (ACTR2), mRNA	Homo sapiens ARP2 (actin-related protein 2, vesst) homolog (ACTR2), mRNA	Homo saplens cysteine-rich repeat-containing protein S52 predictor mRNA complete cuts	Homo sapiens NRAS-related cene (D1S155E) mRNA	Homo sapiens DNA, MHC class I region, 7.1 ancestral hanlohme	Homo saplens T-cell Ivmphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	N-CAM≈145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 Inti	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 Inti	Homo sapiens prosnero-related home-show 4 (DBOX4) mDMA	ZW66d12r1 Sogres testis NHT Homo serions ANN class 1880 Eigennate	601283012F1 NIH MGC 44 Homo seniens cDNA clara IMA CERSESSOR	601501242F1 NIH MGC 70 Home sapiens CDNA clane IMAGE: 3003018 5	EST91020 Synovial sarcoma Homo saciens cDNA 5' and similar to similar to ribosomal and sin	Human mRNA for alpha-actinin	Human mRNA for alpha-actinin	Homo sapiens activin A receptor, type IIB (ACVR2R) mRNA	Homo sapiens hypothetical protein d.1462023.2 (D.1462023.2) mRNA	Homo sapiens hypothetical protein d.1462023.2 (D.1462023.2) mRNA	601118337F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3028204 F	601118337F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3028304 5	mrg=mas-related [human, Genomic, 2416 nt]	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CI IISTER PECION DECTEIN .	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens CDNA clone IMAGE:2413549 3' similar to TR:Q12844 O12844 BREAKPOINT CI IISTER PEDIDINE PROPERTY	Homo sabiens syndecan 4 (amphichran pardocan) /CIDCA m.DNA	Homo sablens calcineurin hinding number 1 (KIA A0330) TIDIA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
2000	Top Hit Database Source	NT	NT	TN	NT	IN	TN	NT	F	F	IN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	Į.	FN	F	IN	EST HUMAN	EST_HUMAN	N	EST HUMAN	EST HUMAN	TN	FX	TN	NT	۲ _N
	Top Hit Acession No.	5031570 NT	5031570 NT	7.0E-92 AF167706.1	6005738 NT	7.0E-92 AB031007.1	4507500 NT	4507500 NT	7.0E-92 S71824.1	S71824.1	4508118 NT	7.0E-92 AA446206.1	6.0E-92 BE390882.1	3.0E-92 BE909714.1	3.0E-92 AA378336.1	3.0E-92 X15804.1	3.0E-92 X15804.1	4501898 NT	11422946 NT	11422946 NT	2.0E-92 BE299190.1	2.0E-92 BE299190.1	S78653.1	2.0E-92 AI818119.1	2.0E-92 AI818119.1	4506860 NT	6912457 NT	4F231919.1	2.0E-92 AF231919.1	5803180 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	5.0E-92	3.0E-92	3.0E-92	3.0E-92	3.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92 S78653.1	2.0E-92	2.0E-92	20E-92	2.0E-92	2.0E-92 AF23191	2.0E-92	2.0E-92
	Expression Signal	1.67	1.67	2.32	5.01	1.04	0.92	0.92	1.61	1.61	1.45	4.87	0.93	2.45	3.74	5.7	5.7	1.53	2.83	2.93	1.38	1.38	2.74	1.55	1.55	4.71	37.64	1.02	1.02	4.99
	ORF SEQ ID NO:	21923	21924					23024	24165	24166	24752	24836		22494	25575	28281		19803	19958	19959	20497	20498		21667	21668	21787	22381	23265	23266	23332
	Exon SEQ ID NO:						_	15068	14378	14378	14978	15142	11473	12600		_]		_	10143	10143	10664	10664	11588	11789	11789	11895	12491	13476	13476	13545
	Probe SEQ ID NO:	2139	2139	2517	2693	2724	3301	3301	4484	4484	5110	5219	1569	2738	5583	8146	8146	প্ত	172	172	732	732	1686	1894	1894	2002	2623	3562	3562	3831

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	T	Т	Т	Т	T-	Т	Т	Т	Т	Т	Т	Т	T		T	-	1	<del>'' -</del>	-7	<del>-1110</del>	_	7,171	T	Ť	1	<u> </u>	<del>~~~</del>
Top Hit Descriptor	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds	DKFZp434C0414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5	Homo sapiens mRNA for KIAA1068 protein, partial cds	Human NPV Y1-like receptor pseudogene mRNA, complete cds	hd02h02x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2908371 3' similar to TR:002711 002711 PRO-POL-DUTPASE POLYPROTEIN :	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA	Homo sapiens mRNA for KIAA1093 protein, partial cds	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	yi80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element	WIEN'I repeatuve element;	tg01b02x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element ;	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'	EST188414 HCC cell line (matastasis to liver in mouse) Il Homo sapiens cDNA 5' end similar to ribosomal protein L29	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'	Homo sapiens ribosomal protein L10a (RPL10A), mRNA	601460521F1 NIH_MGC_66 Homo sapiens cDNA clane IMAGE:3863908 5'	Hamo sapiens chromosome 21 unknown mRNA	Homo sapiens mRNA for KIAA0611 protein, partial cds	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'	Homo sapiens chromosome 21 segment HS21C001	Human skeletal muscle 1.3 kb mRNA for tropomyosin
Top Hit Database Source	LN LN	N	EST_HUMAN	N	LN TN	EST HUMAN	N IN	N	N	EST_HUMAN	EST HUMAN	E	100	ESI HOMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	N-	EST_HUMAN	N	NT	EST_HUMAN	EST_HUMAN	NT	NT
Top Hit Acession No.	M10976.1	2.0E-92 AF136523.1	AL040437.1	-		3W340174.1	11434900 NT	2.0E-92 AB029016.1	6912457 NT			4506668 NT			· 🕶	1.1	9.0E-93 AA316723.1	.1	-:	11418526 NT	8.0E-93 BF036364.1	1.1	<u></u>	1	1	.2	
Most Similar (Top) Hit BLAST E Value	2.0E-92 M10976.1	2.0E-92	2.0E-92	2.0E-92 AB028991	2.0E-92 U67780.1	2.0E-92 AW34017	2.0E-92	2.0E-92/	2.0E-92	1.0E-92 R78078.1	1.0E-92 R78078.1	1.0E-92	A OE OO A LOGICAE	1.05-32/	1.0E-92 Al380356.	9.0E-93 AU12168	9.0E-93	9.0E-93 AF223391	9.0E-93 BE38857	9.0E-93	8.0E-93	7.0E-93	5.0E-93 AB014511	5.0E-93 AI674184	5.0E-93 AI674184	5.0E-93 AL163201	5.0E-93 X04201.1
Expression Signal	1.02	67.0	2.53	2.49	2.25	1.37	5.91	2.55	26.65	1.11	1.11	34.72	2	4.04	4.04	3.14	9.21	1.46	0.95	9.6	2.49	6.24	1.25	5.39	5.39	0.95	2.42
ORF SEQ ID NO:	23869	24323		26017		27211	28276	25274	22381	21582	21583	21810	032260	27300	27361	21769			23267		26003	20028	21121	21145	21146		22925
Exen SEQ ID NO:	14091	14534	14801	15894	16273	17018	18030	19172	12491	11704	11704	11919	17187		17162	11876	11890	12478	13477	18719	15879				]		13120
Probe SEQ ID NO:	4191	4648	4922	6869	6420	7141	8142	9589	6836	1807	1807	2028	7286	7200	7286	1983	1996	2610	3563	8911	5975	246	1359	1385	1385	1459	3195

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Table 4
Single Exon Probes Expressed in Heart

				-	_	_	_	_	_	_	<del></del>	_	_	_	_	_	<del></del>	100		<del></del>	mir.	nunt	-	-thu. en	419 - 91			1,1,11	41.01 A
	Top Hit Descriptor	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product	Homo sapiens secretory pathway component Sec31B-1 mRNA alternatively solited complete and	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA	Homo sapiens nucleobindin 2 (NUCB2), mRNA	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA	2x50e09.s1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM:	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1) mRNA	Homo sapiens pescadilio (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5	Homo sapiens chromosome 21 segment HS21C101	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA	y694c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSF EI FMENT.BINDING DECTEN SDE 700 UNANA	AV692051 GKC Homo sapiens cDNA clone GKCDRE07 5'	602246554F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE-4330138 51	602246554F1 NIH MGC 62 Homo sapiens cDNA clane IMAGE-4330036 5'	Homo sapiens tensin mRNA, complete cds	th 29g03 x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE 2189076 3'	th29g03.x1 NCI_CGAP_Brn25 Homo sepiens cDNA clone IMAGE:2169076.31	Homo sapiens GCN5 (general control of amino-acid swithesis usest homoloxy) like 3 (20 Miles).	wb02d05x1 NCI CGAP GC6 Home septems aDNA clone IMAGE: 2304486 31	Chlorocebus aethiops mRNA for ribosomal protein S4X complete cds	Chlorocebus aethiops mRNA for ribosomal protein S4X complete cds	Homo sapiens chromosome 21 segment HS21C085	Hómo sapiens chromosome 21 segment HS21C085
	Top Hit Database Source	LΝ	NT	NT	NT	NT	EST_HUMAN	TN	N	N	L	N	NT	NT	N	TN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	L	EST HUMAN	EST_HUMAN	L	EST HUMAN	N-	N	LN	LN L
	Top Hit Acession No.	5.0E-93 AF067136.1	AF274863.1	5032156 NT	11439599 NT	11417877 NT	4.0E-93 AA459933.1	4557879 NT	4557879 NT	7657454 NT	7657454 NT	8923658 NT	7.1	1.2	7656972 NT	4504654 NT	746864.1	1.1	Γ	3F690630.1	3.0E-93 AF225896.1	-	_	11426182 NT	-	-		2	2
Most Similar	(Top) Hit BLAST E Value	5.0E-93	5.0E-93		5.0E-93	5.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93 AF04767	4.0E-93 AL16330	4.0E-93	4.0E-93	4.0E-93 T46864.1	4.0E-93 /	3.0E-93 BF69063(	3.0E-93 BF69063(	3.0E-93/	3.0E-93 AI553853	3.0E-93 AI553853.	3.0E-93	3.0E-93 AI824829.	2.0E-93	2.0E-93 /	2.0E-93 AL163285	2.0E-93 AL163285
	Expression Signal	3.67	2.07	1.31	3.01	1.84	4.72	1.75	1.75	1.33	. 1.33	2.08	5.06	0.84	2.18	1.44	4.81	19.24	5.99	5.99	2.7	1.58	1.58	1.32	4.15	8.31	8.31	69.9	7.68
	ORF SEQ ID NO:	26577	27613	27715		25173		20204				20923	21712			23647	25445	28613	23302	23303		25520	25521	25979	28314	19970	19971	. 20100	20100
ij	Exon SEQ ID NO:	16398	17400	17494	18085	19423	10066	10381	10381	10685	10685	11078	11829	12229	12435	13869	15385	18348	13515	13515	14042	15452	15452	15857	18066	10155	10155	10282	10282
O. C.	SEQ ID NO:	6540	7549	7644	8200	9487	82	437	437	755	755	1166	1934	2349	2564	3962	5465	8475	3601	3601	4142	5535	5535	5952	8178	183	183	320	321

Page 313 of 413 Table 4 Single Exon Probes Expressed in Heart

		٦	T	7	٦	П	7	٦	П	T	٦	Т	Т	Ţ	Т	14	_	7	$\neg$	-1	Ť	-		-"	- 74	<u>"- </u>	Ť	<del>"" 1</del>		۳	تسائيات	إسلا
onigie ckui riobes Expressed in neam	Top Hit Descriptor	Homo sapiens fensin mRNA commissionals	Human Olk-associated BS cyclobrilin CARS. On mBNA Commissional	601117586F1 NIH MGC 16 Homo sanlons Anna Alexa MA CE 2255550 E	601116810F1 NIH MGC 16 Home seniors CDNA clare IMA OF 225220 5	EST376458 MAGE resembles MAGH Home senions and A	Homo sapiens hypothetical profels (1 OC54348) WBNA	UI-HE-BND-aks-0-09-0-UI I'M MGC 50 Homo conforc o'DNA along MAA OF 300-000-01	dp78b10x1 Scares fefal find NhH 10W Home senions only of the 11/4 of 1500 1200	229c10.s1 Soares pregnant uterus NhHPI Home cantern child Alega 144 CE 5000 CE.	Homo sapiens CYP17 dene. 5' end	601458531F1 NIH MGC 68 Home saniens chNA close (NAACE 398-388 FI	Homo saplens CTR1 pseudonene	Homo sapiens CTR1 bseudocene	Homo sapiens hypothetical protein (DJ328E19 C1.1) mRNA	oy84b08.x1 NCI_CGAP_CLL1 Homo sepiens cDNA clone IMAGE:1672503 3' sImilar to TR:Q62384 Q62384 ZINC FINGER PROTEIN	Homo sapiens DNA for amyloid presureor protein complete add	Homo sabiens hypothetical protein El 190304 (El 190304).	Homo sapiens hypothetical protein El 120204 (F 120204) - Entry	Homo sapiens mRNA for KIAA1563 profela martial cate	Homo sapiens dysteine-rich reneat-containing professions SS2 professions CN14	SD Shald IIVAN COmpany of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the compan	Homo septens MHC Alexa 4 series.	Novel human gene manning to phomograms 4	60177688F1 NIH MGC 17 Homo canions all A Character and All A Character and All A Character and All A Character and All A Character and All A Character and All A Character and All A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character and A Character	601177686F1 NIH MGC 17 Home emisses CDN 4 1 114 OF CREES 5	Homo sapiens DNA for amyloid precursor matein complete add	Homo sapiens chromosome 21 segment HS21 Ch84	Homo saplens alucocorticoid recenter (GRI) name infram D man E	Homo sapiens glucocorticold receptor (GRL) gene infrom D. exert 5, and infran E.	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA	Homo sapiens protein kinase C heta 1 (PRK/DR1)DNA
שום בעחון בוח	Top Hit Database Source	NT	NT	EST HUMAN	EST HUMAN	EST HUMAN	N	EST HUMAN	EST HUMAN	EST HUMAN	TN TN	EST HUMAN	N	NT	FN	EST HUMAN	IN	FZ	Z-	LN	NT	NIT	NT	LN	T HUMAN	HUMAN	Т	TN				
TIPO I	Top Hit Acession No.	2.0E-93 AF225896.1	2.0E-93 U40763.1	2.0E-93 BE252982.1	T		88	2.0E-93 AW 502002.1		Γ		Γ	Γ	1.0E-93 AF238997.1	7657016 NT	1.0E-93 AI146755.1		8923270	8923270 NT	4B046783.1	1			Γ				2			4557792 NT	11431590 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93	1.0E-93	1.0E-93	1.0E-93	1.0E-93	1.0E-93 D87675.1	1.0E-93	1.0E-93	1.0E-93 AB04678	1.0E-93 /	1 0F-03 AF23408	1.0E-93 /	1.0E-93 /	1.0E-93 E	1.0E-93 BE29736	1.0E-93 D87675.1	1.0E-93 AL163284	1.0E-93 U78509.1	1.0E-93 U78509.1	1.0E-93	1.0E-93
	Expression Signal	1.48	1.02	0.89	1.02	4.59	1.52	1.32	2.87	1.52	1.31	2.75	1.64	1.64	2.56	3.75	3.32	6.41	6.41	1.55	1.68	70	4.16	1.09	2.69	2.69	4.33	1.44	1.62	1.62	9.15	2.06
	ORF SEQ ID NO:	21363	21868	22210	24732	25049	25442		29093				19897	19898	20262	20330	20631	20974	20975	21083	21085	22070	22190		21030	21031	22627	24010	25391	25392	25604	26197
	Exon SEQ ID NO:	11503	11973			15245		15918	_ [				$\perp$		10449	10523	10781	11125	11125	11228	11230	12172	12292	12336	11181	11181	12830	14228	15338	15338	15522	16051
	Probe SEQ ID NO:	1598	2083	2436	5088	5325	5462	6014	9668	9386	9465	9724	96	98	607	585	854	1217	1217	1321	1323	2289	2415	2459	2792	2792	2903	4331	5417	5417	. 5607	6067

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Table 4
Single Exon Probes Expressed in Heart

		T	T	T		T	T	Ī	T			T		1	T	T		T	T	Ť	Ī	Ī	Ī	15265		T	T	T	T	T	
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Human mRNA for NF1 N-isoform-exon11, complete cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	H.sapiens mRNA for MEMD protein	Homo sapiens protein kinase Inhibitor gamma (PKIG) mRNA, complete cds	Homo sapiens mRNA for KIAA1485 protein, partial cds	Homo sapiens Trio isoform mRNA, complete cds	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)	Human PreA4 gene for Alzhelmer's disease A4 amyloid protein precursor (excn 9)	qm03c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:T19B4.4   CE13742;	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens transcription enhancer factor-5 mRNA, complete cds	Homo saplens mitogen-activated protein kinase 12 (MAPK12), mRNA	Homo sapiens mRNA for KIAA0612 protein, partial cds	Homo sapiens mRNA for KIAA0612 protein, partial cds	zg87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594.3*	ot83d05.s1 Soares_total_fetus_NbZHF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'	yd98b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'	Homo sapiens mRNA for KIAA0027 protein, partial cds	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	Homo sapiens ribosomal protein L27 mRNA, complete cds	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA	tw11f10.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE;	And - 7 (And 19) will be where the most of misser of the most of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the ser	Homo sapiene solite carrier family 22 formanic carian transmarks.	Homo saplens hypothetical protein FL12455 (FI J12455) mRNA	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 nene	Homo sapiens complement component 5 (C5) mRNA	Homo saplens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
JIB EXON Pro	Top Hit Database Source	NT	NT	NT	LN	NT	N	ΤN	NT	EST HUMAN	LN L	LN TN	N	LN.	Z	N	EST HUMAN	EST_HUMAN	EST HUMAN	TN	둗	TN	LN	EST_HUMAN	<u> </u>	5	Z	Z	닏	NT	N
)IIC	Top Hit Acession No.	042072.1	1.0E-93 AB037832.1	/10183.1	1.0E-93 AF182032.1	·	1.0E-93 AF091395.1	(13474.1	(13474.1	VI268262.1	11417856 NT	8.0E-94 AL163209.2	AF142482.1	11418351 NT	\B014512.1	\B014512.1	5.0E-94 AA722434.1	1015800.1	89398.1		9558724 NT	L05094.1	4506008 NT	4.0E-94 Al591312.1	11440670 NT	11440670 NT	11545792 NT	\B022785.1	4502506 NT	\F167706.1	3.0E-94 AF167706.1
	Most Similar (Top) Hit BLAST E Value	1.0E-93 D42072	1.0E-93	1.0E-93 Y10183.1	1.0E-93	1.0E-93 /	1.0E-93 /	1.0E-93 X13474.	1.0E-93 X13474.1	1.0E-93 AI268262	1.0E-93	8.0E-94 /	6.0E-94 /	6.0E-94	5.0E-94 AB01451	5.0E-94 AB01451	5.0E-94	5.0E-94 AI015800	5.0E-94 T89398.1	5.0E-94 D25217.2	5.0E-94	4.0E-94	4.0E-94	4.0E-94	4.0E-94	4.0E-94	4.0E-94		3.0E-94	3.0E-94 AF16770	3.0E-94 /
	Expression Signal	4.09	2.04	1.18	1.59	1.8	1.22	4.54	4.54	5.92	2.33	122	1.74	1.67	3.05	3.05	1.72	1.63	4.68	1.27	1.26	4.55	0.86	3.02	1.84	1.84	1.72	1.17	1.17	1.05	1.05
	ORF SEQ ID NO:	26320	26876	27039	27093	26640	26643	27589	27590	25132			23579		25019			26218	24911				22379	24295	25921	25922	28142	20339	20462	21477	21478
	Exan SEQ ID NO:	16163	16686	16848	16901	16450	16453	17380	17380	19494	19257	17875	13791	19331	15217	15217	15598	16069	19736	19378	19384	11697	12489	14506	15798	15798	17898	10531	10637	11607	11607
	Probe SEQ ID NO:	6288	6807	6971	7024	7437	7440	7529	7529	9051	9716	8025	3880	9830	5296	5296	5689	6183	9361	9901	2066	1799	2621	4618	5892	5892	8749	. 595	704	1706	1706

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Table 4
Single Exon Probes Expressed in Heart

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Chigo Lyon I opea Lypressed III nealt	Top Hit Descriptor	Homo saplens E1A binding protein p300 (EP300) mRNA	Zw63g08.r1 Soares total fetus Nb2HF8 9w Horno saniens cDNA clone IMA CE: 777,782 E	Homo sapiens zinc finger protein 277 (7NE)771 mRNA	Homo saplens chromosome 21 open reading frame 18 (C210PE18)	Homo sabiens protocadherin alpha 13 (PCDH-alpha13) mBNA complete alpha13	Homo sapiens mRNA for KIAA0679 protein partial cde	Homo sapiens glycogenin-1L mRNA complete cds	Homo sapiens axonal transport of synaptic vesicles (ATSV) mPNA	Human cbl-b truncated form 1 lacking lengths ginner mRNA complete and	601175762F1 NIH MGC 17 Homo seniens cinva clore MAGE:0531030 E1	801111696F1 NIH MGC 16 Homo sapiens CDNA clone IMAGE:33875E0 E1	601111696F1 NIH MGC 16 Hmm canians COLM close IMAGE CASESEES	Homo sablens hypothetical protein (FI 1207248) mRNA	Homo senjens nained how mane & Call lineage and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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consequent II 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 4 consequent III 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III 4 consequ	ap22e02 x1 Schiller olindendronliome Home conjune CNNA - 1 1100 C Schiller olindendronliome Home conjune	Ocea45 NEURAL CELL ADHESION PROTEIN BIG-2 PRECIESOR .	601175762F1 NIH MGC 17 Homo septems CDNA close IMACE 2521028 E	Homo saplens TNF-alpha stimulated ABC profein (ABC50) mRNA commission	Homo sapiens KIAA0255 gene product (KIAA0255) mRNA	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo sapiens progressive ankylosis-like protein (ANK) mRNA. complete cals	we09e04.xf NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN)	we09e04.x1 NCI_CGAP_Lu24 Home spiens cDNA done IMAGE:2340606 3' similar to gb:K00568	Honoral Art Civil (TOWAY),	normo saprens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA	rioring sapiens processome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA	nomo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo saplens KIA 005E 200 - 11 (KIAA0255), mRNA	Homo saplens proline dehydrogenase (proline oxidase) (PRODH) mRNA
01 1100	Top Hit Database Source	Į.	EST HUMAN	Į.	Ν	Į.	Z L	\ N	F	N.	EST HUMAN	EST HUMAN	EST HUMAN	NT.	F	EST HUMAN	LN	IN	EST_HUMAN	EST HUMAN	NT	F	F	L	EST HUMAN	EST HIMAN	NT.	- E	E E	E L	L	NT
5	Top Hit Acesslon No.	4557556 NT		11496268 NT	11526228 NT	3.0E-94 AF152309.1	AB014579.1	4F087942.1	4757821 NT		3E295714.1	1.0E-94 BE253433.1	3E253433.1	9506692 NT	11428710 NT		1855an 1		N272244.1	3E295714.1	VF027302.1	7662027 NT	662027	.1	8.0E-95 AI700998.1	-	428E20	44426530 NIT	E020907 4	770007	11420944 NT	5174644 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-94	3.0E-94 AA46480	3.0E-94	3.0E-94	3.0E-94	3.0E-94 AB01457	3.0E-94 AF08794	3.0E-94	3.0E-94 UZ6711.	1.0E-94 BE29571	1.0E-94	1.0E-94 BE25343	1.0E-94	1.0E-94	1.0E-94 BE78047	1 0F-94   185590 1		1.0E-94 AI272244	1.0E-94 BE29571	9.0E-95 AF02730;	9.0E-95	9.0E-95	9.0E-95 AF274753	8.0E-95	8.0E-95 A1700998	A OF OF	80E08	R OF OR A FORDER	0.0L-30.	8.0E-95	8.0E-95
	Expression Signal	3.45	0.82	3.58	4.16	1.16	3.79	4.36	1.75	2.27	2.24	1.91	1.91	1.13	1.83	1.41	2.49		2.19	1.98	1.55	1.13	1.13	1.87	1.59	1.59	183	1 83	205	4 73	1.73	2.82
	ORF SEQ ID NO:	21504	23772	25466		26838	27062		28580		19937	22769	22770	23938	27439	27707	28546			19937	21230	22839	22840	26869	24119	24120	26314	26315	26837	27515	27516	27744
	Exon SEQ ID NO:				15787	16650	16869		- 1	18736	10117	12977	12977	14160	17235	17487	18292		18500	10117	11366	13043	13043	16680	14331	14331	16158	16158	16649	17309	17309	17517
	Probe SEQ ID NO:	1735	4095	5484	5881	6771	6992	7533	8448	8928	143	3050	3050	4261	7331	7636	8418		8635	9759	1461	3118	3118	889	4436	4436	6294	6294	6770	7394	7391	7992

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Table 4
Single Exon Probes Expressed in Heart

		complete cds	imilar to contains L1.t1 L1											seudoinflammatory) (TIMP3)	•				iferase theta 1 (GSTT1)	ANG						3' similar to WP:T23G7.4			786457 5'	20000	0 /0100/	
Top Hit Descriptor	Homo sapiens mRNA for KIAA1395 protein, partial cds	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1	repetitive element;	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C046	Human homeobox protein (PHOX1) mRNA, 3' end	602071146F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE-4214147 5	Homo sapiens H factor 1 (complement) (HF1) mRNA	Homo sapiens KIAA0255 gene product (KIAA0255) mRNA	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)	NA	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	Homo sapiens glycine cleavage system protein H (aminomethy carrier) (GCSH) = BNA	Homo sapiens H factor 1 (complement) (HF1) mRNA	Homo sapiens Usurpin-damma mRNA, complete cds	Homo sapiens unconventional myosin-15 (LOC51168), mRNA	Homo sapiens unconventional myosin-15 (LOC51168), mRNA	Homo sapiens mRNA for KIAA1386 protein, partial cds	qm01c02.x1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705;	Homo saplens hypothetical protein (HS322B1A) mRNA	Homo sapiens KIAA0187 gene product (KIAA0187) mRNA	2x11d07.r1 Soares total fetus Nb2HF8 9w Homo septens CDNA clume IMACE-798457 5	2X11d07.r1 Soares total fetus Nb2HF8 9w Homo sapiens CNNA class NAACE:788157 5	Homo saplens CGI-48 protein (LOC51096), mRNA	Homo sapiens CGI-48 protein (LOC51096), mRNA
Top Hit Database Source				HUMAN						HUMAN						HUMAN								Ho F		EST HUMAN CEC		T _O T	HUMAN	HUMAN		
Top Hit Acession No.	\B037816.1 NT	8.0E-95 AF112152.1 NT		8.0E-95 AA629056.1  EST				L163246.2 NT	495929.1 NT	F526041.1 EST	4504374 NT	7662027 NT	7662027 NT		4507512	BE393873.1 EST	5453665 NT	5453665 NT	2.0E-95 AF240786.1 NT	38423	4504374 NT	AF015452.1 NT	7705900 NT	7705900 NT	B037807.1 NT	4.	7657185	7661979 NT		=	7705764	7705764 NT
Most Similar (Top) Hit BLAST E Value	8.0E-95 AB03781	8.0E-95 A	1	8.0E-95	7.0E-95 D87675.1	7.0E-95 D87675.1	7.0E-95 M95708.	7.0E-95 AL16324	7.0E-95 M95929.1	3.0E-95 BF52604°	2.0E-95	2.0E-95	2.0E-95	10.00		2.0E-95 B	2.0E-95	2.0E-95	2.0E-95 A	2.0E-95	2.0E-95	2.0E-95 A	2.0E-95	2.0E-95	2.0E-95 AB03780	2.0E-95 AI290264	2.0E-95	2.0E-95	2.0E-95 AA44793	2.0E-95 AA44793	2.0E-95	2.0E-95
Expression Signal	2.83	2.41		8.68	9.46	9.46	5.94	1.38	1.03	1.76	98.0	1.6	1.6	i	8):)	3.3	1.3	1.3	16.55	2.46	0.86	3.51	2.78	2.78	96.0	1.02	2.3	2.57	0.98	96.0	3.69	3.69
ORF SEQ ID NO:		28236	•		20058	20059	23947		24623	25087	20694	21387	21388	OFFICE	7/017	21676	22147	22148	22191	22235	20693	22842	23232	23233	23268	23390	23940	24615	24663	24664	25121	25122
Exan SEQ ID NO:	17531	17987	_	_Ĺ			١		14857	15261		11529	11529	44700	1	-	ļ	12256	12294	12342	10846	13045	13433	13433	13479	13604	14163	14846	14895	14895	15287	15287
Probe SEQ ID NO:	7681	8096	000	5895 6	274	274	4270	4316	4982	5340	922	1625	1625	1007	/801	139	2376	2376	2417	2466	2787	3120	3517	3517	3565	3690	4284	4971	5022	5022	5367	5367

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Table 4
Single Exon Probes Expressed in Heart

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בייפור בייפור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור ביישור בי	Top Hit Descriptor	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA complete cds	Homo saplens huntingtin (Huntington disease) (HD), mRNA	Homo sapiens bone morphogenetic protein receptor, type (A (BMPR1A) mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	Homo sapiens adenylosuccinate Iyase (ADSL), mRNA	223h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6;	223h04.11 Scares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2 6:	IRGE-FN0019-290600-011-G11 FN0019 Homo canions CDNA	RC6-FN0019-290600-011-G11 FN0019 Homo saniens CDNA	601437232F1 NIH MGC 72 Homo saniens cDNA clane IMAGE 2022423 Et	601497608F1 NIH MGC 70 Homo sepiens cDNA clone IMAGE-SRoozer 5'	601497608F1 NIH MGC 70 Homo saplens cDNA clone IMAGE 3899761 5'	PM0-LT0019-090300-002-409 LT0019 Homo sapiens cDNA	Homo sapiens chromosome 21 unknown mRNA	MRO-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C001	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	Homo sapiens mRNA for KIAA1172 protein, partial cds	Homo sapiens mRNA for KIAA1172 protein, partial cds	Homo sapiens mRNA for KIAA1172 protein, partial cds	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDF6A), mRNA	Homo sapiens transient receptor potential channel 5 (TRPCS) mRNA	H.sapiens DNA for monoamine oxidase type A (7) (partial)	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA	Human type IV collagenase (CLG4B) gene, exon 5	Human type IV collagenase (CLG4B) gene, exon 5
	Top Hit Database Source	ΡN	뉟	N	NT.	Þ	F	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	IN	EST_HUMAN	칟	K	NT	TN	IN	NT	NT	N.	N	IN	LN.	NT	N.	NT	NT
	Top Hit Acession No.	M59724.1	2.0E-95 AF257737.1	11435773 NT	4757853 NT	2.0E-95 AF240786.1	11418164 NT	1.0E-95 AA284651.1	1.0E-95 AA284651.1	1.0E-95 BF370000.1	1.0E-95 BF370000.1	9.0E-96 BE897259.1	3E907607.1	3E907607.1	8.0E-96 AW836047.1	1.	1.	2	A26873.1	7662289 NT	7662289 NT	8923939 NT	5.0E-96 AB032998.1		5.0E-96 AB032998.1	11416767 NT	6912735 NT		11424399 NT	11424399 NT		
	Most Similar (Top) Hit BLAST E Value	2.0E-95 M59724.1	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	1.0E-95	1.0E-95	1.0E-95	1.0E-95	9.0E-96	8.0E-96 BE907607	8.0E-96 BE907607	8.0E-96	7.0E-96	6.0E-96 BE171984	6.0E-96 AL163201	6.0E-96 M26873.1	6.0E-96	6.0E-96	6.0E-96	5.0E-96 A	5.0E-96	5.0E-96 ₽	5.0E-96	5.0E-96	5.0E-96 X60812.1	5.0E-96	5.0E-96	5.0E-96 M68347.1	5.0E-96 M68347.1
	Expression Signal	4.54	2.25	1.62	2.36	1.98	4.34	7.73	7.73	4.85	4.85	1.67	0.82	0.82	2.66	96.0	0.85	96.0	26.15	1.98	1.98	2.09	2.7	3.06	3.06	2.31	0.98	1.22	4.23	4.23	1.81	1.81
	ORF SEQ ID NO:		25984		28245	25285	25211	25427	26428	26460	26461	26835	20201	20202			22003	22997	23159	28927	28928	28972	20096	20599	20600		22713		26193	26194	26788	26789
	_ <u>w</u>				17996	19084	19338	15371	16371	16298	16298	16646	12666	12666	15302			[	13354	18644	18644	18682	10279	10751	10751	12447	12919	14694	16048	16048	16599	16599
	Probe SEQ ID NO:	5734	5957	6055	8106	9452	9840	5450	5450	6437	6437	6767	435	435	5383	3834	2213	3276	3437	8831	8834	8870	317	824	824	2576	2891	4810	6065	6065	6719	6719

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	yr87h12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA	Homo sapiens chromosome 21 segment HS21C048	RC3-HT0230-040500-110-q02 HT0230 Homo seniens cDNA	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5	2819351.5prime NIH MGC 7 Homo sapiens cDNA clone IMAGE:2819351 5'	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes	EST367124 MAGE resequences, MAGC Homo sapiens cDNA	EST367124 MAGE resequences, MAGC Homo sablens cDNA	Homo sapiens flavin containing monooxydenase 2 (FMO2) mRNA	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA	Human hepatocyte growth factor gene, exon 1	Human hepatocyte growth factor gene, exon 1	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOG63214), mRNA	Homo sapiens secretory nathway commonent Sec218 1 mDNA attended:	Home senione MRM for KIAA200 median account in the control and an incidental control of the KIAA200 median account of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont	Homo sapiens mRNA for KIAA1290 protein, partial cds	601863712F1 NIH MGC 57 Homo sablens cDNA clone IMAGE-AR84202 E	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'	zv97e12.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125 G1304125 PMS4 MRNA	RC0-BT0812-250900-032-a09 BT0812 Homo sepiens cDNA	MRO-HT0241-150500-010-b02 HT0241 Hamo sepiens cDNA	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens CDNA	CM0-BN0106-170300-293-a06 BN0106 Homo sepiens CDNA	Homo sapiens brefeldin A-inhibited aganine nucleofide exchange protein 2 (RIC2) mRNA	Homo sapiens mRNA for GalNAc alpha-2, 6-slalytransferase I, Iong form	Homo sapiens mRNA for GalNAc alpha-2. Sisia/dransferasa I Inno form	Homo sapiens v-src avian sercoma (Schmidt-Ruppin A-2) viral oncodene homolog (SRC) mRNA	Homo sapiens mRNA for KIAA0594 protein, partial cds
	Top Hit Database Source	EST HUMAN	1	FN	EST HUMAN	EST HUMAN	EST_HUMAN	NT L	EST HUMAN	EST_HUMAN	N	N F	LN LN	NT	TN	TN	L	LZ	Z	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	 	뒫	N.	ZT.	ZZ.
	Top Hit Acession No.	H68656.1	4503098 NT	2.0E-96 AL163248.2	BE148074.1	2.0E-96 AV689461.1			1.0E-96 AW955054.1	AW955054.1	4503756 NT	4503756 NT	1.	Į.	J51472.2	11419429 NT	1.0E-96 AF274863.1	Γ	6.1			VL043314.2	5.0E-97 AA418026.1	2.1	5.0E-97 BE148597.1	7.1	6.1	5453572 NT			11421793	4.0E-97 AB011166.1 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-96 H68656.	2.0E-96	2.0E-96	2.0E-96 BE14807	2.0E-98	2.0E-96	1.0E-96 Y18890.1	1.0E-96	1.0E-96 AW9550	1.0E-96	1.0E-96	1.0E-96 M75967	1.0E-96 M75967	1.0E-96 U51472.	1.0E-96	1.0E-98	1.0E-96 AB03311	1.0E-96 AB03311	6.0E-97	6.0E-97	5.0E-97	5.0E-97	5.0E-97 BF15491	5.0E-97	5.0E-97 BE14859	4.0E-97 BE00443	4.0E-97	4.0E-97 Y11339.2	4.0E-97 Y11339.2	4.0E-97	4.0E-97
	Expression Signal	822	3.49	1.56	1.58	5.08	2.05	1.69	2.03	2.03	0.89	0.89	1.33	1.33	1.88	20.65	1.98	1.64	1.64	0.95	2.75	1.76	10.79	2.76	1.87	1.87	1.26	1.08	6.1	6.1	1.41	1.17
	ORF SEQ ID NO:			20494	24326			20408	21510	21511	21580	21581	21969	21970	22009	27125	27208	27938	27939	23006		26747	26804	27643	28929	28930	20697	21638	26167	26168	26939	27433
	Exon SEQ ID NO:	13997	10355	10662	14537	17068	18902	10590	11643		'		12068	12068	12650	16935	17015	17693	17693	13206	16319	16552	16614	17429	18645	18645	10849	11764	16027	16027	16746	17232
	Probe SEQ ID NO:	4097	409	730	4651	7191	9151	655	1742	1742	1806	1806	2181	2181	2219	7058	7138	7843	7843	3285	6429	6672	6735	7578	8832	8832	924	1868	6082	6082	6867	7328

Page 319 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Top Hit Database BLAST E No. Source Source	AB011166.1 NT	1.76 4.0E-97 11863122 NT Homo saplens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA	1.76 4.0E-97 11863122 NT Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA	TN	NT	4.0E-97 AB033116.1 NT	418318 NT	1.17 3.0E-97 AB032998.1 NT Homo sapiens mRNA for KIAA1172 protein, partial cds	10.96 3.0E-97 4502166 NT Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	10.96 3.0E-97 4502166 NT Homo saplens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	4758813 NT			3470 NT	1.0E-97 BE5664	1.0E-97 11427757 NT	11427757 NT	1.0E-97 AA553761.1 EST_HUMAN	11426272 NT	1.0E-97 11426272 NT	T_HUMAN		4758119 NT	9.0E-98 4758119 NT	X06989.1 NT	1321580 NT ·	1.39 9.0E-98 AB037786.1 NT Homo sapiens mRNA for KIAA1365 protein, partial cds	9.0E-98 AB023222.1  NT	NT	9.0E-98 BE090973.1 EST_HUMAN	8.0E-98 AB033768.1 NT	1.04 8.0E-98 5031810 NT Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
ŀ	1.	4.0E-97 AF	4.0E-97	4.0E-97	4.0E-97 AF	4.0E-97 AE	4.0E-97 AE	4.0E-97	3.0E-97 AE	3.0E-97	3.0E-97	3.0E-97		3.0E-97	1.0E-97	1.0E-97 BE	1.0E-97	1.0E-97	1.0E-97 A	1.0E-97	1.0E-97	9.0E-98 BE	9.0E-98	9.0E-98	9.0E-98	9.0E-98 XC	9.0E-98	9.0E-98 AE	9.0E-98 AE	9.0E-98 AE	9.0E-98 BE	8.0E-98 AE	8.0E-98
	Expression Signal	1.17	1.76	1.76	15.68	2.31	2.31	3.83	1.17	10.96	10.96	1.77	1.92	1.14	12.55	2.19	3.41	3.41	2.82	13.54	13.54	8	1.29	4.74	4.74	277	2.41	1.39	2.24	2.24	4.97	0.89	1.04
	ORF SEQ ID NO:	27434	28641	28642	28124	28128	28129		20026	20633	20634	21195	22161	22948	24349	25897			28768	28156			21012					27423	28497	28498			21303
	Exon SEQ ID NO:	17232	18376	18376	17882	17885	17885	19012	10210	10783	10783	12694	12652	13147	14556	15778	17979	17979	18494	17912	17912	10809	11162	16503	16503	17148	17195					11256	11444
	Probe SEQ ID NO:	7328	8503	8503	8733	8736	8736	9331	243	856	856	1423	2389	3223	4670	5872	8088	8088	8629	8763	8763	883	1255	6623	6623	7271	7319	7355	8369	8369	9345	1350	1540

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Table 4
Single Exon Probes Expressed in Heart

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Chigie Laur riobes Expressed in Hear	Top Hit Descriptor	Homo sapiens II 2-inducible T-cell kinase (ITK)	Homo sepiens PMS9116 mRNA nertiel cde	Homo saniens PMS21 16 mRNA nartial cds	Human mitochondrial greetine kinese (PRAT) and	Homo saplens chromosome 21 segment HSA Continues	htesto2x1 NCI CGAP 1.124 Homo cantons a DNA clana MA CE 24 54 52 500 51	AJ403124 3.4 (downregulated in lang carringma) Home conjugated DNA - Line	Homo sapiens mRNA for KIAA0707 protein peries adverse contents	7818H01 Chromosome 7 Fetal Brain cDNA Library Home souless CDNA Chromosome 7 Fetal Brain cDNA Library Home souless	Homo sapiens activator of S phase kinase (ASK) mRNA	Homo sabiens activator of S phase kinase (ASK), minute	wd700g rt Scares and the procedure of the National Action of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the 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ada	Homo sapiens Ran GTPase activation profess 1 (RANGAD4) ADMA	601172658F1 NIH MGC 17 Home sanions of Alexandra HA CE 252424 F1	Homo saniens chromosome 21 segment HS21 Chop	Homo sabiens boleselim channel submit (LIED 5) DAIA	Homo sapiens fathracid-Chenzime & lines Inning A Complete Cas	Homo saplens attractin precursor (ATRN) gene expn 16	Homo sapiens attractin precursor (ATRN) gene even 18	Homo sapiens low density lipoprotein receptor related protein-deleted in himor (I BDNIT) DNIA	Homo sapiens low density lipoprotein receptor related protein-deleted in trimor (1 BD) IT. DNA	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA	Homo sapiens PDZ domain-containing quanine professive archange fortail (1.0054225)	Homo sapiens SH3-domain GRB2-like 2 (SH3G) 2 mRNA	Homo sapiens SH3-domain GRB2-like 2 (SH3GI 2) mRNA	H.sapiens arginase gene expn 3 (EC 3.5.3.1)	Homo sapiens AIM-1 protein (LOC51151) mRNA	Homo sepiens chromosome 12 open reading frame 3 (C12ORF3) mRNA	tw36b04.x1 NCI_CGAP_Uff Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW-RI 2R HI IMAAN
	Top Hit Database Source	IN IN	¥	Z	L	¥	T HUMAN	T	Į.	Т			T HIJMAN	Т	Т	T			T HUMAN					Į.										
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	Most Similar (Top) Hit BLAST E Value	8.0E-98	8.0E-98	8.0E-98	8.0E-98	8.0E-98 AL16320	4.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98 H46698.1	3.0E-98 AJ40312	3.0E-98 AJ40312		3.0E-98 U59309.1	3.0E-98	2.0E-98 BE29428	2.0E-98 AL16320;	2.0E-98 AF03289	2.0E-98	2.0E-98 AF218902	2.0E-98 AF21890;	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98 X12664.1	2.0E-98	2.0E-98	
	Expression Signal	1.04	96.0	0.98	5.03	0.88	1.29	1.21	1.85	2.09	1.7	1.7	3.31	1.6	1.6		5.15	2.47	29.05	1.45	96.0	4.94	1.51	1.51	6.39	6.39	1.09	4.66	3.87	3.87	1.5	1.18	1.43	00 07
	ORF SEQ ID NO:	21304	21468	21469	23424		25220	21917	52329		26159	26160	27153		27760		28448		21816	21983	23880	23916	24390	24391	24711	24712	24795	25028	27073	27074	27572		25301	700
	Exon SEQ ID `NO:	11444	11597	11597	13638		19258	12019	12436	12582	16020	16020	16960	17535	17535		18199	18373	11924	12078	14099	14143	14606	14606	14939	14939	15029	15224	16881	16881	17367	17801	19026	10015
	Probe SEQ ID NO:	1540	1695	1695	3726	5049	9717	2131	2565	2720	6147	6147	7083	7685	7685		8322	CASA	2033	2191	4199	4244	4720	4720	5069	2069	5163	5303	7004	7004	7497	7951	3350	000

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Single Exon Probes Expressed in Heart

Top Hit Descriptor	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA	w23f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human :	zp98c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5 similar to TR:G806562 CRARGES NERI II N.	Homo saplens bela-fullulin mRMA complete ods	Homo sapiens befa-tubulin mRNA complete cde	EST380711 MAGE resequences, MAGJ Homo saniens cDNA	tm69h07x1 NCI_CGAP_Bm25 Homo sapiens cDN4 clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST :	tm69h07x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST	200002.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G882994 G68294 GPI-ANCHORED PROTEIN D437	Human endogenous retrovirus, complete genome	Homo saplens oscillir (hi n) dene exan 5	Homo sapiens NK-receptor (KIR-G2) nana Ilinkar radian ayan	Homo sabiens dysteine-rich reneat-containing produced in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the c	Homo saplens cysteine-rich repeat-containing protein S52 preciirear (10054222), Lona	EST388473 MAGE resequences, MAGN Homo saniens cDNA	Homo sapiens CD34 antigen (CD34) mRNA	Homo saplens polycystic kidney disease (PKD1) gene, exons 27-30	Homo saplens polycystic kidney disease (PKD1) gene, exons 27-30	H. sapiens mRNA for estrogen receptor	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds	Homo sapiens lodestar protein mRNA, complete cds	Homo sapiens lodestar protein mRNA, complete cds	Homo sapiens BH3 interacting domain death agontst (BID), mRNA	Human protein C inhibitor (PCI-B) mRNA, complete cds	Human protein C Inhibitor (PCI-B) mRNA, complete cds	H.sapiens IMPA gene, exon 8	Homo sapiens T cell receptor beta locus. TCRBV7S3A2 to TCRRV/12S2 regions	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1) mRNA	801513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
Top Hit Database Source	EST_HUMAN F	EST_HUMAN F	EST HIMAN	Т		T HUMAN				1					T HUMAN		H H	H.							H	H			EST_HUMAN   60
Top Hit Acession No.	1.0E-98 AW998611.1	1.0E-98 N49818.1	1.0E-98 AA195854 1	T	Γ		9.0E-99 AI479829.1	9.0E-99 AI479829.1	9.0E-99 AA134604.1	635487	7.0E-99 AF035808.1	_	430555	11430555 NT	6.0E-99 AW976364.1	4502660 NT				1		6.0E-99 AF080255.1	11526299 NT	•			5.0E-99 AF009660.1	4758697 NT	5.0E-99 BE890177.1
Most Similar (Top) Hit BLAST E Value	1.0E-98	1.0E-98	1.0E-98	1.0E-98	1.0E-98	9.0E-99	9.0E-99	9.0E-99	9.0E-99	8.0E-99	7.0E-99	7.0E-99	6.0E-99	6-30-9	6.0E-99	6.0E-99	6.0E-99 L43610.1	6.0E-99 L43610.1	6.0E-99 X99101.1	6.0E-99 /	6.0E-99 /	6.0E-99 /	6.0E-99	5.0E-99 U35464.1	5.0E-99 U35464.1	5.0E-99 Y11365.1	5.0E-99	5.0E-99	5.0E-99 E
Expression Signal	2.38	16.96	96.9	1.36	1.36	4.29	2.6	2.6	1.84	1.19	9.2	2.31	0.93	0.93	1.87	1.16	2.36	2.36	121	2.18	3.57	3.57	3.72	0.86	0.86	2.36	1.35	2.46	2.1
ORF SEQ ID NO:	20212	21526	24953	27266	27267	25692	28602	28603	28817	27134	25550	28988	21863	21864	23517	24318	26047	26048	26787	27160	27213	27214	28241	20671	20672	21698	24148	24709	
Exen SEQ ID NO:	10391	11655	15178		17080	15590	18338	18338	18533		15477	18695	11970	11970	13726	14530	15917	15917	16598	16966	17020	17020	17992	10827	10827	11817	14357	14936	19032
Probe SEQ ID NO:	447	1756	5256	7203	7203	5681	8465	8465	8716	7065	5561	8884	2080	2080	3814	4642	6013	6013	6718	080/	7143	7143	8102	302	8	1922	4463	5066	9360

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Top Hit Descriptor	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds	xp09e08.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN):	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds	2b46d06.r1 Scares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HI IMAN):	Homo saplens myosin X (MYO10) mRNA, complete cds	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products	Human interferon-alpha receptor (HulFN-alpha-Rec) mRNA, complete cds	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14	Homo sapiens fatty acid amide hydrolase (FAAH) gene. excn 14	Homo sapiens chromosome 21 segment HS210081	Homo saplens ALEX1 protein (LOC51309), mRNA	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711 002711 PRO-P0L-DUTPASE POI YPROTEIN ·	Homo sapiens mRNA for KIAA1005 protein, partial cds	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens chromosome 21 segment HS210047	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA	xv78b11.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824805.3	Homo sapiens chromosome 21 segment HS21C006	Homo sapiens chromosome 21 segment HS21C049	EST02975 Fetal brain, Stratagene (cat#936206) Horno sapiens cDNA clone HFBCR32
Top Hit Database Source	Ę	EST HUMAN	F	K	EST HUMAN	N	N F	E	F	Į.	Ę	F	E	뉟	Z Z	뉟	₽ F	Į,	EST HUMAN	NT		NT	N	N	Ę	F	EST_HUMAN	F	F	EST_HUMAN
Top Hit Acession No.	3.0E-99 M95586.1	2.0E-99 AW274792.1	2.0E-99 M30938.1	03.1	2.0E-99 W23507.1	7	37.1	11526150 NT	.1		AF192523.1	4503730 NT	4503730 NT		8.1	8.1	1.0E-99 AL163281.2	1276	1.0E-99 AW340174.1	1.0E-99 AB023222.1				1.0E-100 AL163247.2	11418230 NT	11418230 NT		6.2		
Most Similar (Top) Hit BLAST E Value	3.0E-99	2.0E-99	2.0E-99	2.0E-99 AF0957	2.0E-99	2.0E-99	1.0E-99 AF1144	1.0E-99	1.0E-99 M30938	1.0E-99 AF1925;	1.0E-99	1.0E-99	1.0E-99	1.0E-99 J03171.	1.0E-99 AF09801	1.0E-99	1.0E-99	1.0E-99	1.0E-99	1.0E-99		1.0E-99	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100 AW2752	1.0E-100	1.0E-100	1.0E-100 T05087.
Expression Signal	5.37	3.46	1.08	3.15	9.75	3.83	1.53	1.04	2.11	1.47	1.47	1.1	1.1	0.89	2.74	2.74	1.18	1.15	1.68	2.4		3.76	1.13	1.93	1.48	1.48	1.52	1.16	1.01	2.43
ORF SEQ ID NO:			22947	24127	27121	28583	20093			21298	21299	21656			23960				27557	28854			19780	19780	19859	19860	19883	19950	20095	20114
Exon SEQ ID NO:	16723	11128	13144	14337	16930	18324	10274	10329	11306	11441	11441						15063	17181	17353	18571		18884	8888	9989	10048	10048	10065	10135	10276	10299
Probe SEQ ID NO:	6844	1219	3220	4443	7053	8451	312	375	1401	1537	1537	1885	1885	3046	4283	4283	5200	7305	7483	8683		9126		2	62	8	<u>ه</u>	162	314	340

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Table 4
Single Exon Probes Expressed in Heart

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Onigie Lyon riones Expressed in near	Top Hit Descriptor	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	G.garilla DNA for ZNF80 gene homolog	RC3-HT0625-040500-022-b09 HT0625 Homa sepiens cDNA	Homo saplens DKFZP586M0122 protein (DKFZP586M0122) mRNA	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA	UI-H-BI1-afk-c-07-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE -2722164 3	qf62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81061 CYSTATIN	Rat mRNA for short type PB-cacherin, complete cris	H.saplens mRNA for IFN-damma (pKC-0)	Homo sapiens KIAA0957 protein (KIAA0957) mRNA	Homo saplens RGH2 gene, retrovirus-like element	Homo seplens myotubularin-related protein 1a mRNA partial cris	Homo sapiens follicle stimulating hormone recentor (FSHR) mRNA	Homo sapiens small optic lobes (Drosophila) homolog (SQLH) mRNA	Homo sepiens small optic lobes (Drosophila) homolog (SOLH) mRNA	801863164F1 NIH MGC 57 Homo saciens cDNA clone IMAGE Angropa F	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA10030A55	Homo saplens NF-E2-related factor 3 gene, complete cds	AU140214 PLACE2 Homo saplens cDNA clone PLACE2000137 5'	yf38c08.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE-120134 र	MR1-TN0046-060900-004-b05 TN0046 Homo seplens cDNA	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA	Human mRNA for kidney epidermal growth factor (EGF) precursor	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5	Homo sapiens chromosome 21 segment HS21C003	Homo saplens mRNA for KIAA1485 protein, partial cds	wr37g09.xf NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element	MER22 repetitive element;	PMO-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA	Homo sapiens mRNA for KIAA1626 protein, partial cds	Homo sepiens mRNA for KIAA1626 protein, partial cds	hh83c11.y1 NCL_CGAP_GU1 Homo sepiens cDNA clone IMAGE:2969396 51
old Exoll F10	Top Hit Database Source	Į.	ΝŢ	EST HUMAN	1	₽ F	EST HUMAN	EST HUMAN	Į.	¥	Z	Ę	F	F	N I	E	EST HUMAN	EST HUMAN	¥	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	뉟	EST_HUMAN	ΝŢ	TN		EST_HUMAN	EST_HUMAN	TN	NT	EST_HUMAN
	Top Hit Acession No.	1.0E-100 AF003528.1		1.0E-100 BE180609.1	7661685 NT	7661685 NT	55.1	Al200857.1			11418976 NT		1.0E-100 AF057354.1	4503792 NT	5032104 NT	5032104 NT	9.1		1.0E-100 AF135116.1				3.1		3.1		1.0E-100 AB040918.1		_		3.1		1.0E-100 AW630487.1
	Most Similar (Top) Hit BLAST E Value	1.0E-100	1.0E-100 X89631.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100 AW2075	1.0E-100 A 200857	1.0E-100 D83349.	1.0E-100 X62468.1	1.0E-100	1.0E-100 D11078.	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100 BF24421	1.0E-100	1.0E-100	1.0E-100 AU14021	1.0E-100 R10887.1	1.0E-100	1.0E-100	1.0E-100 X04571.1	1.0E-100	1.0E-100 AL163203	1.0E-100		1.0E-100 /	1.0E-100 AW99861	1.0E-100 /	1.0E-100 AB04684(	1.0E-100 /
	Expression Signal	1.53	7.04	4.17	2.43	2.43	1.33	1.46	1.45	1.08	1.87	2.45	1.49	1.87	3.07	3.07	1.8	1.4	1.55	5.1	1.41	4.4	1.4	6.99	6.19	5.44	3.2		1.53	1.67	1.73	1.73	1.69
	ORF SEQ ID NO:			20255		20764		21294		22160			23796	23816	24665	24666	24924	25478	25496	25946	26049	26146	26147	26151	27033		27398		10000	20625	27587	27588	27740
	Exon SEQ ID NO:	10375	10425	10442		$\sqcup$	11433	11437	L	12267	12539			14043			15156				- 1	- 1	16010	16013	16841	16860	17198	170	150	10430 105431	17378	17378	17514
	Probe SEQ ID NO:	430	481	500	1002	1002	1528	1533	2195	2388	2674	2985	4116	4143	5024	5024	5232	5496	5514	5915	6015	6116	6116	6119	6963	6983	7322	7960	2000	7420	/957	7527	7664

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	Top Hit Descriptor	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'	Human endogenous retrovirus HERV-K, pol gene	MR0-BN0070-270300-008-h11 BN0070 Homo saplens cDNA	H.saplens CD97 gene exon 4	H.sapiens CD97 gene exon 4	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens golgin-like protein (GLP) gene, complete cds	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	Homo sapiens mRNA for KIAA0446 protein, partial cds	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	Homo sapiens ventral enterior homeobox 2 (VAX2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo saplens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylgnycinamide synthetase, care phosphoribosylgninidazole synthetase (GART) mRNA	Homo sapiens of cardiac alpha-myosin heavy chain gene	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5	qg99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336.3'	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo saplens carboxypeptidase A1 (pancreatic) (CPA1) mRNA	RC3-ST0281-160600-016-h09 ST0281 Homo saplens cDNA	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA	H.saplens EWS gene, exon 5	Homo sapiens RIBIIR gene (partial), exon 12	Homo sapiens RIBIIR gene (partial), exon 12	Homo saplens genomic downstream Rhesus box	Homo sapiens gamma-glutamytitansferase 1 (GGT1) mRNA
	Top Hit Database Source	EST_HUMAN	IN	EST_HUMAN	N	LN.	NT	N L	N	N		IN I	Z	N	NT	N	TN	R	NT	N		N	EST_HUMAN	EST_HUMAN	IN	F	FN	EST_HUMAN	N	NT	F	TN.	NT	LN L
	Top Hit Acession No.	1.0E-100 AW630487.1	r10391.1	3F327292.1	K94633.1	<b>(94633.1</b>	70.3	Γ	1.0E-100 AL163247.2	AF266285.1		1.0E-100 AF240786.1	11545/3ZNI	11417974 NT	7110714 NT	7110714 NT	15.2	7110734 NT	7110734 NT	7657454 NT	4503914 NT	1	18.1	8.1	7662183 NT	7662183 NT	4502996	70.1	5729892 NT		1.0E-101 AJ237744.1		2.1	4885270 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-100	1.0E-100 Y10391.	1.0E-100 BF3272	1.0E-100 X94633	1.0E-100 X94633.	1.0E-100 AF1111	1.0E-100	1.0E-100	1.0E-100	7 04 400	1.0E-100/	1.05-100	1.0E-100	1.0E-101	1.0E-101	1.0E-101 AB0079	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 Z20856.	1.0E-101 BF68121	1.0E-101 AI22187	1.0E-101	1.0E-101	1.0E-101	1.0E-101 BE84307	1.0E-101	1.0E-101 X72993.	1.0E-101	1.0E-101	1.0E-101 AJ25231	1.0E-101
	Expression Signal	1.69	1.29	5.23	2.14	2.14	4.58	4.56	1.96	1.86	i i	9.58	777	3.38	122	122	1.16	4.45	4.45	1.32	1.28	3.44	12.74	1.63	0.87	0.87	1.62	1.6	1.66	4.4	2.56	2.56	12.14	2.51
	ORF SEQ ID NO:	27741			28745	28746	28831	28832	19780			1			19871	19872	20422	20447	20448	20521	20612	20679	20741	20796	21483	21484	21677	21792	22080	22335	22468	22469		22897
	Exon SEQ ID NO:	17514	17866		18473		18549	18549	6866	18738			1302/	19409	10055	10055	10605	10621	10621	10684	10762	10832	10892	10954	11613	11613	11797	11902	12718	12443	12576	12576	12852	13092
	Probe SEQ ID NO:	7664	8016	8141	8606	9098	8660	8660	8688	8930	9700	8048 0254	1008	9940	2	2	671	688	688	754	835	808	696	1036	1712	1712	130	2010	2301	2572	2714	2714	2925	3167

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Single Exon Probes Expressed in Heart

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מוסר באסוו ווסר	Top Hit Database Source	EST HUMAN	EST HUMAN	NT	NT	L	NT	NT	EST HUMAN	NT	LN.	LN L	N.	T HUMAN	Т	T	Τ		THUMAN				EST_HUMAN	L HUMAN		₽N		T HUMAN		EST HUMAN		LN		
5	Top Hit Acession No.	1.0E-101 BF035327.1	1.0E-101 AW965556.1	1.0E-101 AJ237744.1	1.0E-101 AJ237744.1	1.0E-101 AB022785.1	5921460 NT	5921460 NT	AW965139.1	7427512	7427512 NT	AF208970.1	0.1	75.1	1.0E-101 BE257384.1	1.0E-101 BF330759.1	1.0E-101 BF029174.1		-			9845492	7.1	7.1	11429127 NT		5.1	1.1	2	2	1557534		11437146 NT	11437146 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 AW9651	1.0E-101	1.0E-101	1.0E-101	1.0E-101 AF20897	1.0E-101 AW0084	1.0E-101	1.0E-101	1.0E-101		1.0E-101	1.0E-101 X60069.1	1.0E-101 X60069.1	1.0E-101	1.0E-101 BE61966	1.0E-101 BE61966	1.0E-101	1.0E-101 S38327.1	1.0E-101 AB02062	1.0E-101	1.0E-102 AL163303	1.0E-102 BE252470	1.0E-102	1.0E-102 M10976.1	1.0E-102	1.0E-102
	Expression Signal	2.16	1.67	1.75	1.75	4.83	1.67	1.67	1.4	3.73	3.73	4.16	4.16	5.63	1.56	5.3	2.65		C.1.	16.52	16.52	18.4	5.64	5.64	1.76	2.88	1.78	11.62	3.24	0.89	1.46	1.95	1.39	1.39
	ORF SEQ ID NO:			22468	22469	23499	24609	24610	24954	25658	25659		26357	26441		26581	26764	12020	21214	26650	26651	27468	27694	27695	28040	28381	28586		20111	20350	20526	20859	21002	21003
	Exen SEQ ID NO:	13127	13254	12576	12576	13712	14840	14840	15179	15563	15563	16196	16196	16278	16330	16402	16573	17005	20071	10438	16458	17263	17474	17474	1,800	18132	18327	19189	10297	10540	10688	11017	11154	11154
	Probe SEQ ID NO:	3203	3334	3354	3354	3800	4965	4962	5257	5651	5651	6333	6333	6416	6471	6544	6693	7200	7446	0	9	7454	/623	7623	000	8252	8454	9610	88	8	728	1101	1247	1247

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Table 4
Single Exon Probes Expressed in Heart

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	. Top Hit Descriptor	601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5/	em60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.;	am60c10.x1 Johnston frontal corfex Homo sapiens cDNA clone IMAGE:1639954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-95.	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'	Homo sapiens chromosome 21 segment HS210007	601107843F1 NIH_MGC_16 Homo sapiens cDNA clane IMAGE:3343882 5'	y32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds	Homo sapiens histone deacetylase 7 (HDAC7), mRNA	Homo sapiens histone deacetylase 7 (HDAC7), mRNA	ar82f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137	Homo sapiens mRNA for Centaurin-alpha2 protein	AV710738 Cu Homo septens cDNA clone CuAAKD03 5'	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5'	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'	Homo sapiens mRNA for KIAA0454 protein, partial cds	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	RC-BT074-260499-014 BT074 Hamo sapiens cDNA	RC-BT074-260499-014 BT074 Homo sapiens cDNA	on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2. [1];	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'
Section of	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	7661979 NT	EST_HUMAN	EST_HUMAN	IN	EST_HUMAN	EST_HUMAN	ΝΤ	NT	NT	FN.	EST HIMAN	LN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
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	Most Similar (Top) Hit BLAST E Value	1.0E-102 BE40844	1.0E-102 A1124669	1.0E-102 A1124669	1.0E-102	1.0E-102 AU14100	1.0E-102 AU14100	1.0E-102 AL163207	1.0E-102 BE25131	1.0E-102 R66488.1	1.0E-102 AF06713	1.0E-102 AB03495	1.0E-102	1.0E-102	4 0F-102 A1450825	1.0E-102 AJ238994	1.0E-102	1.0E-102	1.0E-102 BE91055	1.0E-102 AV69481	1.0E-102 AV69481	1.0E-102 AB00792;	1.0E-102 T70393.1	1.0E-102	1.0E-102 AU12462	1.0E-102	1.0E-102	1.0E-102 AI905037	1.0E-102 A1905037	1.0E-102	1.0E-102 BE89746
	Expression Signal	90.24	1.34	1.34	1.51	5.61	5.61	1.46	2.11	1.09	1.88	7.27	3.46	3.46	2 5.4	6.56	2.53	42	2.53	1.36	1.36	4.06	1.52	1.52	3.58	2.03	2.03	2.9	2.9	2.3	2.38
-	ORF SEQ ID NO:	21162	22044	22045		22815	22816	23814	23994	24705	22022		25522	25523	25818			L	26904		27015	27069	27448			28052	28053	28070	28071		28549
	Exan SEQ ID NO:	11303	12145	12145	12954	13021	13021	14039	14211	14933	15221	15433	15453	15453	45708	16214			16711	16823	16823	16878	17243			17811	17811	17831	17831		18295
	Probe SEQ ID NO:	1398	2261	2261	3026	3094	3094	4139	4314	5063	5300	5515	5536	5536	5800	6351	6495	6787	6832	6945	6945	7001	7374	7374	7415	7961	7961	7981	7981	8005	8421

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	Top Hit Descriptor	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA	Human chromosome 16 creatine transporter (SLO6AB) and (CDM) paralogous genes, complete cds	Homo saplens chromosome 21 segment HS21C080	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'	601500405F1 NIH_MGC_70 Homo saplens cDNA clone IMAGE:3902305 5'	Homo sapiens mRNA for KIAA0235 protein, partial cds	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds	yw91d08.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259599 3'	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'	UI-H-BW0-ajt-h-11-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'	Homo sapiens mRNA for KIAA1459 protein, partial cds	Macaca mulatta cyclophilin A mRNA, complete cds	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains	element LTR10 repetitive element ;	Homo sapiens neuropilin 1 (NRP1), mRNA	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'	Homo sapiens septin 2 (SEP2) mRNA, partial cds	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
TO LIVE OF	Top Hit Database Source	TN	TN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	NT	LN	IN	NT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT		EST_HUMAN	۲	EST_HUMAN	NT	NT	EST_HUMAN
5	Top Hit Acession No.	4507822 NT	.4507822 NT	3F359243.1	J41302.1	AL163280.2	4W300862.1	1.0E-103 BE908158.1	3E908158.1	D87078.2	5453793 NT	1.0E-103 AJZ78348.1	3E877541.1	1.0E-103 AF012872.1	7657592 NT	4502428 NT	4502428 NT	AU134991.1	AF060568.1	N32770.1	BE744722.1	1.0E-103 AW 298245.1	1.0E-103 AB040892.1	AF023861.1		1.0E-103 AA485663.1	11430876 NT	T23683.1	1.0E-103 AF179995.1	AF053490.1	AI590071.1
	Most Similar (Top) Hit BLAST E Value	1.0E-102	1.0E-102	1.0E-102 BF359243	1.0E-102 U41302.1	1.0E-102 AL163280	1.0E-102 AW30086;	1.0E-103	1.0E-103 BE908158	1.0E-103 D87078.2	1.0E-103	1.0E-103	1.0E-103 BE877541	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 AU134991	1.0E-103 AF060568	1.0E-103 N32770.1	1.0E-103 BE744722	1.0E-103	1.0E-103	1.0E-103 AF023861		1.0E-103	1.0E-103	1.0E-103 T23683.1	1.0E-103	1.0E-103 AF053490	1.0E-103 AI590071
	Expression Signal	1.99	1.99	2.78	4.04	2.82	4.77	0.82	0.82	8.1	0.83	1.01	7.29	2:32	1.04	1.27	1.27	1.57	2.22	0.86	2.43	3.44	1.06	2.41		1.16	1.39	3.02	1.72	5.37	1.68
	ORF SEQ ID NO:		28554		29051		25247	19861	19862	19894	19989	20734	20985	21342	21643	21708	21709	22040	22175	22340			23108					23611	25619	26027	26069
	Exon SEQ ID NO:	18298	18298	18525	18755	18837	19183	10049	10049	10078	10173	10888	11131	11482	11768	11827	11827	12141	12278	12449		13253	13310	13609	1		13670	13831	15534	15903	15936
	Probe SEQ ID NO:	8424	8424	8708	8947	9054	9601	အ	ස	66	201	965	1223	1578	1872	1932	1932	2257	2401	2578	3030	3333	3333	3692		3725	3757	3922	5619	5998	6033

Page 328 of 413 Table 4 Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	tmBBb05x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;	Homo sapiens dystrophin (muscular dystrophy, Ducherne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m,	mRNA	Homo saplens dystrophin (muscular dystrophy, Duchenne and Becker types), includes UXS.142, UXS.104, DXS206, DXS230, DXS239, DXS239, DXS238, DXS269, DXS270, DXS272 (DMD), transcript variant DP427m,	mRNA CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF 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ricacezonos 14 5	7160e03.x1 Soares_NSF_FB_9W_OI_PA_F_ST Home saperis contribution contributions of the SW.PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1;	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LIBF-2)	EST375749 MAGE resequences, watch home sapiens conva-	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cUNA cicrie IMACE2016320 5 Similia 10 TR:015046 015046 KIAA0338 ;	olo2d06.y5 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084	PROSTROLIFYSE CIVE STOCKES 1 2 and 3	Honno septems NOD 1 potent (NOD 1) gene, covere 1, at and 3	Homo sapiens NOU1 protein (NOU1) gene, excits 1, 2, and 3	AU136283 PLACE1 Homo sapiens convergence reace rocess 3	Homo sapiens polycystic kidney disease (PKD 1) gene, excits 27-30	7608a10.X1 Sogres_NSF_F6_9W_OI_FA_F_STRUINS saprens curv. clare invocations of contains MER29.t3 MER29 repetitive element;
Social Libra Billio	Top Hit Database Source	EST_HUMAN		NT		- 1	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	1	L	NT	EST_HUMAN	EST HUMAN		EST HUMAN	Į,		EST_HUMAN	본	EST_HUMAN
BIIIC	Top Hit Acession No.	1590071.1		5032282 NT		5032282 NT	W965776.1	1.0E-103 BE748158.1	1590071.1		AI590071.1	T31080.1	1.0E-103 AU140344.1	1.0E-103 AU140344.1	1 0E-103 BF109244.1	F005921 NT	6005921 NT	237976.1	1.0E-103 AW963676.1	1 0F-103 AI878956.1			AF149773.1	AF149773.1	AU136283.1	L43610.1	BE644611.1
	Most Similar (Top) Hit BLAST E Value	1.0E-103 AI590071		1.0E-103		1.0E-103	1.0E-103 AW9657	1.0E-103	1.0E-103 AI590071		1.0E-103 AI590071	1.0E-103 T31080.1	1.0E-103	1.0E-103	1.0E-103	1.0E-103	İ		1.0E-103	1 0F-103						1.0E-103 L43610.	1.0E-103 BE64461
	Expression Signal	1.68		1.68		1.8	1.64	3,21	3.28		3.28			1.17	1.43								2.74	2.74	2.56	6.49	3.42
	ORF SEQ ID NO:	02030		24878		24879						26896					1						1 28353	1 28354	9 28852		8 29070
	Exon SEQ ID NO:	15038	0000	15102		15102	16153	16201	46478	10450	16426	16702	16887	16887	1	İ	17144	17637	.l_	J	07//	18004	18101			丄	18778
	Probe SEQ ID 8 NO:	600	2000	6000		6092	6280	8338	0000	8000	8258	6823	7010	7010	1000	7367	7967	7787	7815	107	0/0/	8115	8218	8218	8681	8743	8973

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Homo sapiens gene for AF-6, complete cds	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sepiens cDNA clone DKFZp564H1072 5'	DKFZp564H1072_r1 564 (synonym: htbr2) Homo sapiens cDNA clone DKFZp564H1072 5	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (ВМРв) mRNA	2022c06.s1 Stratagene colon (#9372c4) Homo saplens cDNA clone IMAGE:587626 3' similar to ab:Z14116 mat CD59 GLYCOPROTEIN PRECIRSOR (HI IMAN):	601577460F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3926438 5	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds	H.sapiens gene encoding phenylpyruvate tautomerase II	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end	Homo sapiens mRNA for KIAA1276 protein, partial cds	Homo sapiens mRNA for KIAA1276 protein, partial cds	Homo saplens mRNA for KIAA1172 protein, partial cds	Human mRNA for fibronectin (FN precursor)	Homo saplens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Human Down Syndrome region of chromosome 21 DNA	Human Down Syndrome region of chromosome 21 DNA	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN ;contains element LTR7 repetitive element :	wj03b12x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' sImilar to TR:Q14145 Q14145 KIAA0132 PROTEIN ; contains element LTR7 repetitive element	601150451F1 NIH MGC 19 Homo sapiens oDNA clone IMAGE:3503220 5	801150451F1 NIH MGC 19 Homo sapiens cDNA done IMAGE:3503220 57	Homo sapiens edaptor-related protein complex 2, beta 1 subunit (AP2B1) mRNA	nad16g11x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'	Homo sapiens Trio isoform mRNA, complete cds	Homo sapiens Trio isoform mRNA, complete cds
	Top Hit Database Source	N	LN L	N	EST_HUMAN	EST_HUMAN	N	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	N	N	N	EST_HUMAN	NT	NT	본	ΙN	Ā	٦	NT	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	ľ	EST HUMAN	NT	Ŋ
	Top Hit Acession No.	AF224669.1	11526291 NT	AB011399.1	AL037549.3	AL037549.3	4502428 NT	AA132975.1	BE744628.1	BF334221.1	BF334221.1	5031570 NT	M34671.1	Y11151.1		2.1	AB033102.1	1.0E-104 AB032998.1	K02761.1	1.0E-104 AF231920.1	4F231920.1	143379.1	J43379.1	AI768797.1	41768797.1	3E314182.1	1.0E-104 BE314182.1	11425572 NT	3F448230.1	1.0E-104 AF091395.1	1.0E-104 AF091395.1
	Most Similar (Top) Hit BLAST E Value	1.0E-103	1.0E-103	1.0E-103 AB011390	1.0E-104 AL037549	1.0E-104 AL037549	1.0E-104	1.0E-104 AA13297	1.0E-104 BE744628	1.0E-104 BF33422	1.0E-104 BF33422	1.0E-104	1.0E-104 M34671.1	1.0E-104 Y11151.1	1.0层-104	1.0E-104	1.0E-104 AB03310;	1.0E-104	1.0E-104 X02761.1	1.0E-104	1.0E-104 AF231920	1.0E-104 U43379.1	1.0E-104 U43379.1	1.0E-104 AI768797	1.0E-104 AI768797	1.0E-104 BE314182	1.0E-104	1.0E-104	1.0E-104 BF448230	1.0E-104	1.0E-104
	Expression Signal	1.72	2.65	2.21	2.6	2.6	1.81	7.16	1.91	1.15	1.15	1.55	7.64	2.82	1.54	66.0	0.89	0.91	4.28	6.0	0.9	1.33	1.33	8.46	8.46	1.52	1.52	2.38	2.24	4.66	4.66
	ORF SEQ ID NO:			25323	20016	20017	21617	21932	21944		22098		22559			23260	23261	23564	23957	24182	24183	25615	25616	25919	. 25920	26204	26205	26309	27363	27442	27443
	Exan SEQ ID NO:	18833	18855	18979	i I	10202	11741	12035			12199		12770				13465	13772	14179	14397	14397	15532	15532	15797	15797	16056	16056	16152	17164		17239
	Probe SEQ ID NO:	9049	9079	9275	233	233	1845	2147	2157	2318	2318	2387	2842	2886	3345	3550	3550	3861	4280	4504	4504	5617	5617	5891	5891	6073	6073	6288	7288	7370	7370

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Тор Hit Descriptor	11.3-H70619-080900-249-F07 H70619 Home seriens «DNA	11.3-HT0619-080900-249-F07 HT0619 Home saniens cDNA	601581503F1 NIH MGC 7 Home saniens cDNA Alone IMA CE 2025077 F	601581503F1 NIH MGC 7 Homo sepiens CDNA Alme NAA CE 2025477 51	AV728070 HTC Homo septens cDNA clone HTCBYAN7 5	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP2001308 8'	Human beta4-integrin (ITGB4) gene, exons 19 20 21 22 22 and 25	RC0-HT0885-310700-021-b09 HT0885 Homo saniens citals	RC0-HT0885-310700-021-b09 HT0885 Homo sabiens cDNA	602141215F1 NIH MGC 46 Homo saniens clans IMAACE:4202607 E1	601312181F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3658676 5'	Homo sapiens amydid hefa (A4) predimed worksis (westerness)	Homo sapiens Meist (mouse) homolog (AFP), mRNA	Homo sapiens potassium channel subjunit (HERG-3) mBNA complete and	Homo sapiens potassium channel subunit (HERG-3) mRNA complete cds	Homo sapiens chromosome 21 seament HS21Chan	Human mRNA for KIAA0128 cene, partial cds	EST 20609 Spleen I Homo sepiens cDNA 5' and similar to autoimmine anticon VII 201-20 - 11	Ino10d05.s1 NCI CGAP Phet Homo sepiens cDNA clone IMACE-1400368 21	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21022: serment 1/2	Homo sapiens bromodomain adjacent to zinc finger domain 28 (RAZ2R) mRNA	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ28) mRNA	Homo sapiens dermatopontin (DPT), mRNA	EST373761 MAGE resequences, MAGG Homo saplens cDNA	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE 3850156 51	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5	Homo saplens chromosome 21 segment HS21C008	Homo sapiens mRNA for KIAA0796 protein, partial cds	Homo sapiens mRNA for KIAA0866 protein, complete cds	Homo saplens mRNA for KIAA0796 protein, partial cds	Homo sapiens GTPase activating protein-like (GAPL), mRNA	Homo sapiens GTPase activating protein-like (GAPL) mRNA
JIB EXON Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N-	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	Į	L L	N.	N	NT	Į.	EST HUMAN	EST HUMAN	LN	NT	나	T			T_HUMAN			NT			
JIIO	Top Hit Acession No.	1.0E-104 BF352841.1		13.1	13.1	70.1		F.					4502166 NT	4505150 NT	1.0E-105 AF032897.1	•	1.0E-105 AL163280.2	_	59.1	38.1	1.1	7304922	7304922 NT	11425532 NT	88.1	я.1	н.1		19.1		1.0E-105 AB018339.1 N	11419196 NT	11419196 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-104	1.0E-104	1.0E-104 BE7917	1.0E-104 BE7917	1.0E-104	1.0E-104 AU1307	1.0E-104	1.0E-104 BE7201	1.0E-104	1.0E-104	1.0E-104	1.0E-105	1.0E-105	1.0E-105	1.0E-105 AF03289	1.0E-105	1.0E-105 D50918.	1.0E-105 AA3183	1.0E-105 AA5848	1.0E-105 AJ22904	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105 BE86888	1.0E-105 BE86888	1.0E-105 AL16320	1.0E-105	1.0E-105 AB02067	1.0E-105,	1.0E-105	1.0E-105
	Expression Signal	3.84	3.84	3.14	3.14	1.42	4.51	4.24	1.84	1.84	4.49	1.37	2.86	16.85	322	3.22	1.16	1.75	1.64	0.87	2.57	0.93	0.93	1.26	2.15	0.84	0.84	3.74	0.95	2.23	1.3	3.06	3.06
	ORF SEQ ID NO:	26630	26631	27898	27899	28037	28057	28110	28755	28756	28783		20062	19777	20323	20324	21:553	21655	21928			23032	23033		23689	24313	24314		24690	24740	24690	24840	24841
	Exan SEQ ID NO:	16443	16443	17659	17659	17797	17816	17864	18484	18484	18505	19340	12637	9866	10517	10517	11676	11780	12030	12554	12902	13228	13228	13508	13914	14526	14526	14/35	14916	14965	14916	15124	15124
	Probe SEQ ID NO:	7430	7430	7809	2809	7947	7966	8014	8617	8617	8641	9842	277	419	579	579	1777	1884	2142	2689	2975	3307	3307	3592	4008	4638 88	4638	4833	2044	2032	5167	6167	010

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		rto		23'			TR:P87892								ment	ment			speat											
	Top Hit Descriptor	we50c10x1 NCI_CGAP_Bm25 Homo sapiens dDNA clone IMAGE:2500626 3' similar to SW:ACSA PENCH Pagessa A CETYA COENTA LE COURT INTEREST.	U-H-Bion-ah-h-12-0-11 c1 NC1 CGAP S: 12-0-12-12-12-12-12-12-13-13-13-13-13-13-13-13-13-13-13-13-13-	Homo sapiens SMARCA4 isoform (SMARCA4)	Homo sapiens COI 446 gene for as/it/) called a complete cds, alternatively spliced	Homo saplens Ran binding profein 11 (1 0.55100) mbNA	wv74f07.xf Soares_thymus_NHFTh Homo sepiens cDNA done IMAGE:2535301 3' similar to TR:P87892	UI-HEBNO-AR-O72-AIII AINIH MCC EN II	Ita79c01 x1 NCI CGAP 1 Ht Home contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the conta	EST377629 MAGE resequences MAGI Home content CNV	Human dihydrofolaha radinctasa pseudosana (z.e. 1944)	Human dihydrofolata reductasa pseuroceae (nei hdd)	Homo sabiens soluble neuropilin 1 mDMA completed at	Human epidermal growth factor recentor (FCRFR) precincer mBNA	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element.	ng41c05.s1 NCI_CGAP_Co3 Homo sepiens cDNA clone IMAGE:937352 3' similar to contains element	MRQ-HT0165-140200-008-410 HT045E U	Homo sepiens of triathione S-framefaces that a 1/05T-11	Homo saplens X-linked anhidrolite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat renins.	Homo saplens sperm membrane protein BS &3 mDN/A	601149783F1 NIH MGC 19 Home seniens cDNA clame INAA CE 2503222 E	d/76h10.x1 Soares NhHMPu S1 Home capiers c/DNA clara MACE 12022022	Homo sapiens digitatione Stransferase there 4 (CCTT4)	Homo sapiens dutathione S-transferase thete 4 (COTTA) - Data	Homo saplens mRNA for KIAA1328 protein hartisl of	Homo sapiens mRNA for KIAA1336 profes and sales	Homo sapiens hypothetical protein FI (11273 (FI (11972) DNIA	Homo sapiens hypothetical projets El 14272 (El 14272)	Homo saplens gene for activin recentor two IIR complete and	Homo sapiens mRNA for KIAA1278 protein, partial cds
	Top Hit Database Source	EST HUMAN	EST HUMAN	NT	NT	NT	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN LN	N	NT	NT	EST HUMAN	FOT LIMAN	EST HUMAN	L			T_HUMAN	T HUMAN			NT	N				LN L
	Top Hit Acession No.	AW007194.1	1.0E-105 AW016879.1	1.0E-105 AF254822.1	D63548.1	7705936 NT	1 7 7	208.1		1.0E-106 AW965556.1	100146.1		12.1	1	1.0E-106 AA527446.1	-		4504184	F003528.1	2	1.1	5.1	4504184 NT	4504184 NT			2965	8922965 NT		
Most Similar	(Top) Hit BLAST E Value	1.0E-105 AW007	1.0E-105	1.0E-105	1.0E-105 D63548.1	1.0E-105	1.0E-105 AW0278	1.0E-108	1.0E-106	1.0E-106	1.0E-106 J00146.	1.0E-106 J00146.	1.0E-106 AF1457	1.0E-106 U48724.	1.0E-106/	1.0E-106.AA5274	1.0E-106 BE14428	1.0E-106	1.0E-106 AF00352	1.0E-106 U64675.	1.0E-106 BE2602(	1.0E-106 AIZ76526	1.0E-106	1.0E-106	1.0E-106 A	1.0E-106 AB037747.1	1.0E-106	1.0E-106	1.0E-106 AB008681.1	1.0E-106 AB033104.1
	Expression Signal	1.8	2.99	5.44	1.8	2.06	2.01	0.96	1.54	1.77	0.79	1.21	2.66	4.51	5.12	5.12	1.08	8.39	1.63	1.25	1.94	4.23	2.97	2.97	5.01	5.01	2.36	2.36	0.8	0.98
	ORF SEQ ID NO:		27304	28428		28740	28968				20334	20334	21272	21444	21533	21534	21858	22052	22229	22322	22324	22487	21183	21184	22635	22636	22867	22868	23053	23109
	Excan SEQ ID NO:		17111	18181	١.,	18469	18679	10119	10170	10473	10527	10527	11413	11576	11661	11661	11965	12163	12333	12420	12431	12591	11319	11319	12837	12837	13068	3000	13248	13311
	Probe SEQ ID NO:	6894	7234	8303	8560	8602	8867	145	198	531	283	8	1508	1674	1762	1762	2075	7269	2456	2557	2559	2729	2795	2795	2911	2911	3143	3143	3328	3394

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Most Similar Top Hit Acession (Top) Hit Top Hit Acession Signal BLASTE No. Source Source	0.98 1.0E-106 AB033104.1 NT	7.22 1.0E-106 AW974650.1 EST_HUMAN	7.22 1.0E-106 AW974650.1 EST_HUMAN	1.21 1.0E-106 BE144286.1 EST_HUMAN		2.98 1.0E-108 AA781155.1 EST HUMAN	6.78 1.0E-108 BF679574.1 EST_HUMAN	16.4 1.0E-106 11545913 NT	16.4 1.0E-106 11545913 NT	5.59 1.0E-109 AA663779.1 EST_HUMAN	4.83 1.0E-106 11429617	1.35 1.0E-106 BE292722.1 EST HUMAN	7.6 1.0E-106 11425503 NT	7.6 1.0E-106 11425503 NT	5,33 1.0E-106 BE741408.1 EST_HUMAN	5.33 1.0E-106 BE741408.1 EST_HUMAN	. 1.48 1.0E-106 AI523066.1 EST_HUMAN	3.16 1.0E-106 AI654123.1	1.86 1.0E-106 AA825307.1 EST HUMAN	1.86 1.0E-106 AA825307.1 EST_HUMAN	2.79 1.0E-106 AI750447.1 EST_HUMAN	1.86 1.0E-108 AI479569.1 EST HUMAN	186 1.0E-106 Al479569.1 PST HI IMAN TAR1 PTR5 repositive element	1.32 1.0E-106 BF027310.1 FST HIMAN	1.32 1.0E-106 BF027310,1 EST HUMAN	5.83 1.0E-106 AA604417.1 EST HUMAN	5.83 1.0E-106 AAG04417.1 EST_HUMAN
ORF SEQ Expressic ID NO: Signed				24176 1.	1.	25022 2.	25722 6.	15891	25892 10	26385 5.		26453 1.		26518		26734 5.		27120 3.			27419 2.	27501 1.	27502				27976 5.
Exon SEQ ID NO:	13311	13860	13860	14391	15047	15219	15619	15772	15772							16537	16633	16929	17158	17158	17219	17291	17291			17730	17730
Probe SEQ ID NO:	3394	3952	3952	4497	5183	5298	5711	5866	5866	6361	6390	6431	6490	6490	6657	6657	6754	7052	7281	7281	7351	7424	7424	7803	7803	7880	7880

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	Top Hit Descriptor	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C002	601453461F1 NIH_MGC_66 Homo sepiens cDNA done IMAGE:3857366 5	601453461F1 NIH_MGC_66 Homo sapiens cDNA done IMAGE:3857366 67	Human ryanodine receptor mRNA, complete cds	Human ryanodine receptor mRNA, complete cds	fh05h11.x1 NIH_MGC_17 Homo sepiens cDNA done IMAGE:2961644 5	601433087F1 NIH_MGC_72 Homo sapiens cDNA done IMAGE:3918524 5	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Human IFNAR gene for Interferon alpha/beta receptor	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sapiens NY-REN-25 antigen mRNA, partial cds	Human IFNAR gene for Interferon alpha/beta receptor	Human IFNAR gene for interferon alpha/beta receptor	Homo sapiens sodium-dependent high-affinity dicarboxylate fransnorter (NADC3) mRNA commisse and	Homo sabiens BAZ1B mRNA for homodomain ediacent to zine finese domaia 4B	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3	Homo sapiens mRNA for KIAA0453 protein, partial cds	Homo saplens mRNA for KIAA0453 protein, partial cds	Human dipeptidyl peptidase IV (CD26) gene, exon 20	601567619F1 NIH_MGC_21 Home sapiens cDNA clone IMAGE:3842309 5'	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'	PM1-CN0031-190100-001-d03 CN0031 Homo saplens cDNA	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	Homo sapiens myotubularin (MTM1) gene, exon 9	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5	wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
2000	Top Hit Database Source	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	M	ĮŅ.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	N	N	N	TN	FN	· LN	L	EST HUMAN	LN	N.	NT	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	1.0E-106 AW363299.1	1.0E-106 AL163202.2	1.0E-106 BF032755.1	1.0E-106 BF032755.1	J05200.1	J05200.1	1.0E-106 AW410405.1	1.0E-106 BE894488.1	1.0E-106 BE894488.1	BE695905.1	1.0E-107 AJ271735.1	X60459.1	4826863 NT	1.0E-107 AF155103.1	X60459.1	X60459.1	1.0E-107 AF154121.1	1.0E-107 AB032263.1	1.0E-107 BF087405.1	4F136275.1	1.0E-107 AB007922.2	1.0E-107 AB007922.2	J13729.1	1.0E-107 BE732460.1	1.0E-107 BE732460.1	1.0E-107 AW842451.1	1.0E-107 AW842451.1	5902097 NT	AF020671.1	1.0E-107 BE867469.1	1.0E-107 AW 503913.1	1.0E-107 AW 503913.1	AI765078.1
	Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106 J05200.	1.0E-106 J05200.1	1.0E-106	1.0E-109	1.0E-106	1.0E-108 BE69590	1.0E-107	1.0E-107 X60459.1	1.0E-107	1.0E-107	1.0E-107 X60459.	1.0E-107 X60459.	1.0E-107	1.0E-107	1.0E-107	1.0E-107 AF13627	1.0E-107	1.0E-107	1.0E-107 U13729.1	1.0E-107	1.0E-107	1.0E-107	1.0E-107	1.0E-107	1.0E-107 AF02067	1.0E-107	1.0E-107	1.0E-107	1.0E-107 AI765078
	Expression Signal	1.86	3.68	5.21	5.21	2.28	2.28	2.87	2.31	2.31	5:35	3.48	1.05	1.07	1.7	98.0	1.16	10.67	0.78	2.13	1.47	0.95	0.95	126	0.86	0.86	1.94	1.94	2.62	3.92	3.26	1.52	1.52	1.83
	ORF SEQ ID NO:	27990	28113	28389		28544	28545			25299							20644	20724	21015	21314	21488	21571	21572	21949	22257	22258	22701	22702	22779	23450	25567	26380		26471
	Exon SEQ ID NO:	17751	17869	18149	18149	18289	18289	19540	19022	19022	19152	10203	10229	10542	10550	10725	10794	10877	11164	11456	11619	11695	11695	12048	12362	12362	12903	12903	12988	13667	15490	16219	16219	16306
	Probe SEQ ID NO:	7901	8019	8269	8269	8415	8415	9122	9342	9342	9554	234	264	909	614	796	898	953	1257	1551	1718	1797	1797	2161	2487	2487	2976	2976	3061	3754	5275	6356	6356	6445

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Table 4
Single Exon Probes Expressed In Heart

Top Hit Database Source Source T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGLYCAN II PRECURSOR (HUMAN);  1970 TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TEOGRAPH TE	unit (HERG-3) mRNA, complete cds unit (HERG-3) mRNA, complete cds (PCM1) mRNA	hi12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 38P-1.; Human hepatocyte nuclear factor 4-alpha gene, exon 2	ne, excn 2 40187), mRNA	t cariane d'IMA	NA clone IMAGE:3848980 5	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 6 Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete	cds Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
Top Hit Database Source Source ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST HUMAN TO THE ST	PROTEOGLYCAN II PRECURSOR (HUMAN); #191610x1 NCI_CGAP_Pr28 Homo sapiens CDI PROTEOGLYCAN II PRECURSOR (HUMAN); bb25b10x1 NIH_MGC_14 Homo sapiens cDNARIBOSOMAL PROTEIN L23 (HUMAN); gb.J05.	Homo sapiens potasslum channel subunit (HERG-3) mRNA, complete cds Homo sapiens potasslum channel subunit (HERG-3) mRNA, complete cds Homo sapiens pericentriolar material 1 (PCM1) mRNA	hi12a1.x1 NCL_CGAP_GU1 Homo sapiens cDNA clo P65194 SH3-BINDING PROTEIN 3BP-1.: Human hepatocyte nuclear factor 4-alpha gene, exon 2	Human hepatocyte nuclear factor 4-alpha gene, exon 2 Homo sapiens KIAA0187 gene product (KIAA0187), mRNA	Homo sapiens PSN1 gene, alternative transcript RC0-HT0372-241199-031-403 HTn372 Homo sanians	601444922F1 NIH MGC 65 Homo sapiens cDNA clone IMAGE:3848980 57	601444922F1 NIH_MGC_65 Homo sepiens cDNA clone IMAGE:3848980 5* Homo sepiens FYVE domain-containing dual specificity protein phosphatase	cds Homo sapiens FWE domain-containing dual speci cds
	EST_HUMAN EST_HUMAN EST_HUMAN	TN TN	EST_HUMAN	N	NT EST HUMAN	EST_HUMAN	EST_HUMAN	z Ł
	1.0E-108 AI686040.1 1.0E-108 AI686040.1 1.0E-108 BE206994.1	1.0E-108 AF032897.1 NT 1.0E-108 AF032897.1 NT 1.0E-108 5453855 NT	1.0E-108 AW664438.1 1.0E-108 U72961.1	072961.1 7661979 NT	1.0E-108 AJ008005.1 1.0E-108 AW384094.1	1.0E-108 BE869016.1	6.1	7.1
(Top) Hit Top Hit / BLAST E Nalue Value 1.0E-107 Al392855 1.0E-107 BF6655 1.0E-107 BF6655 1.0E-107 AR00141 1.0E-107 AR00141 1.0E-107 AR00141 1.0E-108 BF29604 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR0005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR005 1.0E-108 AR	1.0E-108	1.0E-108 1.0E-108	1.0E-108 AW6644.	1.0E-108 U/2961.	1.0E-108	1.0E-108	1.0E-108 BE86901	1.0E-108 AF26471
Signal Signal 1.82 2.73 1.82 4.27 4.27 4.27 4.27 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.5	7.41	0.94	1.33	2.85	2.19	277	2.77	5.06
O.S.		23028 23029 23437			24528			25746
Exen SEQ ID NO: 17978 18193 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17881 17	12166	13226 13226 13654	13967	14320 14585	14748	15312	15312	15640
Probe SEQ ID NO: 8327 8637 8638 8637 8637 9187 9187	2282 2282 2378	3305	4425	4699	4868	5393	5393	5732

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Table 4
Single Exon Probes Expressed in

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and	Homo emiser C evoluin comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments of the comments	Homo canions deline 6 fem. 11 1	Homo saplens connective them and desaurase (FAUSD6) mRNA	Home capiese mBMA 6. Color growth actor-like protein precursor, mRNA, complete cds	EST378958 MACE recently 11	Homo sapiens G protein-control areaster 48 (Obbas) - Paris	ttoffetoxt NCI_CGAP_PY28 Home septem SDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOCI YCAN II ppeculingoso (unimana)	tt91e10.x1 NCI_CGAP_1028 Home saplens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE	HOLD CALLES CAN II PRECURSOR (HUMAN);	Truin superior intriva for FLU0037 protein, partial cds	Uringer TP1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154297 5	i cinical illustra for NLAVOZZU gene, partial cds	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA	Home services fellocation 1, Er-hand calcium binding domain (RCN1), mRNA	Form Saprens (externopeptide repeat domain 2 (TTC2) mRNA	Home earliene TDN A C. 1778 Acces	Homo sopiens minital for Kiladuses protein, partial cds	Homo sapiens nucleolar prosphoprotein BZ3 (NPM1) mRNA, complete cds	Homo ceniene mDNN 6 V/A Accord	Homo saplens chamesons 34	Homo saniens SNES/INIA nano aven 6	อพยิธ์ช01.x1 Soares_fetal liver_splen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' sImilar to	ow85801x1 Source feel liver spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:1654536.3' similar to	Homo senions currented carlo CATHODIC ANTIGEN.;	J2816F Human fetal heart, Lambda ZAP Express Homo saplens cDNA done J2816 Fi cimilar to ZNIC	FINGER PROTEIN ZNF43	CMS-INNOCUS-190400-150-110 NN0009 Home sapiens cDNA	CMS-INNOUGE-190400-150-110 NN0009 Homo sapiens cDNA
gle Exon Pro	Top Hit Database Source	F	NT	NT	IN I	Į.	EST HUMAN	1	EST HUMAN	EST HIMAN	TN TN	EST DIRAM	FIN TOWNS			FX	NT	FX	-N	LN L	LN	LN	Z	EST HIMAN	POT LITHAN	L.		EST HUMAN	Т	٦
ais	Top Hit Acession No.	AJ133269.1			IB	Y12490.1		1.0E-108 11441465 NT	Al686040.1	40 1		T	T	ADDACCA	11438391 NT	4507742 NT	1.0E-109 AB023246 1	T				2				04206		- 60	37	36.1
	Most Similar (Top) Hit BLAST E Value	1.0E-108 AJ133	1.0E-108	1.0E-108	1.0E-108 AF083	1.0E-108 Y1249	1.0E-108	1.0E-108	1.0E-108 AI6860	1.0E-108	1.0E-108	1 0F-108	1.0E-109 D86974 1	1 0F-100	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109 M28699 1	1.0E-109 M28699,1	1.0E-109 D13643.2	1.0E-109	1.0E-109 Y17123.	1.0E-109 AI022328,1	1.0E-109 AI022328 1	1.0E-109	4 OF 400 NOE400	1.0E-109 N63190.	1.0E-109 AWR931	
	Expression Signal	1.37	5.35	3.34	1.93	2.77	4.26	2.03	4.14	4.14	2.79	5.59	6.0	0.92	1.51	3.64	14.64	14.64	9.63	4.89	1.48	2.03	1.97	3.88	3.88	2.75	88	1.45	1.45	
	ORF SEQ ID NO:	25804		26421			28731		22063	22064	25303		19856	19997	20003	20219	20328	20329	20941	20941	21602	21985	21993	22344	22345	22346	22740	23068	23069	
	Exan SEQ ID NO:	15695	16113	16260		15099		18565	12166	12166	19030	19270	10044	10183	10192	10403	10521	10521	11095	11095	11728	12081	12091	12452	12452	12453	12948	13262	13262	
	Probe SEQ ID NO:	5789	6247	6388	6698	8202	8593	8677	8706	8706	9357	9736	58	212	222	459	583	583	1184	1185	1831	2194	2204	2581	2581	2682	3020	3342	3342	
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Table 4
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| Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>(Top) Hit<br>Palue         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13821         23601         1.53         1.0E-109         BE146144.1         EST HUMAN           13821         23602         1.54         1.0E-109         AB011181.2         NT           13956         23732         3.67         1.0E-109         AI655417.1         EST HUMAN | Exon<br>NO:         ORF SEQ<br>Signel         Expression<br>Signel         (Top) Hit<br>BLASTE<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           13390         23195         1.2         1.0E-109 AF240698.1         NT           13821         23601         1.53         1.0E-109 BE14614.1         EST_HUMAN           13922         23732         3.67         1.0E-109 AB011181.2         NT           13972         23749         1.02         1.0E-109 AB65274.1         EST_HUMAN | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal<br>Signal         (Top) Hit<br>Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit<br>Database<br>Source           13390         23195         1.2         1.0E-109 AF240698.1         NT           13620         23601         1.53         1.0E-109 BE146144.1         EST HUMAN           13821         23602         1.54         1.0E-109 AB011181.2         NT           13956         23732         3.67         1.0E-109 AB011181.2         NT           13972         23749         1.02-109 AA662274.1         EST_HUMAN           13972         23750         1.0E-109 AA662274.1         EST_HUMAN | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>(Top) Hit<br>13390         Top Hit Acession<br>23195         Top Hit<br>1.2         Top Hit<br>No.         Top Hit<br>Source<br>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13926         23732         3.67         1.0E-109         AB055417.1         EST HUMAN           13972         23750         1.02         1.0E-109         AA662274.1         EST HUMAN           14202         23986         2.26         1.0E-109         AA662274.1         EST HUMAN | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>Top) Hit<br>Top) Hit<br>Signal         Top Hit Acession<br>Top) Hit<br>Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit<br>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13821         23602         1.54         1.0E-109         AB041181.2         NT           13926         23732         3.67         1.0E-109         AB05417.1         EST HUMAN           13972         23750         1.02         1.0E-109         AA662274.1         EST HUMAN           14202         23986         2.26         1.0E-109         AA662208.1         THUMAN           14390         24175         1.19         1.0E-109         AA662208.1         EST HUMAN | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most
Similar<br>(Top) Hit<br>13390         Top Hit<br>23195         Top Hit<br>12 (Top) Hit<br>14202         Top Hit<br>23602         Top Hit<br>1.64         Top Hit<br>1.05-109         Top Hit<br>100-109         "><td>Exon<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Top Hit<br/>(Top) Hit<br/>13390         Top Hit<br/>23195         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200         Top Hit<br/>1200  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Top Hit<br/>IT Top Hit Acession<br/>Value         Top Hit<br/>Database         Top Hit<br/>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13680         1.53         1.0E-109         BE146144.1         EST_HUMAN           13821         23601         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13822         23732         3.67         1.0E-109         AB05417.1         EST_HUMAN           14302         23759         1.02         1.0E-109         A662274.1         EST_HUMAN           14720         2396         2.25         1.0E-109         A662274.1         EST_HUMAN           14720         24503         1.0B-109         A6622083         NT           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626</td><td>Exon<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Top Hit<br/>IT Top Hit Acession<br/>Value         Top Hit<br/>Database         Top Hit<br/>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13680         1.53         1.0E-109         BE146144.1         EST_HUMAN           13821         23601         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13822         23732         3.67         1.0E-109         AB05417.1         EST_HUMAN           13972         23750         1.02         1.0E-109         AA662274.1         EST_HUMAN           14390         24175         1.02         1.0E-109         AA662274.1         EST_HUMAN           14720         2396         2.25         1.0E-109         A6622083         NT           14720         24503         1.06-109         AB0462208         NT           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626<td>Exon NO:         CRF SEQ ID ID NO:         Expression Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID Accorded Source Notice Source ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID 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1.02         1.0E-109 AF65274.1         EST_HUMAN           14202         23986         2.25         1.0E-109 AF65274.1         EST_HUMAN           14390         24175         1.04         1.0E-109 AF65274.1         EST_HUMAN           14720         225         1.0E-109 AF65274.1         EST_HUMAN           14720         24503         1.0B-109 BE283673.1         EST_HUMAN           14859         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           1536         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           16326         26491         3.66         <td< td=""><td>Exon NO:         CRF SEQ Signal Signal         Most Similar Seq II         Top Hit Acession Top) Hit Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         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ID ID NO:-         Expression Signal Signal ID NO:-         Most Similar Top Hit Acesson No:-         Top Hit Acesson Signal Database         Most Signal No:-         Most Signal Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Database         Top Hit Database         Top Hit Database        
&lt;</td><td>Exon<br/>NO:<br/>1380<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>1</td><td>Exon<br/>NO:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0</td><td>Exon<br/>NO:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<b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| Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>(Top) Hit<br>13390         Top Hit<br>23195         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200         Top Hit<br>1200      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    23601         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13822         23732         3.67         1.0E-109         AB05417.1         EST_HUMAN           14302         23759         1.02         1.0E-109         A662274.1         EST_HUMAN           14720         2396         2.25         1.0E-109         A662274.1         EST_HUMAN           14720         24503         1.0B-109         A6622083         NT           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626</td><td>Exon<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Top Hit<br/>IT Top Hit Acession<br/>Value         Top Hit<br/>Database         Top Hit<br/>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13680         1.53         1.0E-109         BE146144.1         EST_HUMAN           13821         23601         1.54         1.0E-109         AB011181.2     
   NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13822         23732         3.67         1.0E-109         AB05417.1         EST_HUMAN           13972         23750         1.02         1.0E-109         AA662274.1         EST_HUMAN           14390         24175         1.02         1.0E-109         AA662274.1         EST_HUMAN           14720         2396         2.25         1.0E-109         A6622083         NT           14720         24503         1.06-109         AB0462208         NT           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626<td>Exon NO:         CRF SEQ ID ID NO:         Expression Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID NO:         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NT           13821         23602         1.54         1.0E-109 AF240698.1         NT           13972         23750         1.54         1.0E-109 AF65417.1         EST_HUMAN           13972         23750         1.02         1.0E-109 AF65274.1         EST_HUMAN           14202         23986         2.25         1.0E-109 AF65274.1         EST_HUMAN           14390         24175         1.04         1.0E-109 AF65274.1         EST_HUMAN           14720         225         1.0E-109 AF65274.1         EST_HUMAN           14720         24503         1.0B-109 BE283673.1         EST_HUMAN           14859         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           1536         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           16326         26491         3.66         <td< td=""><td>Exon NO:         CRF SEQ Signal Signal         Most Similar Seq II         Top Hit Acession Top) Hit Top Hit Acession Source Nature         Top Hit Acession Source Nature  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      24175         1.0E-109 AE02274.1         EST_HUMAN           14859         24626         0.86 1.0E-109 BE28373.1         EST_HUMAN           15176         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE1828373.1         EST_HUMAN           16326         2260         1.0E-109 BE1828363.1         EST_HUMAN           16326         226492         5.01 1.0E-109 BE182836.1         EST_HUMAN           16832</td><td>Exon NO:-         ORF SEQ. ID ID NO:-         Expression Signal Signal ID NO:-         Most Similar Top Hit Acesson No:-         Top Hit Acesson Signal Database         Most Signal No:-         Most Signal Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit 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| Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>IT Top Hit Acession<br>Value         Top Hit<br>Database         Top Hit<br>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13680         1.53         1.0E-109         BE146144.1         EST_HUMAN           13821         23601         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13822         23732         3.67         1.0E-109         AB05417.1         EST_HUMAN           14302         23759         1.02         1.0E-109         A662274.1         EST_HUMAN           14720         2396         2.25         1.0E-109         A662274.1         EST_HUMAN           14720         24503         1.0B-109         A6622083         NT           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626         0.86         1.0E-109        
BE293673.1         EST_HUMAN           14859         24626 | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>IT Top Hit Acession<br>Value         Top Hit<br>Database         Top Hit<br>Source           13390         23195         1.2         1.0E-109         AF240698.1         NT           13680         1.53         1.0E-109         BE146144.1         EST_HUMAN           13821         23601         1.54         1.0E-109         AB011181.2         NT           13821         23602         1.54         1.0E-109         AB011181.2         NT           13822         23732         3.67         1.0E-109         AB05417.1         EST_HUMAN           13972         23750         1.02         1.0E-109         AA662274.1         EST_HUMAN           14390         24175         1.02         1.0E-109         AA662274.1         EST_HUMAN           14720         2396         2.25         1.0E-109         A6622083         NT           14720         24503         1.06-109         AB0462208         NT           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626         0.86         1.0E-109         BE293673.1         EST_HUMAN           14859         24626 <td>Exon NO:         CRF SEQ ID ID NO:         Expression Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID Accorded Source Notice Source ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded ID Accorded 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Top Hit Acession Pub.<!--</td--><td>Exon         ORF SEQ ID NO:         Expression Signal         Top Hit Accession Value         Top Hit Accession No:         Top Hit Accession Value         Top Hit Accession Source         Top Hit Accession Value         Top Hit Accession No:         Top Hit Accession Source         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit
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Acession Signal         Top Hit Acession Signal         Top Hit Acession Signa</td><td>Exon<br/>NO:         ORF SEQ<br/>Signel         Expression<br/>Signel         (Top) Hit<br/>PLASTE         Top Hit Acession<br/>No.         Top Hit Acession<br/>Source           13390         23195         1.2         1.0E-109 AF240698.1         NT           13821         23602         1.53         1.0E-109 AF240698.1         NT           13822         23602         1.54         1.0E-109 AF240698.1         NT           13821         23602         1.54         1.0E-109 AF240698.1         NT           13972         23750         1.54         1.0E-109 AF65417.1         EST_HUMAN           13972         23750         1.02         1.0E-109 AF65274.1         EST_HUMAN           14202         23986         2.25         1.0E-109 AF65274.1         EST_HUMAN           14390         24175         1.04         1.0E-109 AF65274.1         EST_HUMAN           14720         225         1.0E-109 AF65274.1         EST_HUMAN           14720         24503         1.0B-109 BE283673.1         EST_HUMAN           14859         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           1536         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           16326         26491         3.66         <td< td=""><td>Exon NO:         CRF SEQ Signal Signal         Most Similar Seq II         Top Hit Acession Top) Hit Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         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Expression<br/>Signal<br/>1.0E - 109 Hit<br/>2300         (Top) Hit<br/>2300         Top Hit Acession<br/>23195         Top Hit Acession<br/>1.0E - 109 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit 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        Top Hit Acession<br/>Nation   
     Top Hit Acession<br/>No:         Top Hit Acession<br/>Source           13390         23195         1.2         1.0E-109 AF240698.1         NT           13821         23601         1.54         1.0E-109 AE011181.2         NT           13822         23780         1.0E-109 AE0274.1         EST_HUMAN           13972         23780         1.02         1.0E-109 AE02274.1         EST_HUMAN           13972         23780         1.02         1.0E-109 AE02274.1         EST_HUMAN           14390         24175         1.0E-109 AE02274.1         EST_HUMAN           14859         24626         0.86 1.0E-109 BE28373.1         EST_HUMAN           15176         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE1828373.1         EST_HUMAN           16326         2260         1.0E-109 BE1828363.1         EST_HUMAN           16326         226492         5.01 1.0E-109 BE182836.1         EST_HUMAN           16832</td><td>Exon NO:-         ORF SEQ. ID ID NO:-         Expression Signal Signal ID NO:-         Most Similar Top Hit Acesson No:-         Top Hit Acesson Signal Database         Most Signal No:-         Most Signal Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit 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       14390         24175         1.04         1.0E-109 AF65274.1         EST_HUMAN           14720         225         1.0E-109 AF65274.1         EST_HUMAN           14720         24503         1.0B-109 BE283673.1         EST_HUMAN           14859         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           1536         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           16326         26491         3.66         <td< td=""><td>Exon NO:         CRF SEQ Signal Signal         Most Similar Seq II         Top Hit Acession Top) Hit Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source 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&lt;</td><td>Exon<br/>NO:<br/>1380<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>100<br/>1</td><td>Exon<br/>NO:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0:<br/>10.0</td><td>Exon<br/>NO:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<br/>10.00:<b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| Exon         ORF SEQ ID NO:         Expression Signal         Top Hit Accession Value         Top Hit Accession No:         Top Hit Accession Value         Top Hit Accession Source         Top Hit Accession Value         Top Hit Accession No:         Top Hit Accession Source         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:    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Acession No:-         Top Hit Acession Signal         Top Hit Acession No:-         Top Hit Acession Signal         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit Acession No:-         Top Hit 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    13390         23195         1.2         1.0E-109 AF240698.1         NT           13821         23602         1.53         1.0E-109 AF240698.1         NT           13822         23602         1.54         1.0E-109 AF240698.1         NT           13821         23602         1.54         1.0E-109 AF240698.1         NT           13972         23750         1.54         1.0E-109 AF65417.1         EST_HUMAN           13972         23750         1.02         1.0E-109 AF65274.1         EST_HUMAN           14202         23986         2.25         1.0E-109 AF65274.1         EST_HUMAN           14390         24175         1.04         1.0E-109 AF65274.1         EST_HUMAN           14720         225         1.0E-109 AF65274.1         EST_HUMAN           14720         24503         1.0B-109 BE283673.1         EST_HUMAN           14859         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           1536         24626         0.86         1.0E-109 BE283673.1         EST_HUMAN           16326         26491         3.66 <td< td=""><td>Exon NO:         CRF SEQ Signal Signal         Most Similar Seq II         Top Hit Acession Top) Hit Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession 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AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1         Top Hit Acession<br/>2000 AF240688.1 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       1.0E-109 AE0274.1         EST_HUMAN           13972         23780         1.02         1.0E-109 AE02274.1         EST_HUMAN           13972         23780         1.02         1.0E-109 AE02274.1         EST_HUMAN           14390         24175         1.0E-109 AE02274.1         EST_HUMAN           14859         24626         0.86 1.0E-109 BE28373.1         EST_HUMAN           15176         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE1828373.1         EST_HUMAN           16326         2260         1.0E-109 BE1828363.1         EST_HUMAN           16326         226492         5.01 1.0E-109 BE182836.1         EST_HUMAN           16832</td><td>Exon NO:-         ORF SEQ. ID ID NO:-         Expression Signal Signal ID NO:-         Most Similar Top Hit Acesson No:-         Top Hit Acesson Signal Database         Most Signal No:-         Most Signal
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| Exon NO:         CRF SEQ Signal Signal         Most Similar Seq II         Top Hit Acession Top) Hit Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Nature         Top Hit Acession Source Source Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top Hit Acession Nature         Top 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AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240688.1         Top Hit Acession<br>2000 AF240 | Exon<br>NO:         ORF SEQ<br>Signal<br>NO:         Most Similar<br>Signal<br>No:         Most Similar<br>Signal<br>No:         Most Similar<br>Signal<br>No:         Top Hit Acession<br>Nation         Top Hit Acession<br>Nation         Top Hit Acession<br>No:         Top Hit Acession<br>Source           13390         23195         1.2         1.0E-109 AF240698.1         NT           13821         23601         1.54         1.0E-109 AE011181.2         NT           13822         23780         1.0E-109 AE0274.1         EST_HUMAN           13972         23780         1.02         1.0E-109 AE02274.1         EST_HUMAN           13972         23780         1.02         1.0E-109 AE02274.1         EST_HUMAN           14390         24175         1.0E-109 AE02274.1         EST_HUMAN           14859         24626         0.86 1.0E-109 BE28373.1         EST_HUMAN           15176         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE283673.1         EST_HUMAN           16326         24827         0.86 1.0E-109 BE1828373.1         EST_HUMAN           16326         2260         1.0E-109 BE1828363.1         EST_HUMAN           16326         226492         5.01 1.0E-109 BE182836.1         EST_HUMAN           16832 | Exon NO:-         ORF SEQ. ID ID NO:-         Expression Signal Signal ID NO:-         Most Similar Top Hit Acesson No:-         Top Hit Acesson Signal Database         Most Signal No:-         Most Signal Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit Acesson Database         Top Hit 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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA	2008b12.r1 Soares fetal Jung_NbHL19W Homo saplens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat	Homo sapiens SNF5/INI1 gene, exon 6	Homo sapiens gene for AF-6, complete cds	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA	Homo saplens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA	C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC3467	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA	Human mRNA for Inward rectifier potassium channel, complete cds	Human dystrobrevin (DTN) gene, exon 20	Homo sapiens calcitonin receptor-like (CALCRL) mRNA	Homo saplens BAZ1B mRNA for bromodomain adjacent to zinc fincer domain 18 commists ode	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5	UI-H-BI4-ecs-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:30857843'	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein	(L44L) and F1P3 (F1P3) genes, complete cds	Homo sapiens pregnancy-zone protein (PZP), mRNA	Homo sapiens pregnancy-zone protein (PZP), mRNA	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR: 060312 O60312 KIAA0566 PROTEIN;	ou32b10x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE DEOTEIN DONA 121	AU117812 HEMBA1 Homo segiens cDNA clone HEMBA100224 5'	Homo saplens KIAA1002 protein (KIAA1002), mRNA	601118710F1 NIH MGC 17 Homo saplens cDNA done IMAGE:3028538 5	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA	Homo saplens hypothetical protein FLJ10300 (FLJ10300), mRNA	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'	Homo sapiens mRNA for KIAA0868 protein, partial cds
and a light	Top Hit Database Source	IN	EST HUMAN	LN	N	Į.	님	Į.	EST_HUMAN	N F	NT	Ę	۲	NT	EST_HUMAN	EST_HUMAN	TN	!	ĮN.	Z	NT	EST_HUMAN	EST HUMAN	EST HUMAN	M	EST HUMAN	Z E	N	Z	EST_HUMAN	T_HUMAN	Ę
5	Top Hit Acession No.	4502838 NT	W16510.1	Y17123.1	1.0E-109 AB011399.1	7549804 NT	5803073 NT	5803073 NT	C04498.1	7549804 NT	D87291.1	U84550.1	5031620 NT	AB032253.1	1.0E-110 BE379477.1	1.0E-110 BF508896.1	4503098 NT	, 1.0001	U78027.1	11436041 NI	11436041 NT	1.0E-110 BE018556.1	A1017213.1		7662441 NT	1.0E-110 BE299406.1	11419323 NT	11419323 NT	1.0E-110 M55112.1	1.0E-110 AV714276.1	1.0E-110 AV714276.1	1.0E-110 AB020675.1
	Most Similar (Top) Hit BLAST E Value	1.0E-109	1.0E-109 W1651	1.0E-109 Y17123.1	1.0E-109	1.0E-110	1.0E-110	1.0E-110	1.0E-110 C04498	1.0E-110	1.0E-110 D8729	1.0E-110 U84550.1	1.0E-110	1.0E-110 AB032	1.0E-110	1.0E-110	1.0E-110	777	1.0E-110 U78027	1.05-110	1.0E-110	1.0E-110	1.0E-110 AI0172	1.0E-110 AU1178	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110
	Expression Signal	2,19	4.83	1.65	2.8	1.48	3.88	3.88	30.63	1.67	0.91	1.16	1.09	1.01	1.5	1.86	1.02	7	1.07	/8'.	1.87	0.92	2.06	2.08	2.34	1.9	7.34	7.34	4.36	10.04	10.04	2.7
	ORF SEQ ID NO:	28848	28810	21993		19781	19817			19781			20921		21650					09077	22886	23650	24207	24232		24929	25492	25493	26068	26413	26414	26432
	Exan SEQ ID NO:	18564	18527	12091	19176	9990	10021	10021	10059	9990	10255	10458	11076	11165	ı	11904	12739	12075	19062	3000	13083	13873	14426	14447	14778	15161	15429	15429	19458	16253	16253	16270
	Probe SEQ ID NO:	8676	8710	9259	9294	3	34	34	75	104	291	516	1163	1258	1879	2012	2810	9070	3040	0010	3158	3966	4533	4555	4898	5237	5511	5511	6032	6391	6391	6409

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Public   Ewn   Orf 9 GE   Extraction   Total Hand   Top Ha   Next Shing   Source   Source   Top Hand   Source   Source   Top Hand   Top Hand   Source   Source   Top Hand   Source   Top Hand   Source   Top Hand   Top Hand   Top Hand   Source   Top Hand   Source   Top Hand   Top Hand   Top Hand   Source   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   Top Hand   T				_		_	-			-	-	_		_								· · · · · · · · · · · · · · · · · · ·		بنيوس	ш					214111		******
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RELATED PROTEIN RAL-A (HUMAN);	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA	zn62c12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562774 5' similar to gb:X03740 MYOSIN HEAVY CHAIN SKEI FTAI MITSCE F JUINAANI.	Human betat-integrin (ITGR4) nene avon 13	601847132F1 NIH MGC 55 Homo seniens CONIA clare MAA CE: 40782222 E1	Human mRNA for Integrin alpha-2 sthumit	Human mRNA for Integrin alpha-2 subunit	Homo sapiens Trio isoform mRNA, complete cds
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		ORF SEQ ID NO:				28462	28463							19978		20489	20684	23342	23343	23760	23909	25117	25118	10010	22082	26423	26622	26866		27221	27222	27321
Probe SEQ ID NO: NO: 18130 81334 8134 8134 8134 8134 8134 8134 813		Exan SEQ ID NO:	L						18857	18935	19080	19684	10140	10161	10650	10658	10835	13556	13556	13982	14133	15284	15284	76297	500	10203	16437	16674	16990	17026	17026	17128
		Probe SEQ ID NO:	7523	7915	8130	8334	8334	8740	9081	9204	9444	9578	168	8	718	726	91	3642	3642	4080	4235	5364	5364	223	200	20402	6229	6795	7113	7149	7149	7251

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Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor                            | ae58902.s1 NCL_CGAP_CCB1 Homo sepiens cDNA done IMAGE:825170 3' similar to gb:L09235<br>VACUOLAR ATP SYNTHASE CATALYTIC SUBLINIT A LIBIOLITICI IS (JULIMAN): | 231f01.r1 Scares pregnant uterus NbHPU Horno saniens cDNA clone IMA CF-570845 F | Human thrombopoletin receptor (MPL) gene, exons 1.2.3.4.5 and 6                                                                                                                                                                                                                                                                                                                 | Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1) mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional                                                                                                                                                                                                                                                                                                                                                                                             | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Homo saplens low density [poprotein-related protein 2 (LRP2), mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Homo saplens acetyl-Coenzyme A carboxylase beta (ACACB) mRNA                                  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                                                                                                                                                                                                                                                                                                                      | UI-H-BI4-act-g-04-0-UI.s1 NCI CGAP Sub8 Homo sepiens cDNA clone IMAGE-3086023 31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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L-proline). member 7 (SI CRA7). mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       
                                                                                              | Homo sapiens solute carrier family 6 (neurotranemitter transactor)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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|                                               | Exon ORF SEQ Expression (Top) Hit Acession Signal BLASTE No. Source Source                                                                                   | Exon SEQ ID NO: Signal Value Signal 1.51 1.0E-111 AA504160.1 EST HUMAN          | Exon         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>ID NO:         Top Hit Acession<br>BLAST E<br>Value         Top Hit<br>No:         Top Hit<br>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111 AA131248.1         EST_HUMAN | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>Value         Most Similar<br>I Top Hit Acession<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN<br>EST_HUMAN           17743         27986         6.35         1.0E-111   AA3131248.1         EST_HUMAN<br>EST_HUMAN           18277         28529         4.52         1.0E-111   U68159.1         NT | Exon<br>SEQ ID<br>NO:         CRF SEQ<br>Signal<br>Signal         Expression<br>(Top) Hit<br>BLAST E         Top Hit Acession<br>No.         Top Hit<br>Source<br>Value           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN<br>EST_HUMAN           18277         28529         4.52         1.0E-111   Mat31248.1         EST_HUMAN<br>EST_HUMAN           18825         29110         3.04         1.0E-111   Me8159.1         NT | Exon<br>SEQ ID<br>NO:         CRF SEQ<br>Signal<br>Signal         Expression<br>(Top) Hit<br>PLAST E         Top Hit Acession<br>No.         Top Hit<br>Source           17690         277935         1.51         1.0E-111         AA504160.1         EST_HUMAN           18277         28529         4.52         1.0E-111         AA504160.1         EST_HUMAN           18825         29110         3.04         1.0E-111         U08159.1         NT           19489         25130         1.69         1.0E-111         W22662.1         EST_HUMAN | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>(Top) Hit<br>No.         Top Hit Acession<br>No.         Top Hit<br>Source           17690         27836         1.51         1.0E-11         AA504160.1         EST_HUMAN           17743         27836         6.35         1.0E-11         AA504160.1         EST_HUMAN           18277         28529         4.52         1.0E-11         AA60450.1         NT           19489         25130         3.04         1.0E-11         W22662.1         EST_HUMAN           19482         25130         1.69         1.0E-111         M22662.1         EST_HUMAN           19422         25171         1.39         1.0E-111         M22662.1         EST_HUMAN | Exon Signal NO:         Most Similar Signal         Most Similar Top Hit Acession Signal      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     U68159.1         NT           19489         25130         1.69         1.0E-111         11417901         NT           19422         25171         1.39         1.0E-111         11430450         NT           19528         25372         1.39         1.0E-111         11430450         NT           10528         20335         2.66         1.0E-112         4501854         NT | Exon Signal         Most Similar (Top) Hit Acession NO:         Expression Signal         Top Hit Acession Value         Top Hit Acession Signal         Top Hit Acession No:         Top Hit Acession No:           17690         27836         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27886         6.35         1.0E-111         AA504160.1         EST_HUMAN           18277         28529         4.52         1.0E-111         AA504160.1         EST_HUMAN           19489         25130         1.69         1.0E-111         AA50450.1         NT           19489         25130         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Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Acid Signal         Top Hit Acid Source Source Source Source Source Source Source Source Source Source Source Acid Signal         Top Hit Acid Source Source Source Source Source Source Source Source Source Source Acid Source Source Acid Source Acid Source Acid Source Acid Source Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source Acid Source 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 1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111         AA504160.1         EST_HUMAN           18277         28529         4.52         1.0E-111         AA504160.1         EST_HUMAN           19489         25130         1.69         1.0E-111         M2562.1         EST_HUMAN           19489         25171         1.39         1.0E-111         M2562.1         EST_HUMAN           19489         25171         1.39         1.0E-111         M2562.1         EST_HUMAN           19480         25171         1.39         1.0E-111         M2562.1         EST_HUMAN           19422         25171         1.39         1.0E-112         M2503.1         NT           10530         20335         2.66         1.0E-112         M2503.1         NT           10552         20346         1.48         1.0E-112         M2503.1         NT           10563         2034         1.48         1.0E-112         EST_HUMAN</td> <td>Exon NO:- Signal         Most Similar (Top) Hit Acession NO:- Signal         Expression Signal         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native   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Nation         Top Hit Acession No.         Top Hit Acession Source Source Nation         Top Hit Acession Source Source Nation         Top Hit Acession Source Source Nation         Top Hit Acession Source Source Nation         Top Hit Acession Source Source Source Source Nation         Top Hit Acession Source Source Nation         Top Hit Acession Source Source Source Source Source Source Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top H</td> <td>Exon Signal         Most Similar (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Nation         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Nation         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession 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Accession<br/>P</td> <td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Figure         Most Similar<br/>Value         Top Hit Accession<br/>No:         Top Hit Accession<br/>Value         Top Hit Accession<br/>No:         Top Hit Accession<br/>Value         Top Hit Accession<br/>Value         Top Hit Accession<br/>No:         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit Accession<br/>Source         Top Hit 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Acession No:         Top Hit Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Top Hit Acession No</td> <td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>FIG         Top Hit<br/>Accession         Top Hit<br/>Database<br/>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111         AA431248.1         EST_HUMAN           18827         28529         4.52         1.0E-111         AA431248.1         EST_HUMAN           19429         25130         1.69         1.0E-111         MT           19420         25171         1.39         1.0E-111         MT           10528         20335         2.66         1.0E-112         L1430460         NT           10529         20337         4.49         1.0E-112         L29103.1         NT           10520         20338         4.49         1.0E-112         L29103.1         NT           10552         20364         1.48         1.0E-112         L29103.1         NT           10566         20365         1.72         1.0E-112         BEST HUMAN           10560         2142         1.0E-112         BES0039.1         EST HUMAN           10561         2724         1.0E-112         BES0039.1         EST HUMAN</td> <td>Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No:</td> <td>Exon<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>ID NO:         Top Hit Accession<br/>Signal         Most Similar<br/>ID NO:         Top Hit Accession<br/>Aclude         Top Hit Accession<br/>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111         AA131248.1         EST_HUMAN           18277         28529         4.52         1.0E-111         MA131248.1         EST_HUMAN           19422         25130         1.69         1.0E-111         MA130460         NT           19422         25171         1.39         1.0E-112         MT           10529         25172         1.39         1.0E-112         MT           10530         20337         4.49         1.0E-112         MT           10530         20338         4.49         1.0E-112         BE50939.1         EST_HUMAN           10530         20338         4.49         1.0E-112         BF50939.1         INT           10530         20338         4.49         1.0E-112         BF50939.1         EST_HUMAN           10530         20364         1.74         1.0E-112         BF50939.1         EST_HUMAN</td> <td>Exon<br/>NO:-<br/>17690         ORF SEQ<br/>ID NO:-<br/>Signal         Most Similar<br/>FLASTE         Top Hit Acession<br/>No:-<br/>Signal         Most Simal<br/>ILS         Top Hit Acession<br/>Velue         Top Hit Acession<br/>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111         AA504160.1         EST_HUMAN           18826         29110         3.04         1.0E-111         M2562.1         INT           19422         25170         1.38         1.0E-111         M2562.1         INT           10528         25171         1.39         1.0E-112         M250400         INT           10529         25172         1.39        
1.0E-112         M250400         INT           10529         20335         2.66         1.0E-112         M270400         INT           10520         20335         4.49         1.0E-112         M29040         INT           10520         20335         4.49         1.0E-112         M29033.1         INT           10562         20363         1.44         1.0E-112         M29039.1         EST_HUMAN           10564         20363         1.48         1.0E-112         M29039.1</td> <td>Expn<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal         Expression<br/>Figure         (Top) Hit<br/>Figure         Top Hit Acession<br/>Figure         Top Hit<br/>Figure         >Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Value         (Top) Hit<br/>No.         Top Hit Acession<br/>Signal         (Top) Hit<br/>Value         Top Hit Acession<br/>Source         Top Hit<br/>Action           17690         27835         1.51         1.0E-111         AA504160.1         EST_HUMAN           18774         27986         6.35         1.0E-111         AA5042460.1         EST_HUMAN           18825         29110         3.04         1.0E-111         AA5042480.1         EST_HUMAN           18826         29110         3.04         1.0E-111         AA50460.1         EST_HUMAN           19422         25172         1.39         1.0E-111         A430460         NT           10530         20337         4.49         1.0E-112         LU29103.1         NT           10530         20338         1.48         1.0E-112         LU29103.1         NT           10530         20338         1.49         1.0E-112         LU29103.1         NT           10530         20337         4.49         1.0E-112         LU29103.1         NT           10530         20338         1.48         1.0E-112         LU29103.1         NT           10540         2080         1.72         1.0E-112</td> <td>Exon<br/>NO:         ORF SEQ ID<br/>Signal         Expression<br/>(Top) Hit<br/>Signal         Most Similar<br/>(Top) Hit<br/>Passes         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>Source         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Detail<br/>No.         Top Hit Accession<br/>(Top) Hit<br/>No.         Detail<br/>No.         -></td> | Exon Signal         Most Similar (Top) Hit Acession Signal         Most Similar (Top) Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Acid Signal 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AA504160.1         EST_HUMAN           19489         25130         1.69         1.0E-111         M2562.1         EST_HUMAN           19489         25171         1.39         1.0E-111         M2562.1         EST_HUMAN           19489         25171         1.39         1.0E-111         M2562.1         EST_HUMAN           19480         25171         1.39         1.0E-111         M2562.1         EST_HUMAN           19422         25171         1.39         1.0E-112         M2503.1         NT           10530         20335         2.66         1.0E-112         M2503.1         NT           10552         20346         1.48         1.0E-112         M2503.1         NT           10563         2034         1.48         1.0E-112         EST_HUMAN | Exon NO:- Signal         Most Similar (Top) Hit Acession NO:- Signal         Expression Signal         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Source Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         Top Hit Acession No:- Native         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Hit Acession Source Source Source Source Nation         Top Hit Acession Source Source Nation         Top Hit Acession Source Source Source Source Source Source Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top Hit Acession Nation         Top H | Exon Signal         Most Similar (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Signal         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Nation         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Nation         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.      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Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acessio | Exon<br>NO:-<br>ID NO:-<br>ID NO:-<br>SEQ ID<br>NO:-<br>ID NO:-<br>Signal         Most Similar<br>FLASTE<br>Public         Top Hit Accession<br>Public         Top Hit Accession<br>P | Exon<br>NO:         ORF SEQ<br>Signal         Expression<br>Figure         Most Similar<br>Value         Top Hit Accession<br>No:         Top Hit Accession<br>Value         Top Hit Accession<br>No:         Top Hit Accession<br>Value         Top Hit 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10529         20337         4.49         1.0E-112         L29103.1         NT           10520         20338         4.49         1.0E-112         L29103.1         NT           10552         20364         1.48         1.0E-112         L29103.1         NT           10566         20365         1.72         1.0E-112         BEST HUMAN           10560         2142         1.0E-112         BES0039.1         EST HUMAN           10561         2724         1.0E-112         BES0039.1         EST HUMAN | Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No: | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>ID NO:         Top Hit Accession<br>Signal         Most Similar<br>ID NO:         Top Hit Accession<br>Aclude         Top Hit Accession<br>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111         AA131248.1         EST_HUMAN           18277         28529         4.52         1.0E-111         MA131248.1         EST_HUMAN           19422         25130         1.69         1.0E-111         MA130460         NT           19422         25171         1.39         1.0E-112         MT           10529         25172         1.39         1.0E-112         MT           10530         20337         4.49         1.0E-112         MT           10530         20338         4.49         1.0E-112         BE50939.1         EST_HUMAN           10530         20338         4.49         1.0E-112         BF50939.1         INT           10530         20338         4.49         1.0E-112         BF50939.1         EST_HUMAN           10530         20364         1.74         1.0E-112         BF50939.1         EST_HUMAN | Exon<br>NO:-<br>17690         ORF SEQ<br>ID NO:-<br>Signal         Most Similar<br>FLASTE         Top Hit Acession<br>No:-<br>Signal         Most Simal<br>ILS         Top Hit Acession<br>Velue         Top Hit Acession<br>Source           17690         27935         1.51         1.0E-111         AA504160.1         EST_HUMAN           17743         27986         6.35         1.0E-111         AA504160.1         EST_HUMAN           18826         29110         3.04         1.0E-111         M2562.1         INT           19422         25170         1.38         1.0E-111         M2562.1         INT           10528         25171         1.39         1.0E-112         M250400         INT           10529         25172         1.39         1.0E-112         M250400         INT           10529         20335         2.66         1.0E-112         M270400         INT           10520         20335         4.49         1.0E-112         M29040         INT           10520         20335         4.49         1.0E-112         M29033.1         INT           10562         20363         1.44         1.0E-112         M29039.1         EST_HUMAN           10564         20363         1.48         1.0E-112         M29039.1 | Expn<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal         Expression<br>Figure         (Top) Hit<br>Figure         Top Hit Acession<br>Figure         Top Hit<br>Figure         r>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>Value         (Top) Hit<br>No.         Top Hit Acession<br>Signal         (Top) Hit<br>Value         Top Hit Acession<br>Source         Top Hit<br>Action           17690         27835         1.51         1.0E-111         AA504160.1         EST_HUMAN           18774         27986         6.35         1.0E-111         AA5042460.1         EST_HUMAN           18825         29110         3.04         1.0E-111         AA5042480.1         EST_HUMAN           18826         29110         3.04         1.0E-111         AA50460.1         EST_HUMAN           19422         25172         1.39         1.0E-111         A430460         NT           10530         20337         4.49         1.0E-112         LU29103.1         NT           10530         20338         1.48         1.0E-112         LU29103.1         NT           10530         20338         1.49         1.0E-112         LU29103.1         NT           10530         20337         4.49         1.0E-112         LU29103.1         NT           10530         20338         1.48         1.0E-112         LU29103.1         NT           10540         2080         1.72         1.0E-112 | Exon<br>NO:         ORF SEQ ID<br>Signal         Expression<br>(Top) Hit<br>Signal         Most Similar<br>(Top) Hit<br>Passes         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>Source         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>No.         Top Hit Accession<br>(Top) Hit<br>No.   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Accession<br>(Top) Hit<br>No.         Detail<br>No.         Top Hit Accession<br>(Top) Hit<br>No.         Detail<br>No.         Page 340 of 413
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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	601155323F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3138989 5	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 PUSED TOES;	qi24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES:	PM0-CT0237-141099-001-h02 CT0237 Homo seniens cDNA	ao95f01.x1 Schiller menindicma Homo sepiens CDNA clone IMAGE 105355.3	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE-1053625.31	Human X-linked phosphoglycerate kinase gene, exon 8	ao95f01.x1 Schiller menindioma Homo sabiens cDNA clone IMAGE-1953625 31	UI-H-BW1-ani-f-03-0-UI:s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876.31	Homo sapiens PLP gene	Homo sapiens mRNA for putative RNA helicase. 3' end	Homo sapiens V-els avian erythroblastosis virus F26 oncovene related (FRC), mDNA	Homo sapiens v-ets avian erythroblastosis virus E26 oncodene related (ERC), mRNA	601469465F1 NIH MGC 67 Homo saplens cDNA clone IMAGE:3872536 5	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-TR) (GAI NTR) mRNA	601297709F1 NIH MGC 19 Homo sepiens CDNA clone IMAGE 36272564 F1	601297709F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE 3627854 81	Homo sapiens transmembrane protein 2 (TMEM2), mRNA	UI-HF-BN0-akj-b-12-0-UI.r1 NIH MGC 50 Homo sapiens cDNA clone IMAGE:3077338 F	Homo sapiens glutamate receptor, ionotropic, N-methy D-aspartate 24 (GRIN2A) mBNA	Homo sapiens glutamate receptor, ignotropic, N-methyl D. schartate 24 (CRINI2A) DNA	601105529F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988866 5'	yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to	Secretary And Programmer All reporting element;	From Sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA	Homo septens inflational furnior detection region protein 1 (K I DK1), mRNA	Homo sapiens mRNA for KIAA1276 brotein partial cds	
201	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	N	EST HUMAN	EST_HUMAN	٦	K	ZI.	N F	EST_HUMAN	EST_HUMAN	EST_HUMAN	ħ	EST HUMAN	Г		EST_HUMAN		Ę	EST_HUMAN	EST HIMAN	- 10m2				
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	Most Similar (Top) Hit BLAST E Value	1.0E-112 BE2804;	1.0E-112 AI79260	1.0E-112	1.0E-112	1.0E-113	1.0E-113	1.0E-113 M11965.	1.0E-113 AI365580	1.0E-113 BF51521	1.0E-113 AJ00697	1.0E-113 AJ22394	1.0E-113	1.0E-113	1.0E-113	1.0E-113 AU1272	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113		1.0E-113	1.0E-113	1.0E-113	1 0F-114		4 0F-114	1.0F-114	1.0E-114 AB03310	
	Expression Signal	1.72	1.75	1.75	5	3.71	3.71	6.32	2.94	1.18	96.0	2.34	0.95	0.95	16.27	6.33	3.92	2.05	2.95	2.95	1.29	1.73	2.07	2.07	3.44	7.86	134	3.47	5.63	0.82	
	ORF SEQ ID NO:	28578	28637	28638	28657	20487	20488	20700	21286	.21833	22179	22813	24677	24678		25144	25605	25710	27326	27327	27731	28604	25832	25833	28721	20379	20815	21053	21413	19823	!
	Exan SEQ ID NO:	18319	18373	18373	18393			10852			i	_	14907	14907	19524	15297	16523	15608	17134	17134	17506	18339	15719	15719	18452	10566	10972	11198	11552	10025	
	Probe SEQ (D NO:	8445	8500	8500	8521	725	725	927	1523	2048	2405	3091	5035	5035	5211	5377	2608	5699	7257	7257	7656	8466	8550	8550	8584	629	1055	1291	1648	2773	

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Top Hit Descriptor	Homo sapiens mRNA for KIAA 1276 protein partial cds	Human gene for catalase (EC 1 11 1 8) evon 2 manufacts characters 44 to 1	601869932F1 NIH MGC 19 Home septembly class (MACE: MACE: 12)	Homo sapiens NOD1 protein (NOD1) nene exams 1.2 and 3	zq05e05.rf Stratagene muscle 937209 Homo saplens cDNA clone IMAGE:628832 5' similar to contains MER22 is MFR22 renefitiue element.	Homo sapiens PKY protein kinase mRNA, complete cds	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain (semanhorin) to SEMMEN COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT COMMENT 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capanahoria of the capanahoria of the capanahoria of the capanahoria of the capanahoria of the capanahoria of the capanahoria of the capanahoria of the capanah	Homo saplens NF2 cene	Homo sapiens NF2 nene	Omo sanjens ramma amjaobi taris osid (CABA) A	gv68d06x1 NCI CGAP Bm25 Home series cDNA clears 144 CE 2022 CC	gy68d06.x1 NCI_CGAP_Bm25 Homo saniens cDNA clone living CE: 2017 163 3	Human neural cell achesion molecule CD56 mBNA complete cells	Homo sapiens mRNA for KIAA0561 horiein harfial cde	Homo sabiens mRNA for KIAADESI modelin paratal cus	de03f05.x1 NIH MGC 2 Homo saniens cDNA class (NA CE 2048244 F)	Homo sapiens tyrosine kinase pn60c-src (SRC) reme even 42 and and a significant	Homo sapiens chromosome 21 segment HS21Cn27	ba73g12.yl NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAI PROTEIN SA ILI IMANIN CHAMAGO AND COMPANY CHAMAGO AND COMPANY CHAMAGO AND COMPANY CHAMAGO AND COMPANY CHAMAGO AND COMPANY CHAMAGO AND COMPANY CHAMAGO AND COMPANY 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sapiens TNE-Inducible profession CC324 (TC4224)	Homo sapiens hypothetical protein (D.1104.2% 10.2) mBN/A	Homo saplens hypothetical protein (D.11042/K10.2), m. BNA	Homo sapiens HLA-B associated transcript-1 (DSS81F) mRNA	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
Top Hit Database Source	NT	N	EST HUMAN		EST HUMAN	LN	NT TN	L L	Z			T HUMAN	Г	Г		Z	T HUMAN	Т	Z		EST HUMAN	Г	Τ	Г	Γ					
Top Hit Acession No.	AB033102.1	X04086.1	BF206374.1	AF149773.1	1.0E-114 AA194468.1	AF004849.1	4506880 NT	4506880 NT	-	-	4557600INT	1.0E-114 Al363139.1	9.1	-	33.1				1.0E-114 AL 163227.2		1.0E-114 BE302666.1				1.0E-114 AV733454.1	11418041 NT	11034850 NT	11034850 NT	4758111 NT	4505938 NT
Most Similar (Top) Hit BLAST E Value	1.0E-114	1.0E-114 X04086.	1.0E-114 BF2063	1.0E-114 AF1497	1.0E-114	1.0E-114 AF0048	1.0E-114	1.0E-114	1.0E-114 Y18000	1.0E-114 Y18000.	1.0E-114	1.0E-114	1.0E-114 AI36313	1.0E-114 U63041	1.0E-114 /	1.0E-114 /	1.0E-114 /	1.0E-114 /	1.0E-114		1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-115	1.0E-115
Expression Signal	0.82	2.29	1.2	1.95	12	2.31	1.37	1.37	7.08	7.08	1.86	1.73	1.73	3.39	6.35	6.35	3.79	3.13	1.31		7.14	4.58	4.58	2.86	2.86	3.21	3.06	3.06	3.36	0.95
ORF SEQ ID NO:		22814	22859	23621	24762	24763	25040	25041	26338	26339	26673	26814	26815	27116	27161	27162		26652	27940			28666	28667	28932	28933		25222	25223	19801	19920
Exan SEQ ID NO:	10025	13019	13060	13843	14988	14989	15237	15237	16179	16179	16486	16627	16627	16925	16967	16967	17285	16459	17694	<u>,</u>	18055	18399	18399	18647	18647	19748	19266	19266	10008	1009
Probe SEQ ID NO:	2773	3092	3135	3934	5120	5121	5316	5316	8316	6316	9099	6748	6748	7048	2090	7090	7418	7447	1844		8167	8527	8527	8834	8834	8479	9729	9729	27	125

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Single Exon Probes Expressed in Heart	Most Similar (Top Hit Acession Database No. Source Source	9 1.0E-115 4557887 NT Homo saplens keratin 18 (KRT18) mRNA	1.0E-115 AW804759.1 EST_HUMAN	1.0E-115 A1339206.1 EST HUMAN	1.0E-115 A1339206.1 EST HUMAN	1.0E-115 5174702 NT	1.0E-115 5174702 NT	1.0E-115 4503794 NT	1.0E-115 AF229180.1 NT	1.0E-115 AF229180.1 NT	1.0E-115 AJ277892.1 NT	1.0E-115 U78027.1 NT	1.0E-115 BE745469.1 EST HUMAN	1.0E-115 BE745469.1 EST HUMAN	1.0E-115 AW804759.1 EST HUMAN	1.0E-115 AJ245922.1 NT	1.0E-115 AJ245922.1 NT	1.0E-115 AJ277892.1 NT	1.0E-115 AB002348.2 NT	1.0E-115 AL137163.1 NT	1.0E-115 6912659 NT	1.0E-115 4758279 NT	1.0E-115 AL096857.1 NT	1.0E-115 AL096857.1 NT	1.0E-115]AL163268.2 NT	1.0E-115 AL163268.2 NT	1.0E-115 AW970335.1 EST_HUMAN	1.0E-115 BF665387.1 EST_HUMAN	1.0E-115 11425128 NT	1.0E-116 11425128 NT	1.0E-115 11426038 NT	1.0E-115 7661883 NT
Single Exon	Acession Vo.	4557887 NT	759.1			74702	5174702 NT	4503794 NT	90.1	30.1	12.1	_	EST	39.1 EST	EST	Z					6912659 NT	4758279 NT						EST	11425128 NT	11425128 NT	11426038 NT	7661883 NT
		15	15 AW804	15 Al3392	15 Al3392	15	35	15	15 AF2291	15 AF2291	15 AJ2778	15 U78027	15 BE7454	15 BE7454	15 AW804	15 AJ2459	5 AJ2459	5 AJ2778	5 AB0023	5 AL1371	5	5	5 AL0968	5 AL0968	5 AL 1632	5 AL 1632	5 AW970	5 BF6653	5	2	22	5
	Most Simil (Top) Hil BLAST E Value	1.0E-1	1.0E-1	1.0E-1	1.0E-1	1.0E-1	1.0E-11	1.0E-1	1.0E-1	1.0E-1	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-1	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.06-11	1.0E-11
	Expression Signal	1.99	2.17	1.08	1.08	1.83	1.83	49.82	0.92	0.92	3.14	1.42	0.87	0.87	1.78	. 2.1	2.1	4.03	4.04	1.09	3.41	3.83	2.58	2.58	2.96	2.96	1.75	7.22	2.05	2.05	12.92	1.93
	ORF SEQ ID NO:		20073	20278	20279	20537	20538	20540	21301	21302	21561	21573	21817	21818	-	22795	22796	23149	23640	23844	23983	24014	24254	24255	24482	24483	24977	25055	25369	25370	25876	25960
	Exan SEQ ID NO:	10103	10253	10467	10467	10699	10699	10701	11443	11443	11683	11696	11925	11925	12749	13004	13004	13344	13864	14069	14199	14232	14468	1468 8	14696	14696	15201	15250	15321	15321	20/20	15838
	Probe SEQ ID NO:	129	289	929	625	769	769	177	1539	1539	1785	1798	2034	2034	2820	3077	3077	3427	3956	4169	4301	£33	4578	4578	4813	4813	5279	2330	5402	5402	7000	5933

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Page 344 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	milar Top Hit Acession Database T E No. Source Source	1.0E-116 AB046856.1 NT Homo saplens mRNA for KIAA1636 protein, partial cds	EST_HUMAN	1.0E-116 BE158133.1 EST_HUMAN MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA	EST_HUMAN	EST_HUMAN	1.0E-116 AA354256.1 EST_HUMAN EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2	EST_HUMAN	1.0E-116 BE565507.1   EST_HUMAN   601338268F1 NIH_MGC_53 Hamo saplens cDNA clone IMAGE:3680680 5	T_HUMAN	1.0E-116 11418646 NT Homo saplens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA	1.0E-116 BF335849.1   EST HUMAN   CM2-CT0482-300800-349-e06 CT0482 Homo sapiens cDNA	qq41e04x1 Sogres_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7	EST HUMAN	EST HUMAN	16636 NT	1.0E-117 AF124393.1 NT Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15	1.0E-117 AF123320.1 NT Homo sapiens lymphocyte activation-associated protein mRNA, complete cds	N	1.0E-117 AW957699.1  EST_HUMAN   EST369769 MAGE resequences, MAGE Homo sapiens cDNA	1.0E-117 AA978114.1   EST_HUMAN   op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'	AA316/23.1 EST HUMAN	8659564 N I	0.1 EST_HUMAN	INT	TN	ΤN	1.0E-117 AF134304.2 NT Homo sapiens Scar2 (SCAR2) gene, partial cds	1.0E-117 AB020873.1 NT Homo sapiens mRNA for KIAA0866 protein, complete cds	1.0E-117 BE730508.1 EST_HUMAN   601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'	N	1.0E-117 L76571.1 NT Hamo sapiens nuclear harmone receptor (shp) gene, 3' end of cds
		116 AB0468	116 BF67791	116 BE1581	116 C02944.	116 AV7163	116 AA3542	116 AA3542	116 BE5655(	116 AI21635	116	116 BF3358	116 012674	116 BE25856	116 AL13486	117	117 AF12439	117 AF1233	117 M19816.	117 AW9576	117 AA9781	117 AA3167	711	117 AL04212	117 X89670.	117 X89670.	117 AF13430	117 AF13430	117 AB0206	117 BE7305	117 L76571.	117 176571.
	Most Similar (Top) Hit BLAST E Value																															
	Expression Signal	1.65	72.79	1.8	3.59	7.97	1.99	1.99	1.43	1.98	1.77	3.68	3 23		2.68	1.18	1.59	6.25	2.3	2.99	1.75	3.62				1.35	9.22	9.22	3.36			4.99
	ORF SEQ ID NO:	25782	25877		26156	26295	26949	26950	27239	27330	27642	28216	28615			20296	20821	21489	21564	21952	22953	SSC52	23820	24158	24299	24300	24382	24383	24516	24978	26426	26427
	Exon SEQ ID NO:	15675	15759	15829			16753	16753	17050	17137	17428	17965	18350			10487	12684	11620		12051	13154					14510	14591	Li	14736			16265
	Probe SEQ ID NO:	5768	5853	5924	6145	6275	6874	6874	7173	7260	7577	8074	8477	9591	9776	546	1061	1719	1790	2164	3230	3065	4247	4476	4622	4622	4705	4705	4856	5280	6404	6404

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Table 4
Single Exon Probes Expressed

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	4V747788 DCB Ummo continue Child 1. Bosto : E	AV717788 INCR Home contains adults and a contains and a contains and a contains and a contains and a contains and a contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contai	wp86b07x1 NCI_CGAP Bm25 Home sepiens cDNA clone IMAGE:2468629 3' similar to TR:075065	Homo seriene neural cell adhesive malecula (Alegana)	Homo sapiens mental cell adheering 1. (NCAM1), mRNA	Himen gene for your density is	1001569317F1 NIH MGC 21 Homo contact Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Alexandra Child Ale	zd83b11.r1 Soares fetal heart. NbHH19W Homo sepiens cDNA done IMAGE:347229 5' similar to	Homo sanians mBNA for MEGES 10-4-1 2-2	Home captains minut on MICOTO, plantal dos	ACH ARADASEA NILL MACHOLD ILL.	Home cerions ATD kind.	Home serious ATD binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo cepiens McDC/664 DNA 1.1.	DKFZh424In58 H 434 (cmmm, 11. 2) 11	Homo serieses hundheited Testing (1970) none 3apiens cDNA clone DKFZp434(056 5)	Home seriens shows the cardis house (1.1), mRNA	601281947E1 NILL MCC 44 H	601281947F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5	601281947F1 NIH M.C. 44 Libert September Con Report September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September September Sept	EST363799 MAGE resentations MAGE Local Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control	Human breakpoint cluster region (RCR) was completed.	Human breakpoint cluster region (BCB) was complete as	Homo saniens PRKV exm 7	CODITION OF NOT COMP KINE DAMP CONTINUED TO THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF TH	application in Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control	Human mRNA for phosomal protein county.	Home september selection showed several services in the second services of the second services of the second several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several several s	Homo canians calcium abone 1	Homo sanians francisch zonnter 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Homo sablens latent transforming growth forther hard.	Homo sapiens latent transforming growth factor beta blinding protein 2 (L. 1872) mRNA	WILLIAM (LIDEA) THE CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF
jle Exon Pro	Top Hit Database Source	EST HIMAN	EST HIMAN	FOT HIMAN	NT TOWAR	L L	FZ	EST HUMAN	EST HIMAN	L L	IN	EST HIMAN	LN LN	L	L	EST HUMAN	.1		EST HIMAN	ST HUMAN	EST HIMAN	EST HUMAN	N	N	Į.	EST HUMAN	EST HUMAN	L	L	NT		L	1	
Sin	Top Hit Acession No.	AV717788.1	AV717788.1	A1950145 1	10834989 NT	10834989 NT		122.1		41.1			1848	4501848 NT	1.0E-118 AF161500.1	Γ	7657016	5174680 NT	05.1	05.1	05.1	729.1	_	_		1.4		_	14.1	1.4	20764	4557732 NT	4557732 NT	
	Most Similar (Top) Hit BLAST E Value	1.0E-117 AV717	1.0E-117 AV717	1.0E-117 AI95012	1.0E-117	1.0E-117	1.0E-117 D16524	1.0E-117	1.0E-117 W8060	1.0E-117	1.0E-117	1.0E-117	1.0E-117	1.0E-117	1.0E-118	1.0E-118 AL0458	1.0E-118	1.0E-118	1.0E-118 BE3897	1.0E-118 BE3897	1.0E-118 BE3897	1.0E-118 AW951	1.0E-118 U07000.	1.0E-118 U07000.	1.0E-118 Y13932.	1.0E-118	1.0E-118/	1.0E-118 D23660.	1.0E-118 AF14262	1.0E-118	1.0E-118	1.0E-118	1.0E-118	
	Expression Signal	3.77	3.77	5.93	1.7	1.7	2.28	1.51	10.31	3.96	3.96	15.63	222	222	9.54	2.59	5.09	0.98	2.39	2.39	2.39	3.77	2.38	2.38	3.73	4.51	4.51	79.7	2.02	2.02	1.88	1.87	1.87	
	ORF SEQ ID NO:	26482		26725				27708	28512	28732	28733		28974	28975	19863	19890	20261	20667	21975	21976	21977		22465	22466		22887	22888	23679	25053	25054	25620	28054	26055	
	Exan SEQ ID NO:	16316	16316	16531	16716		17228	17486	18262		18462	18516	18684	18684	10050	10074	10448	12680	12073	12073	12073	12165	12574	12574	12993	13084	13084	13904	15249	15249	15535	15924	15924	
	Probe SEQ ID NO:	6455	6455	6651	6837	6837	7361	7635	8385	8595	8595	8698	8872	8872	64	06	506	896	2186	2186	2186	2284	2711	2711	3066	3159	3159	3668	5329	5329	2620	6020	6020	
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olingie Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sabiens chromosome 2 men reading frame 3 (C300E2)	601469159F1 NIH MGC 67 Home canions CONIA Alone MA OF CONTACT THE	QV0-BT0263-090200-097-h03 BT0263 H000 cm/cm - 201247 5	OV0-BT0263-080200-097-h03 BT0263 Home conjens child	Z98407.r1 Soares NHHMPu S1 Homo sanians cDNA clone NA OE-244720 2:	298407.rt Soares NHMPu St Homo saniens cDNA clans IMAGE: 041720 5:	Human mRNA for KIAA0383 dene, partial cds	Human mRNA for KIAAN3R3 dena pertiel ade	Homo sablens latent transforming grandt fanter hete binding herein 37 mms.	Homo sapiens latent transforming growth faster bots binding protein 2 (L.i. br. 2) mRNA	601144863F2 NIH MGC 19 Homo sapiens cDNA clone IMAGE 316050 57	7n17e09x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PDE-CLI 105.000	EST186814 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light	Given 1, cycopiasmic	UV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA	Home series chiefle change of 0.000 (2000)	Homo sapiens CGL-105 matein (1 OCE 2014) TRNA, complete cds	Homo sapiens mRNA for KIAAAOSA profein and all	Homo sapiens hypothetical protein FI. J10052 (FI. 140052) mBNIA	on10b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2	Homo saplens alutamate recentor innotronic kningto 1 (CDIXA)DNIA	7814F03 Chromosome 7 Felal Brain cDNA   Internations on the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th	AU133399 NT2RP4 Homo saniens CDN4 clare NT2DD46664 51	Human neurofibromin (NF1) gene complete cals	RC1-NN0073-250800-018-006 NN0073 Home carriers CDNA	AV693731 GKC Homo sapiens cDNA clone GKCDHRn3 57	db77c09.xt Scares_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:1706128 3' similar to SW:K1C.J MOI ISF P05835 KFRATIN TYDE I CYTOCKEI ETAL AN	Human c-fessifing brokensonsons	EST386296 MAGE reseminance MACM Lines	601592005F1 NIH MGC 7 Home emission and Act 114 of 02 120
Jie Exon Prot	Top Hit Database Source	¥	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N.	IN.	N	F	EST_HUMAN	EST HUMAN	ECT LIBRARY	COL LICINIAN	EST HUMAN	NT - IN	; 5	Z	5	EST HIMAN		T HUMAN	Т	T	Т	EST_HUMAN	T T	Т	T HUMAN	1
Suio.	Top Hit Acession No.	11431050 NT	223.1	855.1	855.1	024.1	024.1	381.1	381.1	4557732	4557732 NT	134.1	1.0E-118 BF195407.1		T			5607	12	2205	60.1	4504116	1.0E-119 AA077394.1	Γ		21.1	31.1	1.0E-119 AI150703.1 E	_	93.1	14
	Most Similar (Top) Hit BLAST E Value	1.0E-118	1.0E-118 BE781	1.0E-118 BE062	1.0E-118 BE062	1.0E-118 AA443	1.0E-118 AA443	1.0E-118	1.0E-118 AB002	1.0E-118	1.0E-118	1.0E-118 BE263	1.0E-118	1 OF 118	4 0 1 1 10	10F-118	1.0E-119	1.0E-119	1.0E-119 AB023	1.0E-119	1.0E-119 AA9167	1.0E-119	1.0E-119	1.0E-119	1.0E-119 M89914.1	1.0E-119 BE9361	1.0E-119 AV6937	1.0E-119	1.0E-119 X06292.	1.0E-119 AW9741	1.0E-119 BE7966
	Expression Signal	4.13	2.23	7.81	7.81	1.34	1.34	1.16	1.16	1.28	1.28	5.71	1.18	306	77.	1.75	0.81	1.55	2.09	1.81	1.08	1.15	0.95	2.45	14.93	3.32	2.24	7.19	2.79	4.26	1.42
	ORF SEQ ID NO:	56509	26722	26960	26961	26963	26964		27101	27129	27130	27288	28027	28737	28947	28948	20508	20781	21663	22783		23573	24753	24969	24980	24984	25079	25736	25914	25925	26403
	Exon SEQ ID NO:	16341	16528	16763	16763			_	16912	16939	16939	17100	17786	18465	18659	18659	10672	12683	11786	12991	13126	13781	14979	15194	15204	15207	15256	15633	15793	15801	16243
	Probe SEQ ID NO:	6482	6648	6884	6884	6888	6888	7035	7035	7062	7062	7223	7936	8598	8847	8847	741	1021	1891	3064	3202	3870	5111	5272	5282	5285	5336	5726	5887	5895	6381

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	aa3205r1 NCI CGAP GCR1 Home senions CDNA also 1144 OF 24 1000	Homo sepiens nartial II -12RB1 rens for II 12	602186072F1 NIH MGC 45 Home seniors CONA class 1846 CT 4242000	RC3-CT0212-24090a.011-fin3 CT0212 Home Control MAGE: 431U633 5	Homo sapiens mRNA for KIAA0758 profesor parties of a	Homo sablens synaptolanin 1 (SYN II) mRNA	Homo sapiens intersectin 2 (SH3D1B) mRNA commiste add	Homo sapiens intersectin 2 (SH3D4R) mRNA complete cas	1944012.r1 Soares melanocyte 2NHM Home carlone and Alice Line Services	Homo sapiens cysteine-rich reneat-containing profein 652	Homo sapiens gene for AF-6, complete cds	Homo sapiens gene for AE-6 complete cdc	Homo sapiens adjiancin 4 (AODA) militarindasti. — Dita	Homo septems supervision 4 (SVN 14) DNA	Homo sapiens cAMP-energing a home by the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contractions of the contr	Homo sapiens cAMP-specific phosphodiesterase of (PDESA) mKNA, partial cds	Homo saplens stannizednik (STC)	Homo seniens stanniocalcin (STO) cons	dd6103 x1 Soares feetie MHT Home continue cos	602183994F1 NIH MGC 42 Homo content of the IMAGE 1733981 3	602183994F1 NIH MGC 42 Home captains CDNA Clare INACE 43001/4 5	Human TBXAS1 dene for thrombovane emittees away 7	Human gene for neurofilament subunit M (NE-M)	Human gene for neurofilament subunit M (NF-M)	602035352F1 NCI_CGAP Brn64 Homo sapiens cDNA clone IMAGF-4183333 5	Homo sapiens mRNA, chromosome 1 specific transcrint KIAAAAAS	Homo sapiens mRNA, chromosome 1 specific transcript KIA A 0.40s	Homo sapiens mRNA for KIAA0465 protein partial cds	601307739F1 NIH MGC 44 Homo sabiens CONA clane IMACE 3225E44 El	601307739F1 NIH MGC 44 Home capiens CDNA close 144 CE:0001514 5	601888956F1 NIH MGC 17 Homo sapiens CDNA clone IMAGE: 3023544 5	AU133205 NT2RP4 Homo saniens CDNA close NT2D24044 E1	Homo saplens mRNA for KIAA1077 protein partial rde	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
gie Exon Pro	Top Hit Database Source	EST HUMAN	IN	EST HUMAN	EST HUMAN	Z	N	N N	NT	EST HUMAN	N TN	N.	NT	LV.	Z	LN	L V	FZ	NT	EST HUMAN	EST HUMAN	EST HUMAN	NT	F	N	EST_HUMAN	N _T	N	N-L	EST HUMAN	EST HUMAN	EST HUMAN	ST HUMAN	N	EST_HUMAN
	Top Hit Acesston No.	AA465124.1			AW847519.1	1.0E-120 AB018301.1	4507334 NT	1.0E-120 AF248540.1			1.0E-120 AF167706.1			5124	4507334 NT	1.0E-120 AF056490.1	90.1	T	1.0E-120 AF098463.1			27.1		-		9.1							ł		П
	Most Similar (Top) Hit BLAST E Value	1.0E-119 AA465	1.0E-119 AJ2977	1.0E-119	1.0E-119 AW847	1.0E-120	1.0E-120	1.0E-120	1.0E-120 /	1.0E-120 N44873.1	1.0E-120	1.0E-120	1.0E-120/	1.0E-120	1.0E-120	1.0E-120 /	1.0E-120 AF0564	1.0E-120 A	1.0E-120 A	1.0E-120 A	1.0E-120 BF5682	1.0E-120 BF56822	1.0E-120 D34619.	1.0E-120 Y00067.	1.0E-120 Y00067	1.0E-120 BF33759	1.0E-120 AB00796	1.0E-120 A	1.0E-120 A	1.0E-120 BE392102.1	1.0E-120 BE392102.1	1.0E-120 BF306541.1	1.0E-120 AU133205.1	1.0E-120 AB029000.1	1.0E-120 BE296387.1
	Expression Signal	1.48	1.42	9.72	1.37	1.4	1.34	1.67	1.67	4.53	3.87	6.0	6.0	0.84	1.13	1.17	1.17	2.79	2.79	0.89	13.84	13.84	1.49	1.67	1.67	2.44	2.43	2.43	1.33	4.54	4.54	4.72	7.31	2.53	6.4
	ORF SEQ ID NO:	27977	28089			20022			20788	21172	21348	21847	21848	22250	20082	23936	23937	24242	24243	24801	25488	25489	26495	26674	26675	26924	26971	26972	26993	27535	27536	27687	27698	27885	28607
	Exan SEQ ID NO:	17733	17848	18407	19671	10205				11311	11487	11950	11950	12358	10262	14159	14159	14455	14455	15034	15426	15426	16328	16488	16488	16729	16777	16777	16800	17330	17330	17468	17477	17848	18342
	Probe SEQ ID NO:	7883	7998	8535	9348	237	298	1025	1025	1406	1583	2000	2060	2482	3267	4260	4260	4563	4563	5168	9099	2208	6469	999	9099	0820	8689	8888	6922	7470	7470	7617	7626	7798	8469

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sed in Heart	Top Hit Descriptor	Human muscle afvocaen phosphorylase (DVGM) years R117D and war 4	18 calcineurin binding project 1 (KIAA0330) mDNA	S NF2 dene	LACE1 Homo sapiens cDNA clone DI ACE4000B00 E	Is TNF receptor-associated factor 1 (TRAE1) mRNA	is mRNA for KIAA0581 protein, partial cds	Homo sapiens inositol polyphosphate 4-phosphatase, type I 107kD (INPPAA) spline variant a mBNA	e inneifel nalunharabata / akamabatan t - 1 / 7/17/17/17/18/18/18/18/18/18/18/18/18/18/18/18/18/	Homo sapiens metahofronic nintamata recentor 1 heta / mChiod hota / mChiod and nintamata recentor 1 heta / mChiod hota / mChiod hota	602014759F1 NCI CGAP Bridg Home sales of Notice 1846 CE 44 France 1	602014759F1 NCI CGAP Bridt Home seniors child clare IMACE: 4150286 5	s hHb3 gene for hair keratin exons 1 to 9	s hHb3 gene for hair keratin, exons 1 to 9	s mRNA for KIAA1337 protein, partial cds	s mRNA for KIAA1337 protein, pertial cds	Homo saplens adaptor-related protein complex AP-4 ensilon surhunit mRNA complete ada	0x57b01x1 NCI CGAP Part Homo serviens cONA closes IAAGE-2006447	7E-1 gene (exon 17)	90299-075 BT043 Homo sapiens cDNA	s DNA for prostacyclin synthase, exon 8	s DNA for prostacyclin synthase, exon 8	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11) mRNA	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele,	Schloride infracellular channel 4 like (C11041) DNA	W74c01.s1 Scares fetal liver sniegon 1NFI S Homo canions of his class into the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the	Homo sablens T-cell Nmbhoma invasion and metastasis 4 (TTAMA) with A	s intersectin short isoform (ITSN) mRNA complete cde	Homo sapiers T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	s Intersectin short isoform (ITSN) mRNA, complete cds	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable rection (subarrata V kanna III)
pressed in Heart	Top Hit Descripto	Thusde divoden phosphordase (PVGM) and FILLS	Homo sapiens calcineurin binding protein 1 (KIAA0330) mBNA	Homo sapiens NF2 dena	AU134963 PLACE1 Homo sapiens CDNA close PLACE1000800 F	Homo sapiens TNF receptor-associated factor 1 (TRAE1) mRNA	Homo sapiens mRNA for KIAA0581 protein, partial cds	saplens inositol polyphosphate 4-phosphatase, type [, 10]	sniane inceiro nalvahocabata / Assas assas 1	satisms metabotronic di itamata recentor 1 heta / mCir.04	759F1 NCI CGAP Bridg Homo sanions china demails	759F1 NCI CGAP Brn64 Homo saniens CDNA clone II	Homo sapiens hHb3 gene for heir keratin exons 1 to 0	Homo saplens hHb3 gene for hair keratin, excus 1 to 9	Homo sapiens mRNA for KIAA1337 protein, partial eds	Homo sapiens mRNA for KIAA1337 protein, pertial cds	aplens adaptor-related protein complex AP-4 ensilon sur	1.x1 NCI CGAP Pan1 Homo seriens cDNA clone IMAC	H.sapiens ECE-1 gene (exan 17)	CM-BT043-090299-075 BT043 Homo sapiens cDNA	Homo sapiens DNA for prostacyclin synthase, exon 8	Homo sapiens DNA for prostacyclin synthase, exon 8	aplens COX11 (yeast) homolog, cytochrome c oxidase a	apiens UDP-glucuronosyltransferase 2B4 precursor (UC	Homo sapiens chloride intracellular channel 4 like/Ol 1041 - BNA	S1 Scares fetal liver soleen 1NFI S Homo captors cDN	ablens T-cell lymphoma invasion and metastasis 1 (TIA)	Homo sapiens intersectin short isoform (ITSN) mBNA complete cds	apiens T-cell lymphoma invasion and metastasis 1 (TIAN	Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	kappa-immunoglobulin germline bseudogene (Chr22 4) v
Single Exon Probes Expressed in Heart	Top Hit Database Source				T HUMAN						T HUMAN	HUMAN	Т					EST HUMAN ax57bc		EST_HUMAN CM-BT						T HUMAN					
iguis	Top Hit Acession No.	U94774.1	11417862	Y18000.1	63.1	2192	AB011153.1 NT	4755139 NT	TN 9613374	1	78.1	78.1	-		1.0E-121 AB037758.1 NT	1.0E-121 AB037758.1 NT		4.1		1:	D84122.1 NT	D84122.1 NT	11427788 NT	1.0E-121 AF064200.1	10334	_	11526176 NT	1.0E-122 AF114488.1 NT	11526176 NT	1.0E-122 AF114488.1 NT	M20707.1
	Most Similar (Top) Hit BLAST E Value	1.0E-120 U94774.	1.0E-120	1.0E-121 Y18000	1.0E-121	1.0E-121	1.0E-121 AB0111	1.0E-121	1.0E-121	1.0E-121 L76631	1.0E-121 BF3443	1.0E-121	1.0E-121 Y19208.	1.0E-121 Y19208,	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121 X91937.	1.0E-121	1.0E-121 D84122	1.0E-121 D84122	1.0E-121	1.0E-121	1.0E-121	1.0E-121 N59624.	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122 M20707.
	Expression Signal	2.07	1.36	1.04	0.98	1.23	0.39	0.89	. 0.80	1.17	1.05	1.05	3.09	3.09	1.09	1.09	6.61	1.21	2.55	1.03	2.58	2.58	4.44	2.28	4.91	3.48	3.99	2.22	1.54	2.85	3.41
	ORF SEQ ID NO:	29013					21319	21697	21698	21841	22295	22296	22763	22764	23213	23214	23325	23910	24556	24695	26701	26702	28297	28303	28466	28489	20047	20107	20132	20641	20957
	Exan SEQ ID NO:	18722	19111	10052	10328	12674	11461	11818	11818	11945	12404	12404	12969	12969	13408	13408	13538	14134	14781	14922	16512	16512	18045	18051	18213	18240	10232	10292	10312	10790	11111
	Probe SEQ ID NO:	8914	9492	67	374	707	1556	1923	1923	2055	2530	2530	3042	3042	3492	3492	3624	4236	4901	5050	6632	6632	8157	8163	8336	8363	267	333	355	864	1201

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Descriptor Top Hit Descriptor Source	1.32 1.0E-122 AF167706.1 NT Homo sapiens cysteine-rich repeat-containing protein S52 precursor mRNA complete cde	2.01 1.0E-122 11418424 NT Homo sapiens collagen, type XII, alpha 1 (COL124.) mRNA	2.01 1.0E-122 11418424NT Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA	1.0E-122 BE906024.1 EST HUMAN	1.0E-122 BF316170.1 EST_HUMAN	1.0E-122 BF316170.1 EST HUMAN	1.82 1.0E-122 4502166 NT Homo saplens amyloid beta (A.4) preciment profess foundations and in Al-t-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	T HUMAN	EST HUMAN	Т	4.35 1.0E-122 11418187 NT Homo sapiens phosphomannomulase 1 (PMM1) mRNA	1.0F 1.0E-123 U31519.1 NT Human phosphoenobyruvete carboxykinese (PCK1) rene promotes reading and profiled add	74.1 EST HUMAN	74.1 EST HUMAN		5803114 NT	3.35 1.0E-123 4505818 NT Products	1.0E-123 - 4505818INT	A 13886/14	1.0E-123 M55419 1	1.0E-123 M55419.1 NT	Z	7705962 NT		1.75 1.0E-123 L34219.1 NT Homo sapiens retinaldehvide-binding profein (CRA RP) rena complete color	1.29 1.0E-123 BE799746.1 EST HUMAN 601591108F1 NIH MGC 7 Homo saplens CDNA clone IMAGE 3045423 CS	35.1 EST HUMAN	1.3 1.0E-123   U42224.1 NT Human growth hormone releasing hormone gene, exon 7	11.1 EST_HUMAN	П
	Top Hit	AF1677			BE906024.1	BF316170.1	BF316170.1		Itā	BE256039.1			U31519.1	BF345274.1	BF345274.1	AL163249.2				A 1388644 4	M55419 1	M55419.1	M55419.1		1	L34219.1		AU118435.1	U42224.1	BE263001.1	AB007923.1
	Most Similar (Top) Hit BLAST E Value					1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1 OE-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123
	Expression Signal	1.32	2.01	2.01	5.91	10.56	10.56	1.82	1.2	6.41	1.35	4.35	1.07	1.72	1.72	3.79	5.06	3.35	3.35	176	2.98	2.98	2.98	4.5	1.75	1.75	1.29	2.27	1.3	1.95	4.14
	ORF SEQ ID NO:	21435	21458	21459	21549	22215	22216	24409		. 25390	27286		19968	20517	20518	20760	20767	20976	20977	21211	21837	21838	21839		25091	25092	25400	25923	26221	26545	27517
	Exon SEQ ID NO:	L	11586	11586	11671	12318	12318	14623	14797	15337	17096	18869	10153	10681	10681	10916	10923	11126	11126	11344	11942	11942	11942	12151	15265	15265	15346	15799	16071	16368	17310
	Probe SEQ ID NO:	1667	1684	1684	1772	2441	2441	4738	4918	6051	7219	8008	181	751	751	966	1005	1218	1218	1439	2052	2022	2052	2267	5344	5344	5425	5893	6186	6299	7392

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Table 4
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Single Exon Probes Expressed in Heart	Top Hit Descriptor	North printe cimiculus New Zoolond white cleaned and the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment o	602086791F1 NIH MGC 83 Home conjust china de la la la la la la la la la la la la la	602086797F1 NIH MGC 82 Home confers DNA -1 11 A ST 12555	Homo saplens T-cell hymphoma invasion and metastasis 1 (TIAMA) DNA	Homo sapiens T-cell hymnhoma invasion and mediantics (TIAM) IIINNA	Homo sapiens DNA for amyloid precursor profein, commisto odo	Homo saplens chromosome 21 segment HS21026	281b04.rl Strategene schizo brain S11 Homon sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMON OG IDETEDAMON I FILIA IN TANS	281504.r1 Stratagene schizo brain S11 Homo sapiens CDNA clone IMAGE:728719 6' similar to TR:G300482	Human butative ribosomal protein S1 mPNA	Homo sapiens Tirell humbons investor and make to the transfer	Homo sapiens througheiteat modern (HSDC) and Interestation (HAMT) mKNA	Homo sapiens ring finger protein (RNF) mRNA	Homo sapiens alucose transporter 3 gaps exxxx 0 40 and 11.	Homo sapiens alucase transporter 3 gens examp 0.10 and complete das	Homo sapiens mRNA for nicleolar RNA believes (males at 10, and complete cds	601491715F1 NIH MGC 69 Home series ANN And Character at	Homo saciens gene for 8120 even 11	Homo saplens glutamate receptor, ionotronic, kainate 1 (CBIK1)	Homo sapiens ATP-sensitive inwardiv rectifiving K-channel cub (Col. Inform.)	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KON) Israilou	H.Sapiens lactate dehydrogenase B gene expn 1 and 2 (FC 1 1 1 27) (And John 2000)	Homo sapiens T-cell lymphoma invasion and metactacic 1/T/1/1/1/1/ Control Cubs)	Homo saplens alutamete recentor innotronic keinete 4 (CDIVA) - DNA	Homo sapiens gene for B120, exch 11	Human fibronectin dene extra time III reneat (FDIII) avvn v±1	of56h03.x1 Soares testis NHT Home senions of DNA Alexandra Area 144 CE 1475 1600 CE	Homo sapiens hypothetical profein Fi. 140300 (FI. 140300)	602124644F1 NIH MGC 56 Homo sepiers CDNA close IMAGE: 4284555 F1	M.musoulus mRNA for hoxa3 gene	Homo sapiens ribosomal protein L5 (RPL5) mRNA
le Exon Probe	Top Hit Database Source		Т	EST HUMAN 6				上	EST HUMAN G		Т				E L			T HUMAN	T		Ĭ	エ	F.					EST HUMAN OF		EST_HUMAN 60	Т	
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	Expression Signal	12.23	9	Ø	1.1	1.1	1.98	2.11	2.03	2.03	3.67	1.06	1.81	2.59	5.54	5.54	2.35	2.23	0.85	0.85	0.96	96.0	2.95	1.09	1.19	1.58	1.12	2.72	8.97	6.43	3.31	5.66
	ORF SEQ ID NO:	27537	29057	29058		20049		20238	20429	20430	20509	20561	20860	21056	21086	21087	21550	21797	22182	23045	23169	23170	23300	23528	23666	24315	1	24685	24934	25580	26220	26874
	Exon SEQ ID NO:	17331	18765		10233	10233	10239	10421	10609	10609	10673	10720	10812	11200	11231	11231	11672	11907	12285	13240	13383	13363	13512	13737	13890	14527	14731	14911	15164	15505	16070	16684
	Probe SEQ ID NO:	7471	8928	8328	268	<b>588</b>	273	477	676	676	742	797	988	1293	1324	1324	1733	2016	2408	3319	3446	3446	3598	3825	3983	4639	4820	2039	5240	2230	6185	6805

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Single Exon Probes Expressed in Heart	Top Hit Database Top Hit Descriptor	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162 EST_HUMAN		1	Т	EST HIMAN WIGSON A NOT CRAME LANGE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE C	Т	T HUMAN	Τ	EST_HUMAN hi05c06.x1 Soares_NFL_T_GBC_S1 Homo sabiens cDNA clone IMAGE 2020006.21	#19e03.XI NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662		Z181504.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5 similar to TR:G300482 G300482 POI =REVERSE TRANSCRIPTAGE LONGO COMPANA CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTR		NICINOI -		NT Home saplers media for KIA 4472	T HUMAN	Т	Г	•	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' sImilar to	Г		NT Homo serience KIAAA022 ages product, instant elegenthase ( KIAA0744), mRNA		Homo sapiens Usurpin-alpha mRNA, complete cas	
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	Most Similar (Top) Hit BLAST E Value	1.0E-124 AW6121	1.0E-124 AW6121	1.0E-124 AV6456	1.0E-124 AV64563	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124 /	1.0E-124 A	1.0E-124	1.0E-124	1.0E-125 A	1.0E-125 E	1.0E-125 A	1.0E-125 AI110656.1	1.0E-125 A	1.0E-125 AA042813.1	1.0E-125 AL163210	1.0E-125	1.0E-125	1.0E-125 AF015450.1	1.0E-125 AF015450.1	
	Expression Signal	1.35	1.35	2.44	244	7.8	7.8	1.25	2.25	2.25	1.87	1.87	3.98	3.98	1.99	1.39	5.41	3.92	1.63	1.83	124	2.13	1.53	1.83	1.08	3.81	3.81	
	ORF SEQ ID NO:	27002	. 27003		27533	27604				28788	28162	28163	20429	20430	25005	25006		19778	20377	20378	20469	20619	20750	20890	21414	21545	21546	
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	Probe SEQ ID NO:	6930	6930	7466	7466	7542	7542	7676	8404	8645	8767	8767	9173	9173	9846	9846	316	⁴ 20	628	878		842	982	1136	1649	1769	1769	

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Table 4
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Single Exon Probes Expressed in Heart	Top Hit Descriptor	2k53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to	Homo saniens inhihin pinha (INIA) = DNALINE PROTEIN HGMP07E (HUMAN);	Homo seriens inhihin alpha (INLIA) IIIRNA	oh64402 x5 NCI CGAP Kirls Home sonions CDNA decisions and a second control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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sapiens I-REL gene exm 5	X59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284	#59f02.x1 NCI_CGAP_Gas4 Home saplens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284	Home seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 (1) Anna seniors many 6 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gle Exon Prot	Top Hit Database Source	EST HUMAN	4.	LN	EST HUMAN	4	N.	EST HUMAN	1	EST HUMAN	EST HUMAN	EST HIMAN	NT.	Z			Þ	T HUMAN	Т	Т	EST HUMAN		7			T HUMAN	Т	T	Т		
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	Most Similar (Top) Hit BLAST E Value	1.0E-125	1.0E-125	1.0E-125	1.0E-125 AI73296	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-126 X03427	1.0E-125 X03427	1 OE 12E   100200	10.1	1.0E-125 U90288.	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125/	1.0E-125	1.0E-125	1.0E-125	1.0E-125 E	1.0E-125 E	1.0E-125 A	1.0E-126	1.0E-126 M61936.
	Expression Signal	1.15	1.65	1.65	2.45	1.98	1.98	0.84	1.41	3.44	1.48	1.48	6.36	6.36	4 22		1.22	4.31	4.31	3.15	1.86	1.86	5.13	2.92	5.15	2.49	4.36	4.36	1.96	0.88	1.2
	ORF SEQ ID NO:	22228	22315	22316		24136		24195				25994	26093	26094	27043		27044	27343	27344	28211	28289	28290	28616	28748	28754	28804	28896	28897	29044	20525	20528
	Exon SEQ ID NO:		12424				_		15496	15527	15870	15870	15961	15961	16851		16851	17149	17149	17960	18040	18040	18351	18476	18482	18522	18607	18607	18749	10687	10690
	Probe SEQ ID NO:	2455	2551	2551	2555	4450	4450	4516	5581	5612	5965	5965		6201	6974		6974	7272	7272	8069	8152	8152	8478	8609	8615	8704	8793	8793	8944	757	760
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	r	т	-	Т	_	$\overline{}$	_	_	_	_	_	_			_	_	_	_	_		_	<del></del>	-	-	-	- 1111	· · · · ·	w Tw	-112-	_	in.	*111.1	111111
Single Exon Probes Expressed in Heart	Top Hit Descriptor	H.sapiens gene for alphaf-antichymotrypsin, exon 3	Homo saplens RAN binding protein 2 (RANBP2), mRNA	2072c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5	2072c03.r1 Stratagene panoreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'	H.saplens DNA for liver cytochrome b5 pseudogene	Homo sapiens death receptor 6 (DR6), mRNA	Homo sapiens collagen type XI alpha-1 (COL/11A1) gene, exon 63	Homo saplens collagen type XI alpha-1 (COL11A1) gene, exon 63	yx78c06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:287850.5	2x86e03.r1 Soares_total_fetus_Nb2HF8_9w Homo sepiens oDNA clone IMAGE:796444 6' similar to TR-04145880 04145880 TITIN .	Homo saniens mRNA for KIAA1526 protein months and	Homo sepiens mRNA for K/A41575 protein, partial role	Human mRNA for ankyrin (variant 2.1)	602139138F1 NIH MGC 46 Homo saplens cDNA clone IMAGE 4298240 5'	601149404F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE:3502129 5	601577981F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3926685 5	Homo sapiens mRNA for casein kinase l epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens lost on transformation LOT1 mRNA, complete cds	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA	Homo sepiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA	Homo sapiens leukocyte Immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (Lil RA1)	mRNA	Homo sapiens ribosomal protein L26 (RPL26) mRNA	Homo sapiens adlican mRNA, complete cds	Human mRNA for cytokeratin 18	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:789098 5'
Jie Exon Prot	Top Hit Database Source	NT	IN IN	EST_HUMAN	EST_HUMAN	NT	Į.	N	N.	EST_HUMAN	EST HIMAN		L _N	F	EST HUMAN	EST_HUMAN	EST HUMAN	E	F	FN	ᅜ	NT	NT	NT	NT	Τ	F		ムゴ	ΤV	NT		EST_HUMAN
ùis	Top Hit Acession No.	۲.	6382078 NT	4A160709.1	AA160709.1	.1	TN 8607697	AF101108.1	۲.	V34078.1	1.0E-126 AA460075 1	T	T		-	1.0E-126 BE261660.1		Γ			1.1			88.1	.2	4827053 NT	5803065 NT		5803065 NT	4506620 NT	05.1	.1	31.1
	Most Similar (Top) Hit BLAST E Value	1.0E-126 X68735	1.0E-126	1.0E-126 AA160	1.0E-126 AA1607	1.0E-126 X53941	1.0E-126	1.0E-126 AF1011	1.0E-126 AF1011	1.0E-126 N34078.1	1.0E-126	1 0F-126	1.0E-126	1.0E-126 X16609.1	1.0E-126	1.0E-126	1.0E-126	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127 D87675.1	1.0E-127 D87675.1	1.0E-127	1.0E-127 U72621	1.0E-127	1.0E-127		1.0E-127	1:0E-127	1.0E-127 /	1.0E-127 X12881	1.0E-127 AA4501
	Expression Signal	2.03	2.24	6.07	6.07	1.21	2.04	96.0	96'0	1.57	3.68	3.82	3.82	2.77	1.95	241	4.38	3.59	3.59	2.31	2.31	2.35	2.35	1.32	1.28	0.98	1.59		1.59	7.45	4.01	2.78	0.96
	ORF SEQ ID NO:	20670	22317	22757	22758	23281	23307	24356	24357	24400	25795	25813	25814	26737	28366	28910	24890	19954	19955	19954	19955	20056	20057	20640	20669	21433	21800		21801	21939	22075	22330	22341
Ī	Exon SEQ ID NO:	10826	12425	12963	12963	13491	13519	14563	14563	14614	15686	15703	15703	16540	18114	18620	15098	10138	10138	10138	10138	10238	10238	10789	10823	11567	11911		11911	12041	12176	12437	12450
	Probe SEQ ID NO:	901	2552	3035	3035	3577	3605	4677	4677	4728	5779	5797	5797	0999	8233	8806	9635	165	165	166	186	272	272	88	868	1665	2020		2020	2 2 2 3	2294	2566	2579

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Table 4
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| Top Hit Descriptor                            | zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo capiens cDNA clone IMAGE:789098 5                                                                               | au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA done IMAGE:2782594 5' similar to TR.Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22                                                                                                                    | repetitive element;<br>Homo cantans delando ractifier notas si im channel subunit IsV ==DNA                                                   | Homo sapiens chromosome 21 segment HS21C047                                                                                                                                                                                                                                                                                                                                                                                                                      | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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                                                                                                                                                                                                                                   | H.sapiens NOS2 gane, exon 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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Sec31B-1 mRNA, alternatively spliced, complete cds                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              
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sapiens secretary pathway component Sec31B-1 mRNA, alternatively solired, complete and                                                                                                                                                                                                                         | Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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|                                               | Exon<br>SEQ ID<br>NO:ORF SEQ<br>SignalExpression<br>(Top) Hit<br>SignalTop Hit Acession<br>BLAST E<br>ValueTop Hit Acession<br>No.Top Hit Acession<br>Source | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>No:         (Top) Hit<br>BLAST E<br>Value         Top Hit Acession<br>No:         Top Hit<br>Database<br>Source           12450         22342         0.96         1.0E-127 AA450131.1         EST_HUMAN | Exon ORF SEQ Expression (Top) Hit Top Hit Acession Database NO: Signal BLASTE No. Source Value 12450 22342 0.96 1.0E-127 AA450131.1 EST_HUMAN | Exon SEQ ID ID NO:         Signal Value         Most Striller (Top Hit Acession Signal Value)         Top Hit Acession Database Source Value         Top Hit Acession Database Source Signal Value           12450         22342         0.96         1.0E-127 AA450131.1         EST_HUMAN           13652         23435         0.88         1.0E-127 AA450131.1         EST_HUMAN           13929         23706         1.0F-137 AA450181.1         EST_HUMAN | Exon Signal NO:         CRF SEQ Signal NO:         Expression Signal NO:         CTop) Hit Top Hit Acession Signal NO:         Top Hit Acession Signal NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession 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0.88         1.0E-127 AA450131.1         EST_HUMAN           13929         23706         1.09         1.0E-127 AA1632188.1         NT           14028         23802         0.86         1.0E-127 AA163218.1         NT           14050         23833         21.46         1.0E-127 AA163239 NT | Exon Signal NO:         CRF SEQ Signal NO:         Expression Signal NO:         Most Similar (Top) Hit Acession Signal NO:         Top Hit Acession No:         Top Hit Acession Source No:           12450         22342         0.96         1.0E-127 AA450131.1         EST_HUMAN           13652         23435         0.88         1.0E-127 AA450131.1         EST_HUMAN           14028         23502         0.86         1.0E-127 AA1632188.1         NT           14060         23833         21.46         1.0E-127 AT163218.1         NT           14050         23834         21.46         1.0E-127 AT163218.1         NT | Exon NO:         CRF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Acession Signal NO:         Top Hit Acession Patabase No:         Top Hit Acession Patabase No:         Top Hit Acession Database No:         Top Hit Acession Patabase No:         Top Hit Acession Database Source No:           12450         22342         0.96         1.0E-127 AA450131.1         EST_HUMAN           13652         23435         0.88         1.0E-127 AA161297.1         EST_HUMAN           13929         23706         1.09         1.0E-127 AA163247.2         NT           14050         23833         21.46         1.0E-127 AL163247.2         NT           14050         23834         21.46         1.0E-127 AL163239 NT           14221         24075         0.92         1.0E-127 AF262297.1         NT | Exon NO:         CRF SEQ ID NO:         Expression Signal NO:         Most Similar (Top) Hit Acession Signal NO:         Top Hit Acession NO:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Database Source No:         Source Source No:         Ace In In In In In In In In In In In In In | Exon NO:         CRF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Acession Signal NO:         Top Hit Acession No.         Top Hit Acession Patabase Source Nature           12450         22342         0.96         1.0E-127 AA450131.1         EST_HUMAN           13652         23435         0.88         1.0E-127 AA450131.1         EST_HUMAN           13652         23706         1.09         1.0E-127 AA161297.1         EST_HUMAN           14026         23833         21.46         1.0E-127 AA163247.2         NT           14060         23833         21.46         1.0E-127 AA763539.1         NT           14291         24076         0.92         1.0E-127 AA763539.1         NT           14383         24178         4.16         1.0E-127 AA763539.1         NT           14383         24178         4.16         1.0E-127 AA763539.1         NT | Exon NO:         CRF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Acession Signal NO:         Top Hit Acession NO:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Database Source Source No:         Source Source No:         Source No:         Source No:         Ace Top Hit Acession No:         Ace Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Ace Top Hit 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Source No:         Top Hit Acession Source No:           12450         223435         0.98         1.0E-127 AA450131.1         EST HUMAN Source No:         1.08           13929         23706         1.09         1.0E-127 AA450131.1         EST HUMAN No:         1.0E-127 AA450131.1           14028         23833         21.46         1.0E-127 AA163247.1         INT           14050         23833         21.46         1.0E-127 AA163247.1         INT           14050         23834         21.46         1.0E-127 AA163247.1         INT           14405         23834         21.46         1.0E-127 AA163247.1         INT           14428         24178         4.16         1.0E-127 AA163263.1         INT           14428         24252         0.98         1.0E-127 AA163263.1         INT           15450         2553         3.72         1.0E-127 AA163263.1         INT           16436         26620         1.38         1.0E-127 AA060.1         INT           16436         26621         1.38         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Page 355 of 413 Table 4 Single Exon Probes Expressed in Heart

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Table 4
Single Exon Probes Expressed in Heart

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Exon         ORF SEQ         Expression         (Top) Hit Acess         Top Hit Acess           NO:         15614         25715         2.89         1.0E-129         AJ006345.1           16995         26245         5.17         1.0E-129         AJ006345.1           16132         26286         5.17         1.0E-129         AJ006345.1           16132         26286         5.17         1.0E-129         AJ00345.1           16132         26286         3.68         1.0E-129         AJ00345.1           16132         26286         3.68         1.0E-129         AJ03415.1           16132         26286         3.52         1.0E-129         AJ43415.1           16132         26286         3.52         1.0E-129         AJ43415.1           16699         26993         2.04         1.0E-129         AJ43415.1           16699         26994         2.04         1.0E-129         AJ43415.1           16699         26994         2.04         1.0E-129         AJ43415.1           11547         21409         6.81         1.0E-130         BE564219.1           11640         2.1409         6.81         1.0E-130         BE564219.1           12777	old Exoli Pio		Ā	Þ	TN.	N _T		-1.	EST HUMAN	EST HUMAN	EST HIMAN	EST HIMAN	EST HIMAN	EST HIMAN	LN	Ę	EST HIMAN	EST HIMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	<u> </u>	EST HIMANI	NT IN	Į.	EST HUMAN		┰	
Exam         ORF SEQ         Expression         Mo           SEQ ID         ID NO:         Signal         B           15614         25715         2.89           16095         26245         5.17           16036         26245         5.17           16132         25286         7.59           16720         3.68         3.68           16720         3.68         3.62           18424         28693         3.52           18424         28693         3.52           18599         28994         2.04           18699         28994         2.04           11547         21408         6.81           11547         21408         6.81           11547         21408         6.81           11547         21408         6.81           11547         21408         6.81           11655         2.2564         1.17           12777         22564         4.77           12777         22564         4.77           13768         2356         1.09           14302         24673         1.09           14302         24574         1.09     <	ร็	Top Hit Acession No.	AJ006345.1	AJ006345.1	11420850	AB014534.1	AA625528 1			AU143115.1	H83155 1	AL120739.1	BE275192.1	BE275192.1	X04092.1	AJ010230.1	BE564219.1	BE564219.1	AF240698.1	3E564219.1	3E564219.1	4W 503580.1	4W843993.1	4W363299.1	W363299.1	11416777	W956242 1	\B037756.1	A25140.1		A228128 1	4885136	
Exan NO: 15614 SEQ Express SEQ ID NO: Signa 16095 16095 26245 16720 26245 16720 28993 16132 26266 16720 28993 16132 26266 16477 22564 12777 22564 12777 22564 12777 22564 12777 22565 13460 23560 14335 28650 359991 19783 28991 19783 29991 19783 29991 19783 29991 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 197855 19785 19785 19785 19785 19785 19785 19785 19785 19785 19785 19		Most Similar (Top) Hit BLAST E Value	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130 /	1.0E-130	1.0E-130	1.0E-130 /	1.0E-130	0.0E+00	0.0E+00	0.0E+00	
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0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		ORF SEQ ID NO:						26286	28993	28994			21408	21409			22564	22565	23243	22564	22565	23560	24122	24673	24674	26322	27187	27392	28650	19782	19783	19786	
Probe NO: NO: NO: 5706 6229 6229 6226 9630 1643 1643 1643 1643 1643 1643 1643 1643					16132	16720	18424	16132	18699	18699	18960	19203	11547	11547	11835	12605	12777	12777	13446	12777	12777	13768	14333	14902	14902	16165	16996	17190	18385	9991	9991	5993	
		Probe SEQ ID NO:	5706	6229	6267	6841	8554	8618	8888	8888	9250	9630	1643	1643	1940	2743	2849	2849	3530	3703	3703	3857	4438	6029	5029	6301	7119	7314	8513	4	.4	7	

Page 357 of 413 Table 4 Single Exon Probes Expressed in Heart

Proba   Exam   Oper SC   Expression   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He   Top-He					_	_	т		_		_	_		_	_	_			_	_	_				٠,				11 11			<u> </u>	-11
Exon (1000)         ORF SEQ (1000)         Expression (100) Hit (1000)         (100) Hit (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         Top Hit Acession (1000)         <	des Expressed in Heart	Top Hit Descriptor	Homo sapiens hypothetical protein FI 120324 / FI 120324 - Dh.14	Homo sapiens throughlight protein FI (2027) ( FI 12022) 1 mKNA	Homo sapiens DCRR1 mRNA partial rule	Homo sapiens DCRR1 mRNA partial cds	Homo sapiens beta-tributin mRNA complete ade	Human hebarin cofactor II (HCE2) gane exone 1 through 6	Homo sapiens RNA-binding protein S1 serine-rich damain / DNDS21DN14	Homo sabiens mRNA for multidate resistance andein 3 (ABCCs)	Homo sabiens mRNA for multidate resistance protein 3 (ADCCs)	HUM516-108B Human placenta notva+ (TE-lituras) Home comises - TNIA -	HUM516H08B Human placenta noty4+ (TErithuses) Home control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the	Himan ribosomal prodein 1.7 (PDI.17) meMA.	cr48e07.x1 Jia bona marrow stroms Home sentions about 1	Gr48e07 x1. 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A4 mindometel. A	Homo saniens antin hote (ACTD) - DNA	Human polyhomeofic 1 homeles (HDD4) == 1.1	HA1347 Human fetal liver c DNA library Home coming on the	Homo sapiens mRNA for K/AA1363 provision practical cuts	H.sapiens next dene (expn 2)	1838605.X1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE: 2230833 3' similar to TR: 099551 Q99551 MITOCHONDRIAL TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TEDMINATION EACTOR DELCAY SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE SIMILAR TRANSCRIPTION TE S	ts38b05x1 NCI_CGAP_UtH Hono sapiens CDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551	MILLOGI CALLANDONIE I I NO I ENMINA I I ON PACTOR PRECURSOR.
Exon NO:         ORF SEQ Figural NO:         Expression Signal PLASTE 10001         (Top) Hit Value 10001         Top Hit Acess 134         Top Hit Acess 0.0E+00         Top Hit Acess 8223           10001         19792         1.34         0.0E+00         8923 82237.1           10007         19793         1.34         0.0E+00         D83327.1           10007         19793         2.45         0.0E+00         D83327.1           10007         19804         2.45         0.0E+00         D78327.1           10023         19819         2.45         0.0E+00         D78327.1           10038         19847         1.2         0.0E+00         D78327.1           10039         19846         1.4         0.0E+00         D78327.1           10039         19847         1.2         0.0E+00         D7834.1           10042         19849         4.14         0.0E+00         D7834.1           10042         19853         8.1         0.0E+00         D7834.1           10042         19853         8.1         0.0E+00         D7834.1           10044         19853         8.1         0.0E+00         D783270.1           10054         19859         1.77         0.0E+00	שום באחוו הוח		NT	N _T	Z	ᅜ	N N	Z	NT TA	F	N.			LZ	EST HUMAN	EST HUMAN	LN	FZ	TZ.	LN L	NT	TN TN	EST HUMAN	L	LN LN	IN	LN L	EST HUMAN	."	N	EST HUMAN	EST HIMAN	Tana I
Exon         ORF SEQ         Expression         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose Signal         Mose	Ö	Top Hit Acession No.	8923349	8923349	1.	D83327.1	AF141349.1	M58600.1	6857825	Y17151.2	Y17151.2	D78804.1	D78804.1	L16558.1	AW069534.1	AW069534.1	M60676.1	M60676.1	4758977	4758977	4758977	4758977	4A953770.1	4501850	4504444	5016088				1	N623701.1	-	
Exon SEQ ID NO: Signa NO: NO: NO: Signa NO: 10001 19792 10001 19793 10001 19793 10001 19793 10001 19793 10001 19793 10001 19793 10001 19804 10002 19805 10004 19805 10004 19805 10005 19805 10005 19805 10005 19805 10005 19805 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 19806 10007 1980		Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	. 0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	
Exan ORI SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	1.34	1.34	2.45	2.45	5.57	26.0	2.41	1.4	1.4	1.22	1.22	4.14	8.1	8.1	5.8	2.75	1.77	1.77	1.49	1.49	42.13	1.09	14.77	47.55	13.39	1.46	1.03	6.13	1.39	1.88	
		ORF SEQ ID NO:	19792	19793	19799														19869	19870	19869	19870	19875	19877		19886	19889	19895	19896	19901	19906	19906	
Probe SEΩ D NO: NO: 151 152 220 220 220 220 220 240 253 33 33 33 34 35 55 55 55 55 55 55 55 55 55 55 55 55		Exon SEQ ID NO:	10001	10001	10007	10007	10011	10020	10022	10038	10038	10039	10039	10040	10042	10042	10045	10047	10054	10054	10054	10054	10058	10060	10061	10070	10073	10079	10080	10085	10091	10091	
		Probe SEQ ID NO:	15	15	20	8	24	33	32	24	51	25	52	53	55	55	59	61	69	69	71	71	74	76	111	88	88	94	36	192	110	111	

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Table 4
Single Exon Probes Expressed in Heart

		٠,	_		_	_	_	,	_			_	_					_	_		Har. 11-										_
	Top Hit Descriptar	W01h09.r1 Soares melanocyte 2NhHM Homs saviens a PMA Alexandra Alexandra States	WOT109 rt Scarres melanovita 2016 to septents control (1975)	Homo saniens neuroniin 2 (NRD2) mbn/A	Homo sapiens polymerase (PNA) II (ONA 41:-41)	Homo septens polymerase (NNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	va83n04.72 Stratagnera fetal scheen ///////////////////////////////////	yacogo v.r.z. orazagano teta spiretti (#83/ Zuo) Homo sapiens cDNA clone IMAGE:68310 5' va83a04.r2 Stratarene fetal sulaen (#637205) Longo et al.	Homo saniens heterorenenis Principas alternations alternations and the saniens here and the saniens here are a saniens and the saniens here are a saniens and the saniens are a saniens and the saniens are a saniens and the saniens are a saniens and the saniens are a saniens and the saniens are a saniens and the saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are a saniens are	801480375F1 NIH MGC 86 Home senioral color July 2	Homo sapiens heterodeneous product il here.	formo semiento nellaridad transference incolladore propriedad in the Mark Mark Mark Mark Mark Mark Mark Mark	601174270F1 NIH MCC 47 L	601174270F1 NIH MGC 17 Hrms emisses ONA Acro NA OFFICE SECTION F	2d62b05.r1 Soares fetal heart NbHH19W Home sapiens cDNA clone IMAGE:345201 5' similar to	gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);	Homo sapiens zinc finger protein mRNA, complete cds	Homo sapiens chromosome 21 segment HS21 Cn02	Homo sapiens chromosome 21 segment HS21 Chn2	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE.2963854 5' similar to WP:Y57A10A.Z CE22631 :	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z	Homo saniens mRNA for KIA 80794 mentals and all	Homo sepiens mRNA for KIAA0784 protein, pai uai cus	Human gamma-cybolasmic actin (ACTGDO) Transference	Homo sapiens CTCI thimor aptires 2011 3 metric	Homo sapiens CTCL tumor antique set 4.3 mDNA complete cos	Homo saplens chromosome X MSI 3-2 profein mBNA complete cus	Homo saciens chromosome X MSI 3.2 protein mBNA complete das	tq04f08.x1 NCI_CGAP_U3 Homo septens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN II-	tq04f08.x1 NCI_CGAP_Ut3 Homo sepiens cDNA done IMAGE:2207847 3' similar to gb:J03191 PROFILIN I	Homo saplens DNA mismatch repair protein (MLH3) gene, complete cds
101 - 10V- 0:5	Top Hit Database Source	EST HUMAN			L	Į.	EST HUMAN	EST HUMAN	η	EST HUMAN	L	N-	T HIMAN	Т		HOMAN		닏	L	EST HUMAN	T	7		LN LN				LN	EST HUMAN		NT TN
	Top Hit Acession No.	0.0E+00 N36040.1	0.0E+00 N36040.1	4505458 NT	4505938 NT	4505938 NT	, –	T56945.1	450444 NT		450444 NT		0.0E+00 BE295973.1	0.0E+00 BE295973.1	0.05200	W 10875.1	0.0E+00 AF244088.1	PL163202.2	0.0E+00 AL163202.2	3E018970.1	3E018970 1	27.1	27.1	_	0.0E+00 AF273045.1	5.1		0.0E+00 AF167174.1	0.0E+00 AI587308.1		0.0E+00 AF195658.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 T56945.	0.0E+00 T56945	0.0E+00	0.0E+00 BF0368	0.0E+00	0.0E+00 AF1111	0.0E+00	0.0E+00	00+110	00.70	0.00+00	0.0=+00	0.0E+00	0.0E+00 BE0189	0.0E+00 BE0189	0.0E+00 AB0183	0.0E+00 AB0183	0.0E+00 D50659	0.0E+00	0.0E+00 AF27304	0.0E+00 AF16717	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.83	1.83	0.86	3.17	3.17	94.1	1.49	9.05	2.42	15.84	1.36	1.1	1.18	000	200	1.01	16.37	18.37	4.25	4.25	1.98	1.98	130.42	2.83	2.83	2.92	2.92	9.33	9.33	1.94
	ORF SEQ ID NO:	19907	19908	19913	19921	19922	19929	19930		19943		19946	19947	19947	19948	100/0	19949	7066	19953	19960	19961	19964	19965	19976	19981	19982	19984	19985	19991	19992	19994
	Exon SEQ ID NO:			10094	10100	10100	10108	10108	10121	10125	10127	10130	10132	10132	10133	10134	10137	121	10137	10145	10145	10150	10150	10159	10164	10164	10166	10166	12661	12661	10176
	Probe SEQ ID NO:	112	112	115	126	126	135	135	147	151	153	156	158	159	160	161	184		164	174	174	179	173	187	<u>5</u>	192	194	194	203	203	205

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Single Exon Probes Expressed in Heart

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Table 4
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Top Hit Descriptor	Homo sapiens potassium inwardiv-rectifiving channel subfamily. I member 15 (KCN) 115) mBNA	Homo sapiens potassium inwardiv-rectifying channal subfamily I mamber 15 (VCN) 145)	Homo saplens mRNA for KIAA1019 protein, partial cols	Homo sapiens mRNA for KIAA1019 protein partial cds	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, (CADT), phosphoribosylglycinamide synthetase, (CADT), phosphoribosylglycinamide synthetase, (CADT), phosphoribosylglycinamide synthetase, (CADT), phosphoribosylglycinamide synthetase, (CADT), phosphoribosylglycinamide synthetase, (CADT), phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase, ph	ZV8c06.11 Soares NhHMPU S1 Homo saniens china MACE 752004 F	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMO) OG 1) (HAZZAZ)	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAZSOS)	Homo saplens homonally upregulated neu timor-associated kinasa (Uli NK)	Homo sapiens hormonally upregulated neu fumor-associated kinase (HUNK) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLT4) mRNA	Homo sapiens moesin (MSN), mRNA	Homo sapiens X-box binding protein 1 (XBP1) mRNA	Human zinc finger protein zfo31 (zf31) mRNA partial cds	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo saplens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sepiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA) mRNA	Human mRNA for KIAA0184 gene, partial cds	Human mRNA for KIAA0184 gene, partial cds	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 51	Homo sapiens mRNA for KIAA1019 protein, partial cds	one IMAGE:2018457 3' similar to gb:X54199		Δ	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
Top Hit Database Source			H LN				T HUMAN				SWISSPROT TR	ISSPROT						王 N	H	H H	H			Ŧ		EST_HUMAN AU	Г	EST HUMAN PH	Т		
Top Hit Acession No.	4557029 NT	4557029 NT	0.0E+00 AB028942.1		6728	4503914 NT	0.0E+00 AA480002.1	4507152 NT	4507152 NT	0.0E+00 AF114488.1			TN 8127273	7657213 NT	5174574 NT	4505256 NT	4827057 NT	0.0E+00 U71600.1	0.0E+00 AF231919.1	0.0E+00 AF231919.1	0.0E+00 AF231919.1	4	. 4503854 NT			4	0.0E+00 AB028942.1	0.0E+00 Al363014.1	2.	4503680 NT	4503680 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 O14867	0.0E+00 O14867	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	5.26	5.26	. 4.03	3.11	5.3	1.99	2.03	13.28	9.68	2.23	6.0	6.0	4:18	2.31	3.67	0.86	3.76	0.8	2.15	2.15	3.4	0.89	1.4	1.37	1.52	1.13	5.35	1.01	3.43	1.38	2.04
ORF SEQ ID NO:		20075		20086		20087		20088	20088	i		20102	20103	20103	20115	20116	20120	20125	20129	20130	20131	20133	20136	20137	20137	20149	20188	20189	20156	20159	20160
Exan SEQ ID. NO:		10254	10265	10266	12664	10267	10268		10269	10273	10285	10285	10286	10286	10300	10301	10304	10307	10311	10311	12865	10313	10315	10316	10316	10326	10365	10366	10334	10336	10337
Probe SEQ ID NO:	290	290	301	302	303	304	305	306	307	311	324	324	325	326	341	342	345	348	353	353	354	356	358	320	380	372	384	382	387	330	394

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens IgG Fc binding protein (FC(GAMIMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMIMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMIMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMIMA)BP) mRNA	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	Homo sapiens ribosomal protein L19 (RPL19) mRNA	yg09a02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5'	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens SON DNA binding protein (SON) mRNA	Mus musculus truncated SON protein (Son) mRNA, complete cds	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA	EST27054 Cerebellum II Homo sapiens cDNA 5' end	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo saplens chromosome 21 segment HS21C046	Homo sapiens mRNA for KIAA1209 protein, partial cds	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'	PM0-DT0065-130400-002-c06 DT0065 Hamo sapiens cDNA	Novel human gene mapping to chomosome 1	Homo sapiens PC326 protein (PC326), mRNA	Homo sapiens chromosome 21 segment HS21C010	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'
	Top Hit Database Source	TN	TN	NT.	F	N	F	N	N	TN	EST_HUMAN	NT	TN	NT	Į.	LN.	F	EST_HUMAN	EST_HUMAN	IN	TN	TN	TN	IN	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	N FA	Į.	NT	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	4503680 NT	4503680 NT	4503680 NT	4503680 NT	4503680 NT	4503680 NT			4506608 NT	117795.1	4506728 NT	2.1	4507152 NT	4507152 NT	-	4557879 NT	2.1		4504532 NT	4504532 NT	4557887 NT	4557887 NT	0.0E+00 AL163246.2				0.0E+00 AU132898.1	0.0E+00 BE385144.1	0.0E+00 AW938825.1	Ę.	8923955 NT	.2		0.0E+00 BF028005.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00	0.0E+00 R17795.1	0.0E+00	0.0E+00 AB02894;	0.0E+00	0.0E+00	0.0E+00 AF193607	0.0E+00	0.0E+00 AA32426	0.0E+00 BE25444	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AL117233	0.0E+00	0.0E+00	0.0E+00 BE081527	0.0E+00
	Expression Signal	2.04	1.17	1.64	1.64	2.43	6.0	0.84	0.84	43.09	1.31	2.61	2.42	4.7	4.7	3.51	2.01	86.0	0.91	3.15	3.15	1.27	1.27	2.26	7.05	7.05	2.59	1.64	2.17	1.05	1.07	1.64	3.91	1.97	1.13
	ORF SEQ ID NO:	20161		20163	20164	20165	20166	20167	20168		19772						20206				20221		20229		20236				20250	20251	20253	20254			20273
	Exan SEQ ID NO:	10337	10338	10339	10339	10340	10341	10342	10342	10346	9981	10367	10368	10369	10369	10370	10382	10387	10388	10404	10404	10408	10408	10419	10420	10420	10428	10430	10438	12668	10440	10441	10450	12669	10462
	Probe SEQ ID NO:	391	392	393	393	394	395	968	396	400	414	422	423	424	424	425	438	443	444	460	460	465	465	475	476	476	485	487	495	496	498	499	508	515	220

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Most Similar			$\neg$		П				П	ē			T	٦						7	7	-	"Т	<del>د بری</del>	7	71	"	<u></u>	$\vdash$	اانسا	<del>}</del>	1
Exch BLAST E 10473         Most Similar Crop Hit Pub.         Top Hit Acession Signal         Most Similar Top Hit Acession Adules         Top Hit Database Source         Top Hit Source           10488         20280         1.16         0.0E+00         AB040909.1         NT           10471         20283         1.127         0.0E+00         AB040909.1         NT           10472         20284         3.96         0.0E+00         AF04036         NT           10473         20284         3.96         0.0E+00         AF04036         NT           10473         20284         3.96         0.0E+00         AF04036         NT           10474         20284         3.96         0.0E+00         AF04036         NT           10526         20286         1.79         0.0E+00         AF04036         NT           10529         20332         1.73         0.0E+00         AF04036         NT           10529         20336         1.65         0.0E+00         AF04086.1         NT           10534         20341         1.05         0.0E+00         AF04086.1         NT           10549         20351         1.05         0.0E+00         AF04086.1         NT           10540	bes Expressed in Heart	Top Hit Descriptor	Homo sapiens mBNA for KIA 4 4.76 motein mouth of	Homo sapiens transcription elements to protein, parties of the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same transcription elements to the same 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LO 1	Homo sapiens RGH1 gene, retrovirus-like element	Homo saplens ubiquinol-cytochrome creductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial profein mRNA	Human and incontribute A 1 (Ann A-1) come 4	601822627F1 NIH MGC 75 Home conjust of Nik 21 11 11 20 20 20 20 20 20 20 20 20 20 20 20 20	Homo sapiens acety-Coentring A certification has A Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled to the Controlled 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Homo sapiens low density lipoprotein-related protein 2 (LKP2), mRNA	Homo saniens fow density floorontein-related protein 2 (LATZ), mRNA	Z60c07.1 Soares hestis NHT Home sension only also and the contraction of	Homo sapiens RGH2 gene, retrovirus-like element	2h51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBUL IN PRECLIRSOR (HI MANN).	2h51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to	Homo sanjens novel SH2 contehing and the CORSON (HOMAN);	Homo saniens chitamate recentor involvation I I I I I I I I I I I I I I I I I I I	Homo sapiens CCAAT-box-binding francaings 6-11-70550	Human neutral amino acid transporter (ASCT4) accor (CDF2) mKNA	Homo saniene editimizatelium exchange indeas N.O. o N.O. v.	Homo sabiens sodium/calcium exchange isotorm NeCas (NCX1) mRNA, complete cds	Homo saplens protein kinase, X-linked (PRKX) mRNA
Exon         ORF SEQ ID ID NO: Signal         Most Similar Similar Signal         Most Similar Value         No. Hit Acession Value           10468         20280         1.16         0.0E+00         AB040909.1           10472         20284         3.96         0.0E+00         A504           10472         20285         3.96         0.0E+00         A504           10472         20286         3.96         0.0E+00         A504           10485         20296         3.96         0.0E+00         A504           10485         20296         3.96         0.0E+00         A504           10524         20296         3.75         0.0E+00         AF04388.1           10525         20332         1.79         0.0E+00         AF04388.1           10526         20332         1.75         0.0E+00         BF104898.1           10534         20342         1.05         0.0E+00         BF104898.1           10543         20343         1.05         0.0E+00         BF104898.1           10544         20343         1.05         0.0E+00         BF104898.1           10545         20343         1.05         0.0E+00         BF104898.1           10544         20345 <td>Jie Exon Pro</td> <td>Top Hit Database Source</td> <td>LZ.</td> <td>LZ.</td> <td>¥</td> <td>F</td> <td>LZ</td> <td></td> <td></td> <td></td> <td>F</td> <td>EST HUMAN</td> <td>LY</td> <td></td> <td>5</td> <td>Į.</td> <td> -</td> <td>  L</td> <td>5</td> <td>1</td> <td>   -  -</td> <td>ST HUMAN</td> <td>トフ</td> <td>ST_HUMAN</td> <td>NAMINAN</td> <td></td> <td> -</td> <td></td> <td><u></u></td> <td>1</td> <td></td> <td>П</td>	Jie Exon Pro	Top Hit Database Source	LZ.	LZ.	¥	F	LZ				F	EST HUMAN	LY		5	Į.	-	L	5	1	  -  -	ST HUMAN	トフ	ST_HUMAN	NAMINAN		-		<u></u>	1		П
Excn         ORF SEQ         Expression         Mose           SEQ ID         ID NO:         Signal         ID NO:           10468         20280         1.16           10472         20284         3.96           10472         20285         3.96           10472         20286         3.96           10472         20286         3.96           10477         20286         3.96           10485         20295         1.79           10529         20332         1.75           10529         20332         1.75           10524         20342         1.05           10534         20354         1.05           10548         20354         1.05           10549         20355         1.05           10540         20356         0.93           10541         20356         0.93           10542         20357         0.93           10543         20356         0.93           10544         20356         0.93           10560         20372         6.37           10561         20372         6.37           10562         20376         0.93 </td <td>Suic</td> <td>Top Hit Acession No.</td> <td></td> <td>6030</td> <td>4504036</td> <td>4504036</td> <td>18</td> <td>14.1</td> <td></td> <td>5174742</td> <td></td> <td>-</td> <td>1854</td> <td></td> <td></td> <td></td> <td>6918</td> <td>6806918</td> <td>6806918</td> <td>6806918</td> <td>6806918</td> <td></td> <td></td> <td></td> <td></td> <td>885526</td> <td>8009009 V</td> <td>5031624 N</td> <td></td> <td>1.</td> <td>_</td> <td>826947</td>	Suic	Top Hit Acession No.		6030	4504036	4504036	18	14.1		5174742		-	1854				6918	6806918	6806918	6806918	6806918					885526	8009009 V	5031624 N		1.	_	826947
Excn NO:         ORF SEQ ID NO:         Express Signs           NO:         ID NO:         Signs           NO:         10 468         20280         1           10472         20285         1         1           10472         20286         1         1           10472         20286         1         1           10472         20286         1         1           10529         20336         1         1           10529         20342         1         1           10529         20342         1         1           10529         20343         1         1           10529         20343         1         1           10534         20356         1         1           10548         20356         1         1           10549         20356         1         1           10560         20372         6         1           10564         20376         2         1           10564         20376         2         1           10564         20396         1         1           10579         20398         2		Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00 V	0.0E+00 V	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Exen ORI ORI ORI ORI ORI ORI ORI ORI ORI ORI			1.16	11.27	3.96	3.96	5.78	1.79	3.15	2.65	5.28	1.73	1.46	1.05	1.05	1.38	96.0	222	2.22	0.93	0.93	1.34	6.37	3.17	3.17	3.28	2.89	1.06	1.41	2.18	2.18	3.98
		ORF SEQ ID NO:								20318			20336	20342	20343	20351	20354	20355	20356	20357	20358	20368	20372	20375	20376		20388	20391	20395	20398	20399	20404
Probe SEQ ID NO: 526 530 530 531 544 544 561 607 607 607 607 608 603 603 603 604 604 604 604 604 604 604 604 604 604		Exon SEQ ID NO:				10472		10485	10495	10510	10522	10525	10529	10534	10534	10543	10546	10547	10547	10548	10548	10556	10560	10564	10564	10587	10574	10576	10579	10583	10583	10588
		Probe SEQ ID NO:	526	529	530	530	536	544	554	571	584	287	593	208	598	607	610	611	611	612	612	619	623	627	627	630	637	639	642	646	646	652

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Top Hit Descriptor	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Human endogenous retrovirus pHE.1 (ERV9)	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA	Homo sapiens mRNA for KIAA1089 protein, partial cds	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	np49d01.s1 NCI_CGAP_Br1.1 Homo saplens cDNA clone IMAGE:1129833 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);	Human von Willebrand factor gene, exons 23 through 34	Human von Willebrand factor gene, exons 23 through 34	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA	TCAAP1D0779 Pediatric acute myelogencus leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo	Homo canjone MHC class I antiqua (HI A.C.) mDNA DI A.C.4 allala completa add	Homo sapiens MHC class I antition (HI A-G) mRNA HI A-G1 allele complete cde	Homo sapiens chloride channel CLC4 (CIC4) mRNA, complete cds	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Homo sapiens mRNA for KIAA1339 protein, partial cds	Homo sapiens zinc finger protein 212 (ZNF212), mRNA	Homo sapiens mRNA for repressor protein, partial cds	601445647F1 NIH_MGC_65 Homo sapiens cDNA done IMAGE:3849803 5'	yl69g08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154046 5'	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Human mRNA for KIAA0184 gene, partial cds	Human mRNA for KIAA0184 gene, partial cds	H.sapiens mRNA for interferon alpha/beta receptor (long form)	Homo sapiens mRNA for KIAA0910 protein, partial cds	Homo sapiens mRNA for KIAA0910 protein, partial cds	Homo saplens pericentrin (PCNT) mRNA
Top Hit Database Source	ᅜ	뒫	뒫	ᅜ	¥	EST HUMAN	F	Ę	TN	NT	NT TN	E	E LIMAN	Т	Ę	N	NT	N-	NT.	N	NT	EST_HUMAN	EST_HUMAN		TN	NT	P	NT	NT		NT	
Top Hit Acession No.	4826947	X57147.1	4504424 NT	0.0E+00 AB029012.1	7657468 NT	0.0E+00 AA614537.1	M60675.1	M60675.1	5032192 NT	0.0E+00 AF264750.1	0.0E+00 AF264750.1	11545800 NT	0.0F±00 BE241577.1		10	-			0.0E+00 AB037760.1	6912749 NT		0.0E+00 BE869735.1	348915.1	5032086 NT	0.0E+00 AB011399.1	7661965 NT				.1	0.0E+00 AB020717.1	5174478 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M60675.1	0.0E+00 M60675.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	100+HO 0	0.05	0.0E+00	0.0E+00	0.0E+00 J03764.1	0.0E+00 J03764.1	0.0E+00	0.0E+00	0.0E+00 D30612.1	0.0E+00	0.0E+00 R48915.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D80006.1	0.0E+00 D80006.1	0.0E+00 X89772.1	0.0E+00	0.0E+00	0.0E+00
Expression Signal	3.98	0.95	4.56	4.35	2.03	19.46	7.66	7.66	1.45	3.89	3.89	9.78	4.7	1 42	1.12	2.4	1.55	1.55	0.78	1.12	0.81	2.17	3.38	2.4	1.58	2.97	1.17	1.17	2.64	2.37	2.37	6.84
ORF SEQ ID NO:	20405		20419	20423	20438	20450	20454	20455	20464	20470	20471	20474	20484	20505	20506	20507	20510	20511	20512	20513	20514	20515	20519	20520	20529	20533	20544	20545	20549	20553	20554	20560
Exon SEQ ID NO:	10588	12672	10601	10606	10615	10625	10629	10629	10639	10644	10644	10646	10851	10870	10670	10871	10674	10674	10878	10677	12676	10678	10682	10683	10692	10696	10705	10705	10710	10714	10714	10718
Probe SEQ ID NO:	652	658	667	672	682	692	969	969	202	712	712	714	710	730	95	740	743	743	745	746	747	748	752	753	762	765	775	775	780	784	784	789

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Table 4
Single Exon Probes Expressed in Heart

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Oligic Even Topos Expressed in Total	Top Hit Descriptor	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens T-cell lymphoma Invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasts 1 (TIAM1) mRNA	Homo sapiens sodium/myo-inosital cotransporter (SLC5A3) gene, complete cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens mRNA for KIAA0910 protein, partial cds	Homo sapiens mRNA for KIAA0910 protein, partial cds	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453	Inj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5	Homo sapiens hormonally upregulated neu fumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens chromosome 21 segment HS21 C003	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA	QV0-BT0703-280400-211-g11 BT0703 Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]	protein C Inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
ומקדווו ומק	Top Hit Database Source	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT.	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	M	M	TN	M	NT	EST_HUMAN	EST_HUMAN	NT	Z	NT	IN	NT	NT	IN
5	Top Hit Acession No.	4507500 NT	7657213 NT	7657213 NT		1.1	0.0E+00 AF108830.1	4503854 NT	4507500 NT	4507500 NT	1.1	2.1	7.	4507152 NT	2.1	4506728 NT	7.1	7.1	2.1	2.1	3F677694.1	7657213 NT	7657213 NT	7657213 NT	7657213 NT	1163203.2	0.0E+00 BE089592.1	3E089592.1	AL163203.2	4504958 NT	4504958 NT	AF089747.1	569364.1	569364.1	569364.1
-	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF108830	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF027153	0.0E+00 AB02894;	0.0E+00 AB02894;	0.0E+00	0.0E+00 AB02894	0.0E+00	0.0E+00 AB02071	0.0E+00 AB02071	0.0E+00 AA53327	0.0E+00 AA53327	0.0E+00 BF67769	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AL163203	0.0E+00	0.0E+00 BE08959	0.0E+00 AL16320;	0.0E+00	0.0E+00	0.0E+00 AF08974	0.0E+00 S69364.1	0.0E+00 S69364.1	0.0E+00 S69364.1
	Expression Signal	7.06	1.51	4.43	3.91	1.24	1.24	1.14	1.55	1.55	1.57	3.37	3.37	7.38	3.03	2.02	1.25	1.25	1.97	1.97	7.39	1.3	1.3	2.16	2.16	0.87	1.85	1.85	3.93	7.45	3.29	1.5	0.99		66.0
	ORF SEQ ID NO:		20581		20584	20590		20596	20601	20602		20613	20614	20615	20616	20617	20620	20621	20622	20623		20624	20625	20626	20627	20650	20655	20656				20673	20674		20676
	Exam SEQ ID NO:	10719	10736	10737	10739	10744	10744	10749	10752	10752	10759	10763	10763	10764	10765	10766	10770	10770	10771	10771	10772	10776		10777	10777	10799	10806	10806	L	10825	10825	10828	10829		10829
	Probe SEQ ID NO:	790	807	808	810	816	816	821	825	825	832	836	836	837	838	839	843	843	844	844	842	849	849	850	850	873	880	880	890	906	903	904	906	902	905

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	Homo sapiens thyrotrophic embryonic factor (TEF) mRNA	os98e03.s1 NCI CGAP GC3 Homo saplens cDNA clone IMAGE-1613404 3'	los98e03.s1 NCI CGAP GC3 Homo sabiens cDNA clima INACE-1613AAA 21	Homo saplens KIAA0929 protein Msv2 interaction purchast farmat Milham Msv2 interaction	Homo sapiens mRNA for PSP24, complete cds	PM2-GN0014-050900-001-f02 GN0014 Homo saniens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo saniens china	PM2-GN0014-050900-001-f02 GN0014 Homo saniens CDNA	Homo sapiens partial c-for gene, exons 2 and 3	Homo sapiens partial c-for gene, exons 2 and 3	Homo sapiens chromodomain protein, Y chromosome-like (CDYI.) mRNA	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	Homo sapiens 8q22.1 region and MTG8 (OBFA2T1) gene, partial cds	Homo sapiens 14q32 Jagged2 gene, complete cds: and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14d32 Jagged2 gene complete cds; and unknown need	Homo sapiens DKF2P586M/N122 nrotein (TNKF2P586M/N122)DNA	Homo saplens Inner membrane protein, milochondrial (miloflin) (MAAAT), mBNA	aa86g07.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8:
	Top Hit Database Source	Ā	¥	N N	Z Z	F	N N	뉟	FS	N	TN	EST HUMAN	EST HUMAN	- LV	ĮN.	EST HUMAN	EST HUMAN	EST HUMAN	N	Z L	NT	F	TN	TN	LΝ	Ę	Į.	TN	NT.	Ł	NT	NT	EST_HUMAN
	Top Hit Acession No.	1.28101.1	Z20656.1	Z20656.1	Z20656.1	Z20856.1	0.0E+00 M37190.1	M37190.1	M37190.1	4507430 NT	4507430 NT	0.0E+00 Al001948.1	0.0E+00 AI001948.1	7657266 NT	0.0E+00 AB030566.1	BF366974.1	BF366974.1		X52207.1	X52207.1	4757969 NT	J83668.1	J83668.1	J83668.1	AF198490.1	AF198490.1	AF111170.3	4F111170.3	AF111170.3	AF111170.3		5803114 NT	AA458680.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M37190.	0.0E+00 M37190.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF36697	0.0E+00 BF36697	0.0E+00 BF36697	0.0E+00 X52207.1	0.0E+00 X52207.1	0.0E+00	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 AF198490	0.0E+00 AF198490	0.0E+00 AF11117	0.0E+00 AF11117	0.0E+00 AF11117	0.0E+00 AF11117	0.0E+00	0.0E+00	0.0E+00 AA458680
	Expression Signal	2.14	105.13	105.13	167.64	167.64	36.3	13.25	53.71	1.9	1.9	2.48	2.46	7.21	2.52	4.64	4.64	4.64	127	. 127	1.25	1.05	7.48	6.69	1.99	3.49	0.84	1.43	1.81	2.23	228	2.66	1.94
	ORF SEQ ID NO:	20677	20680	20681	78907	20683		20707	20708	20709	20710	20717	20718	20720	20730	20736	20737	20738	20739	20740	20747	20755	20756	20756			20761	20761	20761	20762	20765	20769	
	Exon SEQ ID NO:	10830	10833	10833	10834	10834	10860	10861	10862	10863	10863	12681	12681	10872	10882	10890	10890	10890	10891	10891	10900	10910	10911	10911	10914	10914	10917	10917	10917	10918	10921	10925	10927
	Probs SEQ ID NO:	906	606	606	910	910	935	936	937	938	938	946	946	948	626	296	296	296	896	898	226	888	686	066	88	994	997	866	566	1000	1003	1007	1009

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor  EST5/124 WATMI Homo septens cDNA clone 5/124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTX or p) (EST5/124 WATMI Homo septens cDNA clone 5/124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTX or p) (EST5/124 WATMI Homo septens cDNA clone 5/124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTX or p) (alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Ser and Pro with BLASTX or p) (Alignment Septens RNA) (Alignment Septens Nypotherical protein FLJ20695 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20695 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20696 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20696 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20696 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20696 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20696 (FLJ20695), mRNA (Alignment Septens Pypotherical protein FLJ20696 (FLJ20695), mRNA (Alignment Septens Pypotherical protein RLJ2099 (FLJ20309), mRNA (Alignment Septens Potein Minase X-Kilnked (PRKX) mRNA (Alignment Septens Potein Minase X-Kilnked (PRKX) mRNA (Alignment Septens Potein Minase X-Kilnked (PRKX) mRNA (Alignment Septens BNA for Human P2XM, complete ods (Alignment Septens BNA for Human P2XM, complete ods (Alignment Septens BNA for Human P2XM, complete ods (Alignment Septens MynAB-Human P2XM, complete ods (Alignment Septens MynAB-Human P2XM, complete ods (Alignment Septens MynAB-Human P2XM, complete ods (Alignment Septens MynAB-Human P2XM, complete ods (Alignment Septens MynAB-Human P2XM, complete ods (Alignment Septens MynAB-Human P2XM, complete ods (Alignment P2XM, complete ods (Alignment P2XM, complete ods (Alignment P2X
Top Hit EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1 Homo sa EST51i24 WATM1
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Most Similar (Top Hit BLAST E Natus   Valus   Valus   0.0E+00 N43182.   0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+00    0.0E+
Signal Signal 1.04 1.04 1.04 1.04 1.04 1.04 1.04 1.04
20774 20775 20776 20777 20808 20872 20872 20872 20873 20873 20873 20873 20873 20873 20873 20873 20887 20887 20887 20887 20887 20887 20887 20887
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Probe SEQ ID NO: 1012 1013 1053 1053 1053 1053 1053 1053 1053

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Table 4
Single Exon Probes Expressed in F

σ	Single Exon Probes Expressed in Heart	 1 11074 20920 1.02 0.0E+00 45578R7 NT Home sentions location to AVENTARY - 100 0.0E+00	11101 1.13 0.0F+00 Z6K7236NT	11116 20962 1.14 0.0E+001AE264750.1 NIT	11116 20963 1.14 0.0F+00 AF264750 1 NT	11117 20964 1.31 0.0E+00 AF264750.1	12687 20965 0.95 0.0E+00 AF264750.1 NT	11134 20988 3.62 0.0E+00 AF109718,1 NT	11135 20989 1.3 0.0E+00 4503098 NT	11152 1.48 0.0E+00 Y18000.	11160 21009 45.69 0.0E+00 4506718 NT	11167 21018 3.66 0.0E+00 AF084479.1 NT	11173 21022 1.71 0.0E+00 AB040940.1 NT	11173 21023 1.71 0.0E+00 AB040940.1 NT	11186 21036 6.42 0.0E+00 5174748 NT	11186 21037 6.42 0.0E+00 5174748 NT	11186 21038 6.42 0.0E+00 5174748NT	11187 2.6 0.0E+00 AF096156.1 INT	12689 21050 1.1 0.0E+00 7657529 NT	12689 21051 1.1 0.0E+00 7657529INT	11202 21057 1.71 0.0E+00	11203 21058 0,82 0.0E+00 4508004 NT	11205 21059 1.07 0.0E+00 5803146 NT	11207 21061 4.1 0.0E+00/AB011149.1 NT	21062 1.06 0.0E+00 7661965 NT	21063 4.64 0.0E+00 7681965 NT	11210 21064 4.1 0.0E+00 8567387 NT	11210 21065 4.1 0.0E+00 8567387 NT	11221 21078 1.35 0.0E+00 M14123.1 NT	11291 21147 0.89 0.0E+00 AJ250014.1 NT	21156 9.13 0.0E+00 AJ277892.1 NT	21160 0.96 0.0E+00 Al208756.1 EST_HUMAN	21161 8.18 0.0E+00 6042206 NT
Probe Exon NO: NO: NO: NO: NO: NO: NO: NO: 1161 1110 1110 1110 1110 1110 1110 111	-		Щ	L					$\perp$					$\perp$	$\perp$	_!		_	[			$\Box$	_	_				- 1	I.				

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements	Homo sapiens alpha1-6fucosytransferase (alpha1-6FucT) gene. exon 7	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Human nebulin mRNA, partial cds	Human nebulin mRNA, partial cds	Novel human gene on chromosome 20	Novel human gene mapping to chomosome 1	Human mRNA for KIAA0240 gene, partial cds	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Homo sapiens RFB30 gene for RING finder protein	Human von Willebrand factor pseudogene corresponding to excus 23 through 34	Human von Wilebrand factor bseudogene corresponding to evons 23 through or	Homo saplens hHDC for homolog of Drosophila headcase (LOC51696) mRNA	aa34a03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE-815116 5'	Cercopithecus aethiops cyclophilin A mRNA, complete cds	Cercopithecus aethiops cyclophilin A mRNA, complete cds	Bowine mRNA for neurocalcin	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	Homo sapiens transmembrane ofvcoprotein (GPNMR) mRNA	Homo sapiens transmembrane divoprotein (GPNMB) mRNA	Homo sapiens KIAA0957 protein (KIAA0957), mRNA	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA	Human transglutaminase mRNA, complete cds	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo saplens ribosomal protein L5 (RPL5) mRNA
Jie Exon Pro	Top Hit Database Source	뉟	N-	님	노	Z Z	Z	TN	N N	IN	NT	NT	NT	N-	FX	NT.	F	IN	Z	IN	LA	EST HUMAN	LN TN	TN	NT	IN	Ę	5	F	5	LN	トフ	トフ	<u></u>
illo	Top Hit Acession No.	4505646 NT	4505646 NT	7705565 NT	7705565 NT		0.0E+00 AF038280.1	4507720 NT	4507720			9.1	1.1		6912457 NT	7661965 NT	7661965 NT			_	7706434		0.0E+00 AF023860.1	1.1			4505404	4505404 NT	7662405 NT	7656972 NT	M98478.1	4507720 NT	4507720 NT	4506654 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AJZ38093	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U35637.1	0.0E+00 U35637.1	0.0E+00	0.0E+00 AL13776	0.0E+00 D87077.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y07829.2	0.0E+00 M60676.	0.0E+00 M60676.	0.0E+00	0.0E+00 AA48117	0.0E+00	0.0E+00 AF023860	0.0E+00 D10884.1	0.0E+00 U78027.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.4	1.4	2.54	2.54	5.25	3.51	9.7	9.7	1.02	1.02	3.05	1.03	1.22	4.97	1.51	1.51	76.0	3.65	3.65	1.32	0.95	11.95	11.95	0.97	2.03	3.9	3.9	3.12	8.41	5.02	5.75	5.75	10.12
	ORF SEQ ID NO:	21173	21174	21177	21178		21192	21203			21209	21214	21215			21225	21226		21231	21232	21259	21273	21276	21277	21280		21283	21284	21285		21289	21291	21292	
	Exon SEQ ID NO:	11312	11312	11314	11314		11327	11337	11337	11342	11342	11350	11352	11356	11359	11361	11361	11362	11367	11367	11399	11414	11420	11420	11422	11424	11425	11425	11426	11427	11432	11435	11435	12697
	Probe SEQ ID NO:	1407	1407	1409	1409	1412	1421	1432	1432	1437	1437	1445	1447	1451	1454	1456	1456	1457	1462	1462	1495	1509	1515	1515	1517	1519	1520	1520	1521	1522	1527	1530	1530	1531

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Jingle Exoli Flobes Expressed in Heart	Top Hit Descriptor	Homo sapiens FOXJ2 forkhead factor (I OC55810) mBN (	Human hepatrovite drowth factor gene even 15	Human hepatocyte growth factor cane gover 45	Homo sabiens RNA binding motifications of the management of the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same for the same 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sapiens activating transcription factor 4 (fax-responsive enhancer element Bezy (ATEA)	John Continue and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state 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of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of	Homo sapiens imminoalchin simoaforaili.	Homo saplens imminoalchin supertaniny, member 3 (1937-3) mKNA, and translated products	Homo sabiens Refine derived DOI Lidomein forter 4 (DDE 4)	Homo sapiens Retina-derived POU-domain factor-1 (RPE-1), mixtyA		Troing septens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Homo sepiens potassium voltage-gated channel Shab-related subfamily months.			anjon of Miles in the Constant of Miles and Inc.	
שוני בייטיו בייטי	Top Hit Database Source	IN	LN L	I-X	Z	TN	N	۲	NT	Į	TN	ŢN	TN	T HUMAN		L	Ł		LN L										IN	LN LN	EST HUMAN	П
5	Top Hit Acession No.	8923841 NT	M75980.1	M75980.1	4826973 NT	AB026542.1	594400.1	11545911 NT	AF273841.1		4557556 NT	4557556 NT			4505332 NT		\B002331.1		4502264 NT	4502264 NT	4502264	4504626 NT	4504626 NT	6005855 NT	6005855 NT	TM SEZECT	60 10201	4826783 NT			5.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 M75980.1	0.0E+00 M75980.1	0.0E+00	0.0E+00 AB02654;	0.0E+00 S94400.1	0.0E+00	0.0E+00 AF273841	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U63963.1	0.0E+00 W76571.	0.0E+00	0.0E+00 U14967.1	0.0E+00 AB00233		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+0.0		0.0E+00	0.0E+00 U07147.1	0.0E+00 U07147.1	0.0E+00 AW207280	0.0E+00 AW207280
	Expression Signal	4.65	1.02	1.02	1.43	2.59	2.6	0.87	1.75	13.81	6.0	6.0	1.23	1.13	3.89	7.25	4.6		4.34	4.34	4.34	1.04	1.04	10.22	10.22	3.19		3.19	4.52	4.52	1.47	1.47
	ORF SEQ ID NO:		21448	21449		21460			21481			21518	21521		21525	21538	21541		21342	21543	21544	21558	21559	21586	21567	21576		21577	21578	21579	21584	21585
	Exon SEQ ID NO:		11579					_		- 1	[		11651	11654	12704		11666	L	200	11667	11667	11680	11680	11691	11691	11701		173	11702	11702	11706	11706
	Probe SEQ ID NO:	1672	1677	1677	1680	1685	1687	1699	1710	1745	1749	1749	1751	1754	1755	1765	1767	4780	8	1768	1768	1781	1781	1793	1793	1804		1804	1805	1805	1809	1809

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Single Exor Probes Expressed in Heart	Top Hit Descriptor	601179164F1 NIH MGC 20 Homo seriens cDNA clone IMA GE-3547239 F	601179164F1 NIH MGC 20 Homo saniens cDNA clore MAGE:3647239 E	RC2-BN0126-200300-012-b04 BN0126 Home series CDNA	Homo saplens RAD1 (S. pombe) homology (RAD1) mBNA and females and	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA and translated models	Homo saplens DNA polymerase zata catalytic submit (REV3) mRNA Ammerica.	Human transglutaminase mRNA, complete cds	Human transglutaminase mRNA, complete cds	Homo sapiens transforming growth factor, beta 3 (TGFR3) mRNA	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	Human topicismerase   pseudorene 1	Homo sanjens, hukron-hijin eukfemilu 3. mombar 40./0Thio.ko	Homo saplens histidine ammonia-lyase (HAI) mRNA	Homo sapiens histidine ammonia-lyase (HAL) mRNA	Homo sapiens chromosome 21 segment HS21 Ch52	Homo sapiens nebulin (NEB), mRNA	Homo sapiens nebulin (NEB), mRNA	Homo sapiens actinin, alpha 4 (ACTN4) mRNA	Homo saplens actinin, alpha 4 (ACTN4) mRNA	Homo sapiens mRNA for KIAA0790 protein, partial cds	Homo sapiens mRNA for KIAA0790 protein, partial cds	Human TFEB protein mRNA, partial cds	Human TFEB protein mRNA, partial cds	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE-2670013.3"	X69b01 X1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE: 2570043 3	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA	H. saplens genes for semenodelin I and semenodelin II	H.sapiens genes for semenodelin I and semenodelin II	Homo sapiens mRNA for KIAA1513 prodein partial cds	Homo saplens SMCY (SMCY) gene, complete cits	Homo sapiens SMCY (SMCY) gene, complete cds	
Jie Exon Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	N-	LN FN	¥	Į.	Ł	N F	N N	LN LN	Į.	LN	Į.	R	NT	NT	NT	Z	FN	IN	ΝΤ	NT	NT	EST_HUMAN	Г			LN N					
CIIC	Top Hit Acession No.	0.0E+00 BE277465.1	0.0E+00 BE277465.1	0.0E+00 BE006292.1	4506384 NT	4506384 NT		M98478.1	M98478.1	4507464 NT	4507464 NT	0.0E+00 AF240786.1		5901905 NT	4809282 NT	4809282 NT	AL163252.2	716	8400716 NT	4826638 NT	4826638 NT	3.1	3.1				0.0E+00 AW193024.1	6912457	6912457 NT			3.1	-	Ξ.	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF15747	0.0E+00 M98478.	0.0E+00 M98478.	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M55632.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB01833	0.0E+00 AB01833	0.0E+00 M33782	0.0E+00 M33782.1	0.0E+00 /	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z47556.1	0.0E+00 Z47556.1	0.0E+00 AB040946	0.0E+00 AF273847	0.0E+00 AF27384	
	Expression Signal	2,08	2.08	0.99	3.52	3.52	1.65	4.06	4.06	2.28	2.28	5.25	1.0	96:0	1.97	1.97	1.12	1.15	1.15	8.13	8.13	121	121	2.01	2.01	1.33	1.33	8.4	8.4	0.92	0.92	2.31	0.86	0.86	
	ORF SEQ ID NO:		21604	21623	21651	21652		21661	21662	21669	21670			21678	21685	21686		21700	21701	21702	21703	21715	21716	21720	21721	21722	21723	21724	21725	21727	21728	21737	21759	21760	
	Exon SEQ ID NO:	11729	11729	11748	11777	11777	11785	12707	12707	11790	11790	11794	11799	12708	11808	11808	11819	11821	11821	11822	11822	11832	11832	11838	11838	189	11840	11841	11841	11843	11843	11850	11868	11868	
	Probe SEQ ID NO:	1832	1832	1852	1881	1881	1889	1890	1890	1895	1895	1898	1903	1905	1913	1913	1924	1926	1926	1927	1927	1937	1937	1943	1943	1945	1945	1946	1946	1948	1948	1955	1975	1975	

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Single Exon Probes Expressed in Heart

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Single Exoli Flores Expressed III realt	Top Hit Descriptor	601573895F1 NIH_MGC_9 Homo sepiens oDNA done IMAGE:3835198 5	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5	Homo sapiens coagulation factor IX (plasma thrombopiastic component, Christmas disease, hemophilia B) (F9) mRNA	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA	HSC0IC021 normalized infant brain cDNA Homo sapiens cDNA clone c-0ic02	qv90f08.x1 NCI_CGAP_Utz Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive	SOLARET AND MCC SO Users This Island Construction	COLTAGE TWILL MISCOULD SEPTEMS CLINA CIGHE INVICE: 388//4/ 5	601902604F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5	OU ISOZOVAT I NIN _MOV_ IS NOMO SEPTEMS CLIVIA CIGNE IMAGE:4135320 5	rest of 13-270700-022-d10 C10413 Home sapiens cDNA	RC3-C10413-270700-022-d10 CT0413 Homo sapiens cDNA	Human plasma membrane calcium A TPase isolom 2 (APT 252) mKNA, comiete cds.	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA	Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) denes, complete cds	IL3-CT0219-271099-022-G10 CT0219 Homo sepiens cDNA	QV-BT065-020399-092 BT065 Homo saplens cDNA	QV-BT065-020399-092 BT065 Hamo saplens cDNA	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like	Human DNA-binding protein mRNA, 3'end
die Exoli Fior	Top Hit Database Source	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	LN	N L	EST_HUMAN	EST_HUMAN	· LN	IN	EST_HUMAN		EST HUMAN	TOT TOTAL	EST HUMAN	EST TOWNS	ESI_HUMAN	EST_HUMAN	ĮN.	NT	EST_HUMAN	NT	EST_HUMAN		IN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	LN L
IIO	Top Hit Acession No.	BE743215.1	BE743215.1	4503648 NT	AU140831.1	7705565 NT	7705565 NT	0.0E+00 AA077589.1	0.0E+00 AA077589.1	7657468 NT	4585863 NT	242399.1	7 67077018	RIZ44Z41.1	DEDITES.1	0.0E+00 BF315325.1	0.0E-100 DI 31353.1	DE09/ 123.1	0.0E+00 BE697125.1	00620 1	4758489 NT	0.0E+00 BE767964.1	0.0E+00 AF018963.1	3F027562.1	4503756 NT	0.0E+00 AF240786.1	0.0E+00 AW752708.1	0.0E+00 AI904640.1	A1904640.1	7657252 NT	
	Most Similar (Top) Hit BLAST E Value	0.0E+00 BE74321	0.0E+00 BE74321	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z42399.1	00,100	0.0E+00 AIZ44Z47	0.01.100	0.01+00	0.01100	0.05+00	0.0E+00 BE69712	0.0E+00   00620 1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF02756	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A1904640	0.0E+00	0.0E+00 L14787.1
	Expression	1.09	1.09	0.96	5.46	1.01	1.01	1.95	1.95	2.34	1.6	0.92	2	- C	1	2	5 6	7,77	2.42	2.53	1.32	2.63	1.13	3.09	2	0.99	1.16	1.96	1.96	1.19	1.6
	ORF SEQ ID NO:	21793	21794	21795	21796	21177	21178	21798	21799			21802		21841		21813	07876	21013	21820	21827	21831			21854	21855	21856	21857	21859	21860	~	
	Exan SEQ ID NO:	11903	11903	11905	11906	11314	11314	11908	11908	11910	11912	11913	44045	11020	44000	11922	11028	1 1320	11926	11931	11936	11957	11958	11960	11961	11963	11964	11966	11966	12001	12020
	Probe SEQ ID NO:	2011	2011	2013	2014	2015	2015	2017	2017	2019	2021	2022	7000	2020	1000	2031	2035	2002	2030	2040	2045	2067	2068	2070	2071	2073	2074	2076	2076	2112	2132

Page 373 of 413 Table 4 Single Exon Probes Expressed in Heart

		Т	-	Т	1	_	7	7	_	_	$\overline{}$	_	Т					- 19		-بىن	-11-	_		-	-		*	<del></del>	<u></u> -			<del>11. 11. 1</del> 1
Single Exon Probes Expressed in Heart	Top Hit Descriptor	601122338F1 NIH MGC 20 Homo sabiens cDNA clone IMAGE 3346688 F	Human mRNA for KIAA0244 gene, partial cds	AV738288 CB Homo sapiens cDNA clone CBNBDF08 5'	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'	oo32e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896.3'	Human apolipoprotein B-100 (aboB) dene, exons 22 through 29	602014829F1 NCI_CGAP_Bm64 Homo sabiens cDNA clone IMAGE-4150734 51	601572186T1 NIH MGC 55 Homo sapiens cDNA clone IMAGE:38300123	CM1-TN0141-250900-439-b08 TN0141 Homo saplens cDNA	CM1-TN0141-250900-439-b08 TN0141 Homp segiens cDNA	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5	bb84e02.yi NIH MGC_10 Homo sapiers cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN	2653c07.s1 Scares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to qb:X65857 cds1 OLFACTORY RECEPTOR-I IKE PROTEIN HOMBOTE (ULIMANIA)	263007.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to ab:X65867 adst Ot FACTORY RECEDENCE IME PEDATEIN IMPAGE:486540 3' similar to	Homo sapiens chromosome 21 seriment HS21Ch04	Homo sapiens chromosome 21 segment HS21CD04	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Human beta-prime-adaptin (BAM22) gene, exon 16	Homo sapiens E1A binding protein p300 (EP300) mRNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5	601495208F1 NIH MGC 70 Homo saplens cDNA clone IMAGE:3807457 FI	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5	Homo sapiens mRNA for KIAA1363 protein, partial cds	Homo sapiens differentially expressed in FDCP (mouse homolon) 6 (DEFR) mRNA	Homo saplens differentially expressed in FDCP (mouse homolog) 6 (DEER) mDNA	oz09c07.x1 Soares fetal liver spleen 1NFLS S1 Homo saniens cDNA clone IMAGE 1877/879	ZV78a11.r1 Soares total fetus Nb2HF8 9w Homo saniens cDNA clone MAGGE-7507An F	zv78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE-75:0740.5	602021846F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157339 5'
Jie Exon Pro	Top Hit Database Source	EST HUMAN	Į.	EST HUMAN	EST HUMAN	EST_HUMAN	₽ E	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Z	Z.	Į.	LZ	N P	Z	۲۲.	EST_HUMAN	EST_HUMAN	EST_HUMAN	N F	F	ラ	EST_HUMAN	EST_HUMAN	EST HUMAN	ST_HUMAN
Sing	Top Hit Acession No.	0.0E+00 BE274696.1		0.0E+00 AV738288.1	0.0E+00 AV738288.1	1.1							0.0E+00 BE018750.1	3.1	3.1	4.2	4.2	7662401	7662401 NT	-	4557556 NT	7662401		3.1		0.0E+00 AB037784.1	11545748 NT	11545748 NT	1.	-:	1.1	-
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 D87685	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M19828.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF31361	0.0E+00	0.0E+00 AA04281	0.0E+00 AA04281	0.0E+00 AL16320	0.0E+00 AL16320	0.0E+00	0.0E+00	0.0E+00 U36264.	0.0E+00	0.0E+00	0.0E+00 BE89528	0.0E+00	0.0E+00 BE90556	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI076404	0.0E+00 AA42900	0.0E+00 AA42900	0.0E+00 BF34703
	Expression Signal	1.02	1.09	10.46	10.46	1.4	6.0	17.1	11.29	2.35	2.35	1.77	1.92	0.92	0.92	2:32	2:32	2.63	2.63	1.04	7.56	1.44	1.09	0.87	0.87	1.36	4.16	4.16	2.51	2.21	2.21	2.23
	ORF SEQ ID NO:	21922	21925	21926	21927	21929		21933	21934	21937	21938	21943	21946	21947	21948	21956	21957	21958	21959		21984	21988	21996	21999	22000	22002	22034	22035	22036	22038	22039	22041
	Exon SEQ ID NO:	12026	12028	12029	12029	12031	12033	12036	12037	12040	12040	12714	12046	12047	12047	12055	12055	12056	12056	12061	12080	12086	12093	12096	12096	12098	12137	12137	12138	12140	12140	12142
	Probe SEQ ID NO:	2138	2140	2141	2141	2143	2145	2148	2149	2152	2152	2156	2159	2160	2160	2168	2168	2169	2169	2174	2193	2199	2206	2209	2209	2212	2253	2253	2254	2256	2256	8077

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					21.1.1.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	Ongre Lyon Flores Lypressed III near
유 ^교	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	22047	1.19	0.0E+00	0.0E+00 L02840.1	Ε	Homo saplens potassium channel Kv2.1 mRNA complete cds
	22048	2.03	0.0E+00	6325466 NT	님	Homo saplens flavin confaining monooxygenase 3 (FMO3), mRNA
	22054	<del>-</del>	0.0E+00	0.0E+00 BE676095.1	EST HUMAN	7f22a02.xt NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:094939 O94939 KIAA0857 PROTEIN :
	22056	10.08	0.0E+00		F	Homo sapiens phosphorylase kinase alpha submit (PHKA2) gene axm 32
	22057	272	0.0E+00	0.0E+00 AI625542.1	EST HUMAN	ty57c08.x1 NCI CGAP Utz Homo saplens cDNA clone IMAGE-2283482 31
	22061	1.76	0.0E+00		님	Homo saplens sperm specific antigen 2 (SSFA2), mRNA
	22062	1.76	0.0E+00	5803178 NT	Σ	Homo saplens sperm specific antiden 2 (SSFA2), mRNA
	22072	4.28	0.0E+00	0.0E+00 AF058332.1	F	Homo saplens titin (TTN) gene, alternative splice products partial cde
	22073	4.26	0.0E+00	2.1	Ę	Homo sapiens titin (TTN) gene, afternative splice products, partial cite
	22079	2.88	0.0E+00	5174678	F	Homo sapiens signal regulatory protein, beta 1 (SIRP-RFTA-1) mRNA
	22083	1.75	0.0E+00	0.0E+00 AU131142.1	EST HUMAN	AU131142 NT2RP3 Homo sapiens CDNA clone NT2RP3002084 5'
		5.71	0.0E+00		EST HUMAN	601586843F1 NIH MGC 7 Homo sanians CONA clans MAGE:2044662 5:
	22084	0.98	0.0E+00	0.0E+00 AW867076.1	EST HUMAN	MR1-SN0033-120400-002-e04 SN0033 Homo sanieps c DNA
	22085	1.97	0.0E+00		7662017 NT	Homo saplens KIAA0244 profein (KIAA0244) mRNA
	22086	1.44	0.0E+00	4758497 NT	N _T	Homo saplens hexose-6-phosphate dehydrogenase (ducose 1-dehydrogenase) (HRPD)
	22087	1.44	0.0E+00	4758497 NT	Ę	Homo sapiens hexose-6-phosphate dehydrogenase (dlucose 1-dehydrogenase) (HRPD) mRNA
						Homo saplens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete ods: and cytochrome P450 polypeptide 5 (CYP3A7) genes, complete ods: and cytochrome D450
		2.31	0.0E+00	Σ.	K	polypeptide 5 (CYP3A5) gene, partial cds
	22088	7.57	0.0E+00		EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
	22089	7.57	0.0E+00		EST HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
	22090	7.57	0.0E+00	0.0E+00 AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
- 1		0.96	0.0E+00	0.0E+00 BE814424.1	EST_HUMAN	MRO-BN0070-090600-029-d12 BN0070 Homo saniens cDNA
- 1	22138	1.34	0.0E+00 AU11958;		EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5
		3.64	0.0E+00)	0.0E+00 AI042035.1	EST HUMAN	ox60b02x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:008662 008662 230KDA PHOSPHATIDY INOSITOLAKINASE
	22444	0	0			xv15f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone IMAGE:2813221 3' similar to TR:054924
	4141	0.88	0.0=+00		П	054924 EX084. ;
	1	203	0.05+00		П	601432608F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3918168 57
		1.69	0.0E+00 AB00562	7.	T_HUMAN	AB005622 HeLa cDNA (T. Noma) Homo sapiens cDNA similar to adenylate kinase ispoyune 2
	22168	5.63	0.0E+00	6006002 NT		Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 24 (GRIN2A) mRNA
	22162	2.48	0.0E+00 D85606.1			Homo sapiens gene for chalecystokinin type-A receptor, complete cds
	22163	2.48	0.0E+00 D85606.1		LN	Homo sapiens gene for chalecystokinin type-A receptor, complete cds

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Table 4
Single Exon Probes Expressed in Heart

	_			_	_	_			_			_			_		-				- 4		11	_		السه			تـــــــــــــــــــــــــــــــــــــ	سيد	311	ساف	<u></u>	<u>, , , , , , , , , , , , , , , , , , , </u>
Top Hit Descriptor	Homo saplens Immunoalchuiln-like transcript 1c variant 4 /II T1c) game and 6	602018058F1 NCI CGAP Brief Homo sapiens cDNA clone IMACE: 4153870 F	Homo sapiens collagen, type XII, alpha 1 (COI 1241), mRNA	CM0-MT0033-150600-428-h11 MT0033 Homo seniens cDNA	CM0-MT0033-150800-428-h11 MT0033 Homo saniens cDM4	602184558T1 NIH MGC 42 Homo sepiens cDNA clone IMAGE-4300383 2	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMACE 2872756 21	UI-HF-BP0p-ais-c-07-0-UI-r1 NIH MGC 51 Homo saniens con a clare IMAGE 20222200 E1	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (DDK 6.62) mBNA	Homo sapiens protein kinase. AMP-activated, alpha 2 catalviris subunit (DDVAAA), Daya	RC3-ST0197-300300-016-004 ST0197 Home saniens cDNA	601592530F1 NIH MGC 7 Homo saciens CDNA done IMAGE 3048519 F	Homo saplens death receptor 6 (DR6), mRNA	UI-H-BI4-aoz-b-08-0-UI st NCI CGAP Sub8 Homo saniens cDNA clans MACE:3085525 2	Homo saplens mRNA for membrane transport protein (XK gens)	Homo sapiens platelet-derived growth factor recentor-like (PDCSER) mRNA	601503356F1 NIH MGC 70 Homo seniens CDNA clans IMAGE 2006448 FI	Homo sapiens similar to rat integral membrane altronomiain DOM434 / DOM434141	RC4-HT0276-160200-013-405 HT0276 Home saniens CDNA	Homo sapiens hypothefical protein FI. 120366 (FI. 120366) m. DNA	Human Sec62 (Sec62) mRNA, complete cds	601508211F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE 3909866 F	601489241F1 NIH MGC 69 Homo sapiens cDNA clone IMAGE 3891371 5'	601489241F1 NIH_MGC_69 Homo saptens cDNA clone IMAGE:3891371 5:	Homo sapiens adlican mRNA, complete cds	601064738F1 NIH MGC 10 Homo sabiens cDNA clone IMAGE-2451161 5'	AU143277 Y79AA1 Homo saplens cDNA clone Y79AA1001673 57	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5	601105312F1 NIH MGC 15 Homo sepiens cDNA clime IMAGE: 3087066 El	601105312F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE - 20872655 FT	7q27h12x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:000246 000246	Homo saniens adlicen mDNA consolete - J-	2011/2 Septens autical Illinum, complete cas	Common Mind Middle Septens active come IMAGE:3529159 5
Top Hit Database Source	Į.	EST HUMAN	F	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN LN	N.	EST HUMAN	EST HUMAN	N	EST HUMAN	IN	NT	EST HUMAN	1	EST HUMAN	Ί	N	EST_HUMAN	EST_HUMAN	T_HUMAN	LN	EST HUMAN	Г	Γ	EST HUMAN	Г		Т	T HI IMANI	٦
Top Hit Acession No.	AF106275.1	BF345274.1	5729777 NT	0.0E+00 BE831003.1	0.0E+00 BE831003.1	0.0E+00 BF569144.1	AW 466922.1	AW501010.1	5453965	5453965 NT	4W813853.1	3E795542.1	7657038,NT	0.0E+00 BF509482.1		5453871 NT	8.1	7657468 NT	BE150865.1	8923340 NT		0.0E+00 BE886490.1	1.1	1.1	5.1	3E536921.1	7.1	7.1	5.1	3.1	•			
Most Similar (Top) Hit BLAST E Value	0.0E+00 AF10627	0.0E+00 BF34527	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW4669	0.0E+00 AW5010	0.0E+00	0.0E+00	0.0E+00 AW8138	0.0E+00 BE79554	0.0E+00	0.0E+00	0.0E+00 Z32684.2	0.0E+00	0.0E+00 BE91037	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U93239.1	0.0E+00	0.0E+00 BE87551	0.0E+00 BE87551	0.0E+00 AF24550	0.0E+00 BE53692	0.0E+00 AU14327	0.0E+00 AU14327	0.0E+00 BE292890	0.0E+00 BE292890	0 0F+00 BF233044	0.0E+00 AF24550	0.0E+00 BE29661	
Expression Signal	2.28	0.98	3.95	0.87	0.87	2.27	2.66	3.45	2.08	2.08	2.35	16.13	1.18	1.8	2.25	29:9	1.99	1.96	55.78	1.14	3.21	1.64	4.39	4.39	0.97	1.27	3.8	3.8	1.19	1.19	00.0	7.65	1.05	
ORF SEQ ID NO:				22188			22201	22202	22219	22220					22236		22239	22240	22241	22242	22243	22249	22255	22256	22259	22267	22274	22275	22276	22277	22278	22280	22304	
Exon SEQ ID NO:	12276					_	12305	12307	12321	12321	12334	12339	11792	12340	12343	12345	12347	12348	12349	12350	12351	12357	12361	12361	12363	12379	12383	12383	12384	12384	12385	12388	12414	
Probe SEQ ID NO:	2398	2402	2410	2414	2414	2419	2428	2430	2444	2444	2457	2462	2463	2464	2467	2469	2471	2472	2473	2474	2475	2481	2486	2486	2488	2504	2509	2509	2510	2510	2511	2514	2540	

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	Top Hit Descriptor	Homo sapiens mRNA for KIAA1415 protein, partial cds	Homo sapiens mRNA for KIAA1415 protein, partial cds	UI-H-BW1-amp-f-12-0-UI.s1 NCI_CGAP_Sub7 Hamo saplens cDNA clone IMAGE:3070631 3'	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293612 5	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'	Homo saplens mRNA for KIAA1321 protein, partial cds	tn19b08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMACE:2168055 3' similar to gb:1.20977   CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);	Homo saplens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I)	mRNA	Homo sapiens mRNA for KIAA1438 protein, partial cds	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5	601590108F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3944304 5'	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'	601584930F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3939222 5	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1	Homo sapiens mRNA for KIAA0536 protein, partial cds	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA	7h15h05x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5	601278373F1 NIH_MGC_39 Homo saplens cONA clone IMAGE:3610267 5'	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA	EST188414 HCC cell line (matastasis to liver in mouse) II Homo septens cDNA 5' end similar to ribosomal	protein L29 1601589625F1 NIH MGC 7 Homo sepiens cDNA clone IMAGE 3943591 5	Human beta-prime-adaptin (BAM22) gene, exon 5
201 1 1007 216	Top Hit Database Source	LN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN		NT	님	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	TN	LV	NT	NT.	EST_HUMAN	INT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N		EST HUMAN	NT
	Top Hit Acession No.	0.0E+00 AB037836.1	0.0E+00 AB037836.1	0.0E+00 BF513835.1	0.0E+00 BF672818.1	0.0E+00 BE616695.1	0.0E+00 AB037742.1	AJ571737.1		5032150 NT	0.0E+00 AB037859.1	0.0E+00 BE795445.1	0.0E+00 BE795445.1	0.0E+00 BE293328.1	0.0E+00 BE792472.1	4504686 NT	4507720 NT		AF173227.1	0.0E+00 AB011108.1	0.0E+00 AU133385.1	0.0E+00 M69225.1	AU130403.1	3.1			0.0E+00 BE383165.1	0.0E+00 BE531263.1	8922843 NT	7 44407070	0.0E+00 RF794884 1	0.0E+00 U36253.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI571737		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 (U78027.1	0.0E+00 AF173227	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AU13040;	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	90.70.0	0.00+00	0.0E+00
	Expression Signal	2.37	2.37	3.85	2.8	1.16	1.34	76.0		227	5.78	1.03	1.03	1.1	10.42	2.46	7.02	1.09	5.19	1.17	96.0	1.41	1.21	121	1.29	1	3.25	2.74	1.74	01.0	0.88	3.59
	ORF SEQ ID NO:		22319		22325		22332	22333						22339			22365		22369	22370	22373		22376	22377			22386		22413		22443	
	Exan SEQ ID NO:	12654	12654	12426	12432	12434	12440	12441		12442	12444	12445	12445	12448	12456	12465	12727	12476	12477	12481	12484	12485	12487	12487	12490	12494	12495	12496	12523	1	12556	12562
	Probe SEQ ID NO:	2553	2553	2554	2560	2562	2569	2570		2571	2573	2574	2574	2577	2585	2595	2601	2608	2609	2613	2616	2617	2619	2619	2622	2626	2627	2628	2656	0000	2697	2698

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Top Hit Descriptor	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds	601591991F1 NIH_MGC_7 Homo saplens cDNA done IMAGE:3945983 5'	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'	AV721647 HTB Homo saplens cDNA clone HTBBYE09 5'	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA	Horrio sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA	601580903F1 NIH_MGC_9 Homo sapiens cDNA clane IMAGE:3929472 5'	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C001	UI-H-BW1-amw-e-07-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'	au55d04.y1 Schneider fetal brain 00004 Homo saplens cDNA clone IMAGE:2818663 5' similar to SW:R13A HUMAN P40429 60S RIBOSOMAL PROTEIN 1 13A	602071957F1 NCI_CGAP_Bm67 Hono sapiens cDNA clone IMAGE:4214679 5	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
Top Hit Database Source	NT TN	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	N	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	NT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT
Top Hit Acession No.	7669517 NT	4F110763.1	3E796376.1	3F680632.1	3E563433.1		5174486 NT	5174486 NT	8923441 NT	8923441 NT	0.0E+00 AF290195.1	0.0E+00 AV651066.1	3F377897.1	3F377897.1	47,57963 NT	4757963 NT	3E747193.1	3E176836.1 .	4L163201.2	3F514110.1	4503098 NT	3F677694.1	7427522 NT	4V725534.1	4V725534.1	AI879163.1	3F530661.1	0.0E+00 BE872768.1	0.0E+00 AU131494.1	0.0E+00 AU131494.1	3E300344.1	0.0E+00 BE300344.1	576830.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 AF11076	0.0E+00 BE79637	0.0E+00 BF68063	0.0E+00 BE56343	0.0E+00 AV72164	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00[	0.0E+00	0.0E+00 BF37789	0.0E+00 BF37789	0.0E+00	0.0E+00	0.0E+00 BE74719	0.0E+00 BE17683	0.0E+00 AL16320	0.0E+00 BF51411	0.0E+00	0.0E+00 BF67769	0.0E+00	0.0E+00 AV72553	0.0E+00 AV72553	0.0E+00 AI879163	0.0E+00 BF53066	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE30034	0.0E+00	0.0E+00 S76830.1
Expression Signal	1.08	10.23	10.37	3.2	13.51	1.28	2.17	2.17	6.0	6.0	22	15.67	1.72	1.72	3.21	3.21	2.2	76.0	1.3	3.47	1.07	4.95	1.73	9.56	9.56	11.15	1.97	2.91	1.11	1.11	10.1	10.1	4.6
ORF SEQ ID NO:	22454	22455	22462	22463	22467						22474		22475		22479	22480	22485	22488		22498					22516		22521	22522	22523				19966
Exen SEQ ID NO:	12564	12565		12572		12575		1								12585	12589		12603	12604			12620	12623	12623	12625	12628	12629	12631				10151
Probe SEQ ID NO:	2700	2701	2708	2709	2712	2713	2715	2715	2718	2716	2717	2718	2719	2719	2723	2723	2727	2730	2741	2742	2748	2754	2758	2761	2761	2763	2766	2767	2769	2769	2770	2770	27.75

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SEQ Expression (Top) Hit Acession Signal BLAST E No. Source Value	1.94 0.0E+00 AB032281:1 NT Homo saplens BTRCP2 mRNA for F-hox and Wn-reneate marketin lenders.	1.37 0.0E+00 AF264750.1 NT	20784 3.58 0.0E+00 4503202 NT (CYP1B1) mRNA (CYP1B1) mRNA	3.68 0.0E+00 4503202 NT	0.0E+00 X85980.1 NT	0.0E+00 AF068624.1 NT	10.1 NT	1.07 0.0E+00 AJ238852.1 NT	2.24 0.0E+00 AL163201.2 NT		1.58 0.0E+00 BE154504.1 EST HUMAN	1.58 0.0E+00 BE154504.1 EST HUMAN	0.0E+00 X73428.1 NT	2.84 0.0E+00 AL 163268.2 NT	2.58 0.0E+00 M98478.1 NT	43.46 0.0E+00 D50657.1 NT	43.46 0.0E+00 D50657.1 NT	0.0E+00 AL096857.1 NT	0.0E+00 Y10658.1 NT	0.96 0.0E+00 AF152303.1 NT	25.08 0.0E+00 4503470 NT	25.08 0.0E+00 4503470 NT	2.42 0.0E+00 4507280 NT	1.35 0.0E+00 AL047599.1 EST_HUMAN	1.25 0.0E+00 7661883 NT	0.0E+00 7661883 NT	3.42 0.0E+00 4503098 NT	4.95 0.0E+00 BE081896.1 EST HUMAN	4.95 0.0E+00 BE081896.1 EST HUMAN	Homo sapiens chromosome 21 segment HS21C006	
																	.		7												
Exon ORF SEQ ID NO:	12638	10649 20	10941 20	10941 20		12736	12738						12753						12766											12794 228	
Probe Ex SEQ ID SEC NO: NO		2784 10	2789 10	2789 10			2808 12		$_{\perp}$	]	2822 12	_[					ot	L		70 600					_1		$\perp$			2866 127	

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Table 4
Single Exon Probes Expressed in Heart

		T	Τ		Т	Τ	T	T	Т	T	T	T	Т	T	T	T	4	14	1	70 10	1	T	ή.	<b>"</b> ]"	T	-	"	1
Single Exoli Flores Expressed III near	. Top Hit Descriptor	Homo saplens chromosome 21 segment HS210006	2796b11.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:683517 3' similar to contains Alu	Homo saniens, hHPF dena for hair keralin avvns 1 fn 0	Homo saplens EphA4 (EPHA4) mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	hr18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN.	th18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN .	ZINC FINGER PROTEIN 132	Homo saplens protocadherin gamma C4 (PCDH-gamma-C4) mRNA complete cals	Homo sapiens mRNA for KIAA1287 protein, partial cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens mRNA for KIAA1508 protein, partial cds	Homo sapiens mRNA for KIAA1508 protein, partial cds	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, (MLLT4) mRNA	Homo sapiens myeloid/lymphold or mbæd-lineage leukemia (trithorax (Drosophila) homolog); translocated to, (MLLT4) mRNA	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17293 PROTEIN.	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VI N1 CG17203 PROTEIN	Homo saplens melanoma antiden family R 4 (MAGERA) mRNA	Homo sapiens melanoma antigen, family B. 4 (MAGEB4) mRNA	Homo sapiens verbe avian erythrobiastic leukemia viral processe homologiike 4 (FRRBA) mPNA	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncodena homolog-like 4 (FRBRA) mRNA	Homo saplens neurexin III (NRXN3) mRNA	H.sapiens NF-H gene, exon 4	H.saplens NF-H gene, exon 4	Homo saplens immunoglobulin-like transcript 1c variant 4'(ILT1c) gene, exon 8
JIE EXUIT PIOL	Top Hit Database Source	IN	EST LIMAN	TN - ION	LN L	N-	EST_HUMAN	EST HUMAN	SWISSPROT	TN	¥	¥	N	F	¥	N-	NT.	Ę	EST_HUMAN	NAMIN TSE	TA	Į.	¥	¥	MT	Ę	N	Ę
	Top Hit Acession No.	4L163206.2	0.05+00.045570.4	5	4758279	4503470 NT	1561002.1	AI561002.1		-	2	0.0E+00 AB033093.1		1.1	TM 2061903	7661903 NT	5174574 NT	5174574 NT	0.0E+00 BF110702.1	-	505084	4505084 NT	4885214 NT	4885214 NT	4758827			
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AL163206	00+400	0.0E+00 Y19210.1	0.0E+00	0.0E+00	0.0E+00 AI561002	0.0E+00 AI561002	0.0E+00 P52740	0.0E+00 AF152338	0.0E+00 AB033093	0.0E+00	0.0E+00 AB040941	0.0E+00 AB04094	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE110702	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X15309.1	0.0E+00 X15309.1	0.0E+00 AF106275
	Expression	1.64	4 08	3.09	1.16	18.66	1.25	1.25	1.87	1.5	1.34	1.34	4.98	4.98	2.66	2.66	3.23	3.23	1.27	1.27	203	2.03	0.94	0.94	1.6	1.3	1.3	7.93
	ORF SEQ ID NO:	22589	0522		22599		22601	22602	22604	22605	22617	22618	22619	22620	22623	22624	22625	22626	22630	22631	22642	22643	22645	22646	22651	22654	22655	22657
	Exen SEQ ID NO:	12794	12795	12801	12804	12805	12806	12806	12808	12809	12824	12824	12825	12825	12828	12828	12829	12829	12833	12833	12842	12842	12844	12844	12851	12854	12854	12856
	Probe SEQ ID NO:	2866	2867	2874	2877	2878	2879	2879	2881	2882	2897	2897	2898	2898	2901	2901	2902	2902	2907	2907	2915	2915	2917	2917	2924	2927	2927	2929

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	qf43f09.x1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'	Homo saplens neuropilin 2 (NRP2) gene, complete cds, afternatively spliced	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA	Homo sapiens mRNA for PKU-alpha, partial cds	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	Homo sapiens chromosome 21 segment HS21C046	Human displacement protein (CCAAT) mRNA	Homo sapiens semenogelin I (SEMG1) mRNA	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA	Isoform 2 of a novel human mRNA from chromosome 22	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein. T54 protein.	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes.	complete cds; and L-type calcium channel a>	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA	Human germline gene 16.1 for lg lambda L-chain C region (IgL-C16.1)	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds	Homo saplens SWI-SNF complex protein p270 mRNA, partiál cds	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA	Homo sapiens olfactory receptor-like protein (OLFR 428) gene, OLFR 428-9110 allele, partial cds	Homo sapiens potassium voltace-cated channel. Shab-related subfamily, member 1 (KCNR1) mRNA	Human ferritin heavy chain mRNA, complete cds	Homo saplens mRNA for KIAA0549 protein, partial cds		DNA clone IMAGE:119453 3' similar to SP:S29539
	Top Hit Database Source	EST_HUMAN	N TN	IN IN	N	۲	N	۲	N	NT	F	IN	Į.	۲	¥	F	IN			L	LNT	NT	TN	TN	NT	LN	IN	IN	LN	NT	FN	LN	EST_HUMAN
	Top Hit Acession No.	0.0E+00 AI149880.1	0.0E+00 AF281074.1	0.0E+00 AF281074.1	4506118 NT	0.0E+00 AB004884.1	7662273 NT	5729755 NT	5729755 NT	0.0E+00 AL163246.2	M74099.1	4506882 NT	0.0E+00 AF195953.1	5579469 NT	5579469 NT	0.0E+00 AL359403.1	0.0E+00 AF017433.1			0.0E+00 AF196779.1	4504664 NT	X03529.1	0.0E+00 AF199355.1	0.0E+00 AF064589.1	0.0E+00 AF265208.1	0.0E+00 AF149773.1	7662139 NT	0.0E+00 AF042075.1	4826783 NT	20941.1	4B011121.1	4B011121.1	194870.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00		0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00 M74099.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00	0.0E+00	0.0E+00 X03529.1	0,0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L20941.1	0.0E+00 AB011121	0.0E+00 AB011121	0.0E+00 T94870.1
	Expression Signal	1.13	0.84	0.84	76.0	2.15	1.33	1.59	1.59	0.89	1.04	0.82	4.85	7.86	7.86	5.08	202			1.74	0.99	2.79	1.85	1.89	2.85	3.97	4.21	1.64	3.45	19.64	1.79	1.79	9.41
	ORF SEQ ID NO:		22677		22679	22680			22691			22721		22730			22735					22760					22791		22824				22845
	Exan SEQ ID NO:	12870	12879	12879	12880	12881			12892					12937	12937		12942			12945	12947	12966	12970	12974	12995		13001	13002	13028	13036	13040	13040	13048
	Probe SEQ ID NO:	2943	2922	2922	2953	2954	2964	2965	2965	2990	2992	3001	3006	3000	3009	3011	3014			3017	3019	3038	3043	3047	3068	3069	3074	3075	3102	3111	3115	3115	3123

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Single Exon Probes Expressed in Heart

Top Hit Descriptor		wu12h10.x1 NGL_CGAP_GCG Homo sapiens cDNA done IMAGE:2516803 3'	H.saplens mRNA for gamma-glutamytransferase	H.sapiens mRNA for gamma-glutamytransferase	Homo sapiens neuredin III (NRXN3) mRNA	Homo saplens neurexin III (NRXN3) mRNA	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens CREB binding protein (Rubinstein-Tavbi syndrome) (CREBBP) mRNA	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrame) (CREBBP) mRNA	Π	Γ	Homo sapiens angiostatin binding protein 1 mRNA, complete cds	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA	Homo sapiens titin (TTN) mRNA	Human connexin 43 processed pseudogene	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKIZW), RD, complement factor B	(Bf), and complement component C2 (C2) genes,>	Homo saplens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	#58f08.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11. :contains Alu repetitive element:	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
Top Hit Acession No.	F243336.1 EST_HUMAN	1968086.1 EST_HUMAN	38922.1 NT	38922.1 NT	4758827 NT	4758827 NT	. 4504658 NT	4507720 NT	4507720 NT	28699.1 NT	4502098 NT	4758055 NT	4758055 NT	A774783.1 EST_HUMAN		F286598.1 NT	4557590 NT	4507720 NT	65189.1 NT	*	F019413.1 NT	F055084.1 NT	4502014 NT	4502014 NT	0.0E+00 AF265208.1 NT	8923624 NT	589294.1 EST HUMAN	=	F128893.1 NT	7657213 NT	7657213 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00 BF24333	0.0E+00 AI968086	0.0E+00 X98922.1	0.0E+00 X98922.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M28699.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AA77478	0.0E+00 AF286598.1	0.0E+00 AF28659	0.0E+00	0.0E+00	0.0E+00 M65189.	!	0.0E+00 AF019413.1	0.0E+00 AF05508	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI589294	0.0E+00 AF128893	0.0E+00 AF12889	0.0E+00	0.0E+00
Expression Signal	1.1	1.03	3.99	3.90	1.5	1.5	7.73	3.26	3.26	2.44	2.23	0.82	0.82	26.3	4.53	4.53	1.56	3.35	4.39		1.19	4.15	3.46	3.46	2	0.89	4.86	2.98	2.98	1	1
ORF SEQ ID NO:	22862	22863	22870	22871	22883	22884	22892	22893	22894	22910	22912		22919	22920	22928	22929	22935	22942		<u> </u>	22949	22951			22973	22974	23003	23011	23012	23013	23014
Exan SEQ ID NO:		13065	13070	13070	13081	13081	13088	13089	13089	13105	13108	L	13113	13115	13123	13123	13134	13139	13148		13149		1	15066	13175	13176	13203	13211	13211		13212
Probe SEQ ID NO:	3138	3140	3145	3145	3156	3156	3163	3164	3164	3180	3183	3188	3188	3190	3198	3198	3210	3215	3224		3225	3227	3237	3237	3252	3253	3282	3289	3289	3290	3290

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	T	T		T	T	T	. \$	Ş	T	T	T	T	T	T	T	T	Т	T	T	7	Ť		Τ	T	Ť	†	Τ	Τ	T	T	T	
Top Hit Descriptor	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo sapiens chromosome 21 unknown mRNA	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGF:844387.5'	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGF-844387 5	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'	Homo sapiens zinc finger protein 45 (a Kruppel-associated hox (KRAR) domain podynaenida) /7NEAR) mBAA	601143853F1 NiH MGC 15 Homo sapiens cDNA clone IMAGE-3051373 5	601143853F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE:3051373 5	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNF2) mRNA	te35g12.xf Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:2088742.3' similar to TR:000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sapiens semenogelin II (SEMG2) mRNA	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds	Novel human gene mapping to chamosome X	Homo sapiens mRNA for KIAA1476 protein, partial cds	ox/7c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:T19B4.4 CE13742 :	Homo sapiens butvrophilin, subfamily 3, member A3 (RTN3A3), mRNA	QV0-CT0225-230300-169-e01 CT0225 Homo sabiens cDNA	Homo sapiens gamma-glutamytcysteine synthetase (GLCLC) gene, partial cds	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 51	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'	Homo saplens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA	Homo sapiens KIAA0808 gene product (KIAA0806), mRNA	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo sapiens midline 1 (OpitziBBB syndrame) (MID1) mRNA	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel complete rate	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD) mRNA	Homo saplens WAVE2 mRNA for WASP-family protein, complete cds	
Top Hit Database Source	NT	LN L	NT NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST HUMAN	EST_HUMAN	1.	EST HUMAN	N L	N	LN	F	L	EST HUMAN	LZ.	T HUMAN		EST_HUMAN		EST_HUMAN	HUMAN					Į.		L	
Top Hit Acession No.	0.0E+00 AF045452.1	0.0E+00 AF045452.1	0.0E+00 AF231922.1	0.0E+00 AA626677.1	 	 	4508028 NT	0.0E+00 BE304791.1		4826795 NT	0.0E+00 AI384007.1	M10976.1	4506884 NT	0.0E+00 AF078868.1	AL133204.1	0.0E+00 AB040909.1	0.0E+00 AI081907.1	6325463 NT	0.0E+00 AW852217.1	0.0E+00 AF118846.1	0.0E+00 BF676393.1	3967		0.0E+00 AW664693.1	4826763	7662319 NT	4557752 NT	4557752 NT		7669491 NT	0.0E+00 AB026542.1	
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M10976.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D87327.1	0.0E+00	0.0E+00	
Expression Signal	2.08	2.08	1.23	0.94	0.94	0.94	1.11	223	223	1.43	0.92	96'0	0.82	1.3	1.39	0.96	0.98	126	4.53	0.95	7.43	1.1	0.98	0.98	1.13	0.98	0.79	0.79	1.51	28.67	4.26	
ORF SEQ ID NO:	23163	23164	23172	23175	23176	23177	23180	23182	23183	23185	23191	23194	23217		23225	23226		23242			23250		23269	23270	23274	23277	23282	23283	23297		23316	
Exan SEQ ID NO:	13357		13365			13371	13374	13377	13377	13379	13386	13389	13412	13414	13422	13423	13443	13445	13449	13456	13457	13478	13480	13480	13483	13485	13492	13492	13510	13514	13530	
Probe SEQ ID NO:	3440	3440	.3448	3455	3455	3455	3458	3461	3461	3463	3470	3473	3495	3497	3505	3507	3527	3529	3533	3540	3541	3564	3566	3566	3569	3571	3578	3578	3596	3600	3616	

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											\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \				043340											lar to MXRA5	lar to MXRA5					
Olingia Lyon Frodes Cypressed III near	Top Hit Descriptor	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA	Homo sapiens myosin light chain kinase Isoform 2 (MI CK) mRNA	Homo sapiens myosin light chain kinase isoform 2 (MI CK) mRNA complete case	Homo sapiens 5-hydroxytryptamine (serotonin) recentor 1D (HTR1D) mRNA	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA	Homo sapiens chromosome X open reading frame 5 (CXORE5) mRNA	Human zinc finger protein ZNF134 mRNA, complete cds	Homo sapiens potassium voltare-dated channel. Shah-rajated suhfamiliv member 4 (1/10) And and a subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subseq	Homo sabiens familial mental retardation protein 2 (FMR2) gans 44	Homo sapiens SC35-interacting profein 1 (SRRP129) mRNA	Homo sapiens amphiphysin gene, partial cds	Wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340 O43340 R28830 2 'contains element DTB7 reposition of present	Homo sablens ribosomal profein S8 (RPS8) mRNA	DKFZp434N0413_r1 434 (synonym; htes3) Homo sapiens clona Ciona DK FZp434Nn413 Fi	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GRP1) mRNA	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo sapiens zinc finger protein (KIAA0412) mRNA	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA	MXRA5 Human matrix tissue expression library Homo saplens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5	Home conjunct Franchist Trial (Franchist)	norro saprens r-box protein Fbi3b (FBL3B) mRNA, partial cds soddsecentiil NCC 441	60115323051 NIT MGC 44 Homo sapiens cDNA clone IMAGE:3608800 5	PM2-I Tonga, Annan Long Land Sapiers Conversion (1974) 5	APINE ELECTION INC. 1000-1100 ELECTION ESPIRIS CITIAN
gie Exuit F10	Top Hit Database Source	FN	F	L	F	NT	LN LN	IN	NT	TN	N	IN	NT	NT	EST HUMAN	LZ	EST_HUMAN	LN	N.	TN	TN	NT	L	TN	EST_HUMAN	EST_HUMAN	EST HIMAN	TINE TIME	N I	EST HIMAN	EST HIMAN	
5	Top Hit Acession No.	7662183 NT	0.0E+00 AF069601.2	0.0E+00 AF069601.2	4504534 NT		6912735 NT	4503178 NT	4503178 NT	J09412.1	4826783 NT	F012615.1	4759171 NT	F099117.1	1864727.1	4506742 NT	L040338.1	6005887 NT	6005887 NT	4504138 NT	4505078 NT	AF149412.1	4506758 NT	35642	0.0E+00 BF356295.1	21.1	7			1		1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AL16327	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U09412.	0.0E+00	0.0E+00 AF01261	0.0E+00	0.0E+00 AF09911	0.0E+00 A)864727	0.0E+00	0.0E+00 AL04033	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00 B	0.0E+00 AW8882	0.0F±00 AW88822	0 0F+00 4F120533	0.0E+00 RE37860	0.0E+00.B	0.0E+00 A	
	Expression Signal	2.39	1.31	1.31	1.97	1.61	1.12	5.67	5.67	3.93	1.63	0.99	1.87	0.82	2.54	80.9	1.41	-	1	2.45	1.8	0.87	1.27	1.62	1.75	1.4	4	178	32	127	0.97	
	ORF SEQ ID NO:	23460	23462	23463						23482				23489	23498	23502				23518		23521	23534	23537	23544	23546	23547	23552	23557	23558	23563	
	Exan SEQ ID NO:		13681		13682				13692	13694	13696	13699	13700	13702	13711	13714	13719	13725	13725	13727	13728	13732	13/42	13745	13751	13753	13753	13759	13764	13765	13771	
	Probe SEQ ID NO:	3765	3768	3768	3769	3773	3775	3780	3780	3782	3784	3787	3788	3790	3799	3802	3807	3813	3813	3815	3816	3820	3830	3833	3840	3842	3842	3848	3853	3854	3860	

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Table 4
Single Exon Probes Expressed in

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| Top Hit Descriptor                            | Homo sapiens cancer-testis antigen CT10 (CT10) gans complete and                          | Homo sapiens cancer-testis antigen CT10 (CT10) dena complete cus                                                                                                                                                                                                                                                                                                                                          | Human MHC class Il Ivmphocyte entiden DPw4-heta-2 heardcone accord                                                                                                                                                                                                                                                                                                      | Homo sapiens chromosome 21 seament HS21C103                                                          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                                                                                                                                                         | Homo sapiens KIAA0569 gene product (KIAA0569) mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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Homo sapiens DGCR8 (DGCR8) mRNA, complete cds                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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|                                               | Exon ORF SEQ Expression (Top) Hit Top Hit Acession Database No: Signal BLAST E No. Source | Exan<br>SEQ ID<br>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>BLAST E         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source         Top Hit Acession<br>Source           NO:         Signal<br>Yalue         Value<br>No.         Source         Source           13803         23587         4.6         0.0E+00 AF116195.1         NT | Exan<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>NO:         Expression<br>Signal<br>NO:         (Top) Hit<br>BLAST E<br>Value         Top Hit Acession<br>No.         Top Hit<br>Source<br>Source           13803         23587         4.6         0.0E+00 AF116195.1         NT           13803         23588         4.6         0.0E+00 AF116195.1         NT | Exan<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal<br>Signal<br>Signal<br>NO:         Expression<br>Signal<br>NO:         (Top) Hit<br>Signal<br>Value<br>No:         Top Hit Acession<br>No:         Top Hit<br>Source<br>Source<br>Source<br>13803         Top Hit<br>Signal<br>No:         Top Hit<br>Source<br>No:         Top Hit<br>No:         Top Hit<br>No:         Top Hit | Exan<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal         Expression<br>RLAST E<br>Value         (Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit<br>Source<br>Source           13803         23587         4.6         0.0E+00 AF116195.1<br>0.0E+00 AF116195.1         NT           13813         3.93         0.0E+00 AF116195.1<br>0.0E+00 MZ3910.1         NT           13813         3.93         0.0E+00 AF116135.1<br>0.0E+00 AF116135.1         NT | Exan<br>SEQ ID<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>BLAST E<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>Source           13803         23587         4.6         0.0E+00         AF116195.1         NT           13813         23588         4.6         0.0E+00         AF116195.1         NT           13813         3.83         0.0E+00         AF116195.1         NT           13815         5.44         0.0E+00         AL163303.2         NT           13822         23503         1.53         0.0E+00         AL118494.1         NT | Exan<br>SEQ ID<br>NO:         ORF SEQ<br>Signal         Expression<br>Signal         (Top) Hit<br>BLAST E<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>Source           13803         23587         4.6         0.0E+00 AF116195.1         NT           13813         23588         4.6         0.0E+00 AF116195.1         NT           13813         3.83         0.0E+00 M23910.1         NT           13822         23503         1.53         0.0E+00 AL118494.1         NT           13825         23605         2.89         0.0E+00 AL118494.1         NT | Exon SIGN ID NO:         ORF SEQ ID NO:         Expression Signal         (Top) Hit Acession Signal         (Top) Hit Acession No:         Top Hit Acession No:         Top Hit Acession Database No:           13803         23587         4.6         0.0E+00 AF116195.1         NT           13813         23588         4.6         0.0E+00 AF116195.1         NT           13815         3.93         0.0E+00 AF116195.1         NT           13822         23603         1.53         0.0E+00 AL18494.1         NT           13825         23605         2.89         0.0E+00 AL18494.1         NT           13825         23605         2.89         0.0E+00 AL163284.2         NT           13833         23613         1.46         0.0E+00 AL163289.2         NT | Exon SIGN ID NO:         ORF SEQ ID NO:         Expression Signal SIGN         (Top) Hit Acession Signal NO:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top 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No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit | Exon Signal NO:         CRF SEQ ID ID NO:         Expression Signal Signal         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:      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Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Top Hit Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No.         Accession No. | Exon Signal NO:         Crop Hit Acession Signal NO:         Top Hit Acession Signal Signal NO:         Top Hit Acession Signal NO:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top 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Acession<br/>Value 
       Top Hit Acession<br/>No.<br/>14803         Top Hit Acession<br/>Asian Database<br/>Source           13803         23587         4.6         0.0E+00         AF116195.1         NT           13803         23588         4.6         0.0E+00         AF116195.1         NT           13813         3.83         0.0E+00         AF116195.1         NT           13815         5.44         0.0E+00         AF148303.2         NT           13822         23603         1.53         0.0E+00         AL18494.1         NT           13824         23605         2.89         0.0E+00         AL182384.2         NT           13844         25.76         0.0E+00         AL183268.2         NT           13847         23623         1.18         0.0E+00         A503470         NT           13848         23624         0.0E+00         M90366.1         NT           13867         23645         0.0E+00         A6015610.1         NT           13875         0.0E+00         A6015610.1         NT</td> <td>Exan<br/>NO:<br/>138C3         ORF SEQ<br/>23587         Expression<br/>318C3         (Top) Hit<br/>23587         Top Hit Acession<br/>Value         Top Hit Acession<br/>NO:<br/>138C3         Top Hit Acession<br/>Allows         Top Hit Acession<br/>Source           138C3         23587         4.6         0.0E+00 AF116195.1         NT           138C3         23588         4.6         0.0E+00 AF116195.1         NT           138C3         23588         4.6         0.0E+00 AF116195.1         NT           13813         3.83         0.0E+00 AF116195.1         NT           138L2         23503         1.53         0.0E+00 AF118494.1         NT           138L2         23605         2.89         0.0E+00 AL18494.1         NT           138L2         23605         2.89         0.0E+00 AL18494.1         NT           138L4         25.75         0.0E+00 AL183284.2         NT           138L4         25.75         0.0E+00 AL183288.2         NT           138L4         23624         2.05         0.0E+00 AL1849.1         NT           138L7         23645         0.0E+00 AL271276.1         NT           138R7         3.79         0.0E+00 AL271276.1         NT</td> <td>Exan<br/>NO:<br/>ID NO:<br/>ID NO:<br/>ID SEQ ID<br/>ID NO:<br/>ISGarel         Most Similar<br/>BLAST E<br/>Value         Top Hit Acession<br/>No.<br/>Source         Top Hit<br/>Database           13803         23587         4.6         0.0E+00<br/>OE+00<br/>AF116195.1         AF116195.1<br/>NT         NT           13803         23588         4.6         0.0E+00<br/>OE+00<br/>AF116195.1         NT         NT           13813         3.83         0.0E+00<br/>OE+00<br/>AF118494.1         NT         NT           13822         23503         1.53         0.0E+00<br/>OE+00<br/>AF118494.1         NT           13824         2.89         0.0E+00<br/>OE+00<br/>AF183268.2         NT           13844         25.75         0.0E+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+00<br/>OE+0</td> <td>Exan<br/>NO:<br/>ID NO:<br/>ID NO:<br/>ID SEQ ID<br/>ID NO:<br/>ID Signal         Top Hit Acession<br/>BLAST E<br/>Value         Top Hit Acession<br/>NO:<br/>Value         Top Hit Acession<br/>Asion         Top Hit<br/>Database<br/>Source           13803         23587         4.6         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<td>Exam<br/>NO:<br/>10 NO:<br/>13 SEQ ID<br/>NO:<br/>13803         CAPE SEQ<br/>Signal<br/>23587         Expression<br/>Asian<br/>Asian<br/>3.83         (Top Hit Accession<br/>Asian<br/>Asian<br/>3.83         Top Hit Accession<br/>No.<br/>14803         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>3.83         Top Hit Accession<br/>Asian<br/>Asian<br/>Asian<br/>3.83         Top Hit
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 23587         4.6         0.0E+00         AF116195.1         NT           13803         23588         4.6         0.0E+00         AF116195.1         NT           13813         3.83         0.0E+00         AF116195.1         NT           13815         23603         1.53         0.0E+00         AF118494.1         NT           13824         23605         2.89         0.0E+00         AL18494.1         NT           13847         23605         2.89         0.0E+00         AL18494.1         NT           13848         23624         0.0E+00         AL183284.2         NT           13849         23624         0.0E+00         AL183284.2         NT           13848         23624         0.0E+00         AL18494.1         NT           13848         23624         0.0E+00         AL182183         NT           13848         23624         0.0E+00         AL238617.1         NT           1388         23659         3.28         0.0E+00         AL242020.1</td> <td>Exon SEQ ID ID NO:         Signal Signal 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Similar<br/>Poble         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           13803         23587         4.6         0.0E+00<br/>0.0E+00<br/>1.53         AF116195.1<br/>0.0E+00<br/>0.0E+00<br/>1.53         NT           13813         23587         4.6         0.0E+00<br/>0.0E+00<br/>0.0E+00<br/>0.0E+00<br/>1.53         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    AL182384.2         NT           13844         25.76         0.0E+00         AL183268.2         NT           13847         23623         1.18         0.0E+00         A503470         NT           13848         23624         0.0E+00         M90366.1         NT           13867         23645         0.0E+00         A6015610.1         NT           13875         0.0E+00         A6015610.1         NT | Exan<br>NO:<br>138C3         ORF SEQ<br>23587         Expression<br>318C3         (Top) Hit<br>23587         Top Hit Acession<br>Value         Top Hit Acession<br>NO:<br>138C3         Top Hit Acession<br>Allows         Top Hit Acession<br>Source           138C3         23587         4.6         0.0E+00 AF116195.1         NT           138C3         23588         4.6         0.0E+00 AF116195.1         NT           138C3         23588         4.6         0.0E+00 AF116195.1         NT           13813         3.83         0.0E+00 AF116195.1         NT           138L2         23503         1.53         0.0E+00 AF118494.1         NT           138L2         23605         2.89         0.0E+00 AL18494.1         NT           138L2         23605         2.89         0.0E+00 AL18494.1         NT           138L4         25.75         0.0E+00 AL183284.2         NT           138L4         25.75         0.0E+00 AL183288.2         NT           138L4         23624         2.05         0.0E+00 AL1849.1         NT           138L7         23645         0.0E+00 AL271276.1         NT           138R7         3.79         0.0E+00 AL271276.1         NT | Exan<br>NO:<br>ID NO:<br>ID NO:<br>ID SEQ ID<br>ID NO:<br>ISGarel         Most Similar<br>BLAST E<br>Value         Top Hit Acession<br>No.<br>Source         Top Hit<br>Database           13803         23587         4.6         0.0E+00<br>OE+00<br>AF116195.1         AF116195.1<br>NT         NT           13803         23588         4.6         0.0E+00<br>OE+00<br>AF116195.1         NT         NT           13813         3.83         0.0E+00<br>OE+00<br>AF118494.1         NT         NT           13822         23503         1.53         0.0E+00<br>OE+00<br>AF118494.1         NT           13824         2.89         0.0E+00<br>OE+00<br>AF183268.2         NT           13844         25.75         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0.0E+00         AF116195.1         NT           13803         23588         4.6         0.0E+00         AF116195.1     
   NT           13813         3.83         0.0E+00         AF116195.1         NT           13815         23603         1.53         0.0E+00         AF118494.1         NT           13824         23605         2.89         0.0E+00         AL18494.1         NT           13847         23605         2.89         0.0E+00         AL18494.1         NT           13848         23624         0.0E+00         AL183284.2         NT           13849         23624         0.0E+00         AL183284.2         NT           13848         23624         0.0E+00         AL18494.1         NT           13848         23624         0.0E+00         AL182183         NT           13848         23624         0.0E+00         AL238617.1         NT           1388         23659         3.28         0.0E+00         AL242020.1 | Exon SEQ ID ID NO:         Signal Signal Signal         Most Similar Top Hit Acession (Top) Hit Top Hit Acession Signal NO:         (Top) Hit Top Hit Acession Signal Asignal Signal Signal Signal 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	Probe Excr SEQ ID SEQ I NO: NO:	4044 139	4048 139	4055 139	4056 139	4064 139	4069 139	4071 139	- 4071 139	4081 138	4098 1399	4098 1399		4113 140	4126 140		┙							4198 1406	4206 1410		4224 1412	i

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	Top Hit Descriptor	Homo saplens protein kinase C, nu (PRKCN), mRNA	Human G2 protein mRNA, partial cds	Human G2 protein mRNA, partial cds	Homo sapiens COMPLEMENT COMPONENT C10 RECEPTOR (C10R) mRNA	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds	Human Ig light chain VL1 region germline (humIv1c2c) gene, partial cds	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products,	partial cds	H.sapiens HZB/h gene	H.sapiens H2B/h gene	H.sapiens H4/d gene for H4 histone	H.sapiens H4/d gene for H4 histone	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA	Homo saplens mRNA for KIAA1360 protein, partial cds	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA	Homo saplens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10	Homo sapiens ACTN2 gene for alphe-Actinin 2, exon 10	Homo sapiens HPS1 gene, intron 5	xc68e08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AUNAK	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a. mRNA	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds	Homo sablens chromosome 21 segment HS21Cn07	PM1-HT0305-101199-002-d03 HT0305 Home saniens CDNA	Homo sabiens mRNA for butative ankurin-reneat containing motein (DRE1)	Homo sapiens mRNA for putative ankyrin-repeat containing mortain (ORE1)	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA	Homo sapiens serine-threonine protein kinase (MNBH) mRNA complete cris	H.sapiens pancreatic polypeptide receptor PP1 gene	Homo sapiens ATP-sensitive Inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
	Top Hit Database Source	N.	NT TN	NT	NT	IN	N		NT	NT	IN	LN L	PA	N IN	K	NT	NT	N FN	IN	R	NT	LN TN	EST HUMAN	LN LN	NT	NT	EST HUMAN	NT	K	NT.	Į,	N	NT
	Top Hit Acession No.	6563384 NT	J10991.1	110991.1	6912281 NT	VF153047.2	J03901.1	, , , , ,						7662091 NT	7662091 NT	4885126 NT	1.1	7019456 NT	0.0E+00 AF195953.1	5.1	5.1	3.1	7.	1619	0.0E+00 AF016050.1			ĺ	=	4758467 NT	-		
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 U10991.	0.0E+00 U10991.	0.0E+00	0.0E+00 AF15304	0.0E+00 U03901.	20.700	0.0E+00/L14581.1	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00 X60483.1	0.0E+00 X60483.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB03778	0.0E+00	0.0E+00	0.0E+00 AJ24976	0.0E+00	0.0E+00 AF20062	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AJ278120	0.0E+00 AJ278120	0.0E+00	0.0E+00 AF10883(	0.0E+00 Z66526.1	0.0E+00 S78684.1
	Expression Signal	0.87	1.17	1.17	10.2	1.15	1.59	1	5.17	2.78	2.78	1.58	1.58	8.95	8.95	10.81	86.0	1.1	5.85	8.1	8.1	1.92	40.23	1,91	1.38	7.5	1.29	1.83	1.83	3.91	2.3	1.47	1.12
	ORF SEQ ID NO:	23905	23911		23917		23943			23955	23956	23962	23963	23969	23970	23982	23984	24012		24025	24026		24080		24083		24087	24094	24095	24097	24098	24104	24111
	Exan SEQ ID NO:	14128	14135	14135	14144	14162	14167		.		14177	14183	14183	14187	14187	14197	14200	14230	14238	14243	14243	14264	14296	15073	14299	14302	14304	14310	14310	14312	14313	14318	14324
	Probe SEQ ID NO:	4230	4237	4237	4245	4263	4268	7207	#77#	4278	4278	4284	4284	4289	4289	4299	4302	4333	4341	4346	4346	4368	4401	4403	4405	4408	4410	4416	4416	4418	4419	4424	4429

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חומים ביינון וספים ביינון מפוני	Top Hit Descriptor	Homo sapiens pyrin (MEFV) gene, complete cds	Homo saplens pyrin (MEFV) gene, complete cds	Homo saplens zinc finger protein 195 (ZNF195), mRNA	Homo sapiens syncytin precursor, mRNA, complete cds	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds	Homo saplens zinc finger protein 211 (ZNF211), mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo saptens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA	Homo sapiens iduronate sulphates (IDS) gene, complete cds	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens PTEN (PTEN) gene, exons 3 through 5	Homo saplens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility	complex)	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	Homo saplens DNA for amyloid precursor protein complete ode	70/8008.51 Stratagene fatal reting 03/7002 Homo series - DNA Alone MAA CE. Societa of	Homo sapiens odz (odd Ozlfen-m. Drosobhila) hemolog 1 (ODZ1) mRNA	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens gene for netriuretic protein, partial cds	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds	Homo sapiens inwardly-rectifying potassium channel Kir2 1 (KCN I2) nene aron 9 and animalah	Mus musculus E-cadherin binding protein F7 mRNA complete cds	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
21 110 26	Top Hit Database Source	NT	N	TN	LN	TN	۲N	Į,	N	FZ	N.	K	LN PL	N		NT	ŢN	NT.	EST HIMAN	NT	N N	N	N	NT	N-	N N	NT	Į.	NT	NT	N	Į.
	Top Hit Acession No.	0.0E+00 AF111163.1	0.0E+00 AF111163.1	TN 826909	0.0E+00 AF208161.1		5454175 NT	4503470 NT	4503098 NT	4502556 NT	L35485.1	7662091 NT	7662091 NT			1,7245418.1	0.0E+00 AJ245418.1		2.1	7657410 NT	0.0E+00 AL163284.2		0.0E+00 AL163300.2	0.0E+00 AB037521.1	4557887 NT	4557887 NT	9.1	9.1	1	0277	4507720 NT	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF15233	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF14331		0.0E+00 AJ24541	0.0E+00	0.0E+00 D87675.1	0.0E+00 AA17407	0.0E+00	0.0E+00	0.0E+00 ≠	0.0E+00 ∤	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF15381	0.0E+00 AF15381	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y18890.1
	Expression Signal	1.95	1.95	3.08	5.37	1.92	1.36	15.15	1.47	1.58	2.78	9.78	9.78	2.04		8.67	8.67	28.0	1,5	1.55	122	1.71	4.37	1.89	1.91	1.91	1.3	1.3	1.18	7.43	7.43	21.96
	ORF SEQ ID NO:	24112	24113	24123				24147	24156	24161		24163	24164	24177		24179	24180					24205	24206		24216	24217	24218	24219	24220	23791	23792	24238
	Exon SEQ ID NO:	14325	14325		14338		14346	14356	14367	14371	14375	14377	14377	14392		14394	14394	14404	14416	14419	14421	14422	14423	14424	14434	14434	14435	14435	14436	14013	14013	14452
	Probe SEQ ID NO:	4430	4430	4439	4444	4449	4452	4462	4473	4477	4481	4483	4483	4498		4500	4500	4511	4523	4526	4528	4529	4530	4531	4541	4541	4542	4542	4543	4554	4554	4560

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6453812         NT           14474         24262         1.82         0.0E+00 Acos 6453812         NT           14474         24263         1.03         0.0E+00 Acos 6453812         NT           10108         19929         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.01         0.0E+00 Acos 6453812         NT           14505         24291         3.14         0.0E+00 Acos 646917.1</td><td>Exon<br/>SEQ ID<br/>NO:         Crop Hit<br/>Signal         Top Hit Accession<br/>Value         Top Hit<br/>No.         Top Hit<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14458         24246         2.32         0.0E+00         AB037820.1         NT           14470         24256         2.65         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14471         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24263         1.03         0.0E+00         AB037820.1         NT           14475         24263         1.03         0.0E+00         T56945.1         EST_HUMAN           14476         24263         1.11         0.0E+00         M69197.1         NT           14505         24294         3.14         0.0E+00         M69197.1         NT           14508         24298         1.32</td><td>Exon<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Pub.         (Top) Hit<br/>Pub.<br/>Signal<br/>Signal         Most Similar<br/>Pub.<br/>Signal         (Top) Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         <t< td=""><td>Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No:</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>PIO NO:         Expression<br/>Signal<br/>PIO NO:         (Top)
Hit<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Pa</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Palue         Top Hit Accession<br/>No.         Top Hit Accession<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24257         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB037820.1         NT           14476         24269         1.82         0.0E+00         AE53812         NT           14476         24269         1.03         0.0E+00         AE53812         NT           14476         24267         1.11         0.0E+00         BE30050.1         EST_HUMAN           14505         24294         3.14         0.0E+00         MB0917.1         NT           14508         24294<td>Exan<br/>NO:<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal         Most Similar<br/>FLAST         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00         AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1</td><td>Exon<br/>NO:-<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>14470         Most Similar<br/>Signal<br/>PLASTE<br/>Alubase<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE</td><td>Exan<br/>NO:<br/>1445B         ORF SEQ<br/>24246         Expression<br/>Signal<br/>Public         Most Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03         0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT     </td></td></t<><td>Expn<br/>SEQ ID<br/>ID NO:         ORF
SEQ<br/>Signal<br/>Signal         Expression<br/>Fallon         (Top) Hit<br/>Fallon         Top Hit Acession<br/>Fallon         Top Hit<br/>Database<br/>Source<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         24246         2.32         0.0E+00         AB037820.1         NT           14470         24259         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.65         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.03         0.0E+00         AB0451.1         NT           14470         24269         1.34         0.0E+00         AB0451.1         NT           14470         24260         3.14         0.0E+00         AB0451.1         NT           14505         24291         3.14         0.0E+00         AB0461.1         NT           14506</td><td>Exan<br/>NO:<br/>Inc.         ORF SEQ<br/>Secure<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Value         (Top) Hit<br/>No.<br/>Inc.         Top Hit Acession<br/>Source         Top Hit<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24256         2.0G         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14476         24262         1.82         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB030050.1         EST HUMAN           14502         24290         37.36         0.0E+00         M89197.1         NT           1</td><td>Excn SEQ ID DNO:         Cypression Signal NO:         Most Similar Value NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top 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24257         2.65         0.0E+00 AB037820.1         NT           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24258         2.65         0.0E+00 AB037820.1         NT           14471         24259         2.65         0.0E+00 AB037820.1         NT           14470         24259         2.55         0.0E+00 AB037820.1         NT           14471         24260         1.03         0.0E+00 AB037820.1         NT           14476         24263         1.03         0.0E+00 AB037820.1         NT           14477         24263         1.03         0.0E+00 AB0370.1         NT           14450         24263         1.11         0.0E+00 AB0370.1         NT           1450B         24297         1.12         0.0E+00 AB0370.1         NT           1450B         24298         1.34         0.0E+00 AB0370.1         NT      <tr< td=""></tr<></td></td></td></td></td> | Exon SEQ ID NO:         ORF SEQ ID NO:         Signal Value         Top Hit Acession Value         Top Hit Acession Signal Value         Top Hit Acession Signal Value         Top Hit Acession Signal Value         Top Hit Acession Source Source           14456         24246         2.32         0.0E+00 BE081527.1         EST_HUMAN           14465         2.01         0.0E+00 AF086641.1         NT           14470         24257         2.65         0.0F+00 AR037820.1 | Exon<br>NO:         CRF SEQ<br>ID NO:         Expression<br>Signal<br>NO:         (Top) Hit<br>BLASTE<br>Vatue         Top Hit Acession<br>No.         Top Hit<br>Source<br>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST HUMAN           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24256         2.65         0.0E+00 AB037820.1         NT | Exon SEQ ID NO:         CRF SEQ Signal NO:         Expression Signal NO:         Top Hit Accession Signal Signal NO:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit Accession No:         Top Hit 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       NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT | Exon No:         CRF SEQ ID NO:         Expression Signal NO:         (Top) Hit Top Hit Acession Signal Signal NO:         Most Similar Author No:         Top Hit Acession Signal Signal NO:         Top Hit Acession No:         Top Hit Acession No:           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         2.01         0.0E+00         AF086641.1         NT           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         G453812 NT           14474         24263         1.82         0.0E+00         G453812 NT | Exon No:         CRF SEQ ID NO:         Expression Signal NO:         (Top) Hit Top Hit Acession Signal Signal NO:         Most Similar Author No:         Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession No:           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AR037820.1         NT           14471         24259         2.65         0.0E+00         AR037820.1         NT           14474         24262         1.82         0.0E+00         AR037820.1         NT           14474         24263         1.82         0.0E+00         AR037820.1         NT           14474         24263     
   1.82         0.0E+00         AR037820.1         NT           14474         24263         1.82         0.0E+00         AR037820.1         NT           14474         24263         1.82         0.0E+00         AR037820.1         NT           14474         24263         0.0E+00         AR03812 NT         AR04091           14474         24263         0.0E+00         AR03812 NT           10108         19929         0.0E+00         AR03812 NT | Exon No:         CRF SEQ ID NO:         Expression Signal No:         Top Hit Acession Signal Signal No:         Most Similar Top Hit Acession Signal Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit 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<td>Exon No:         CRF SEQ ID NO:         Expression Signal No:         Top Hit Acession Signal Signal No:         Most Similar Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:   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      2.01         0.0E+00 Acos 641.1         NT           14470         24257         2.65         0.0E+00 Acos 6453812         NT           14471         24256         2.55         0.0E+00 Acos 6453812         NT           14474         24262         1.82         0.0E+00 Acos 6453812         NT           14474         24263         1.03         0.0E+00 Acos 6453812         NT           10108         19929         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.01         0.0E+00 Acos 6453812         NT           14505         24291         3.14         0.0E+00 Acos 646917.1</td><td>Exon<br/>SEQ ID<br/>NO:         Crop Hit<br/>Signal         Top Hit Accession<br/>Value         Top Hit<br/>No.         Top Hit<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14458         24246         2.32         0.0E+00         AB037820.1         NT           14470         24256         2.65         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14471         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24263         1.03         0.0E+00         AB037820.1         NT           14475         24263         1.03         0.0E+00         T56945.1         EST_HUMAN           14476         24263         1.11         0.0E+00         M69197.1         NT           14505         24294         3.14         0.0E+00         M69197.1         NT      
    14508         24298         1.32</td><td>Exon<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Pub.         (Top) Hit<br/>Pub.<br/>Signal<br/>Signal         Most Similar<br/>Pub.<br/>Signal         (Top) Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top 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No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No:</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>PIO NO:         Expression<br/>Signal<br/>PIO NO:         (Top) 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        ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Palue         Top Hit Accession<br/>No.         Top Hit Accession<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24257         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB037820.1         NT           14476         24269         1.82         0.0E+00         AE53812         NT           14476         24269         1.03         0.0E+00         AE53812         NT           14476         24267         1.11         0.0E+00         BE30050.1         EST_HUMAN           14505         24294         3.14         0.0E+00         MB0917.1         NT           14508         24294<td>Exan<br/>NO:<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal         Most Similar<br/>FLAST         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00         AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1</td><td>Exon<br/>NO:-<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>14470         Most
Similar<br/>Signal<br/>PLASTE<br/>Alubase<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE</td><td>Exan<br/>NO:<br/>1445B         ORF SEQ<br/>24246         Expression<br/>Signal<br/>Public         Most Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03         0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT     </td></td></t<><td>Expn<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal         Expression<br/>Fallon         (Top) Hit<br/>Fallon         Top Hit Acession<br/>Fallon         Top Hit<br/>Database<br/>Source<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         24246         2.32         0.0E+00         AB037820.1         NT           14470         24259         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.65         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.03         0.0E+00         AB0451.1         NT           14470         24269         1.34         0.0E+00         AB0451.1         NT           14470         24260         3.14         0.0E+00         AB0451.1         NT           14505         24291         3.14         0.0E+00         AB0461.1         NT           14506</td><td>Exan<br/>NO:<br/>Inc.         ORF SEQ<br/>Secure<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Value         (Top) Hit<br/>No.<br/>Inc.         Top Hit Acession<br/>Source         Top Hit<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24256         2.0G         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14476         24262         1.82         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB030050.1         EST HUMAN           14502         24290         37.36         0.0E+00         M89197.1         NT           1</td><td>Excn SEQ ID DNO:         Cypression Signal NO:         Most Similar Value NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Ac</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>BLAST E         Expression<br/>No:         Most Similar<br/>Signal<br/>PLAST E         Top Hit Acession<br/>Value         Top Hit Acession<br/>No:         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           14456         24246         2.32         0.0E+00 BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24258         2.65         0.0E+00 AB037820.1         NT           14471         24259         2.65         0.0E+00 AB037820.1         NT           14470         24259         2.55         0.0E+00 AB037820.1         NT           14471         24260         1.03         0.0E+00 AB037820.1         NT           14476         24263         1.03         0.0E+00 AB037820.1         NT           14477         24263         1.03         0.0E+00 AB0370.1         NT           14450         24263         1.11         0.0E+00 AB0370.1         NT           1450B         24297         1.12         0.0E+00 AB0370.1         NT           1450B         24298         1.34         0.0E+00 AB0370.1         NT      <tr< td=""></tr<></td></td></td></td> | Exon No:         CRF SEQ ID NO:         Expression Signal No:         Top Hit Acession Signal Signal No:         Most Similar Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit
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ID NO::         Expression Signal No:         (Top) Hit Top Hit Acession Signal No:         Most Similar No:         Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top 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6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.01         0.0E+00 Acos 6453812         NT           14505         24291         3.14         0.0E+00 Acos 646917.1</td><td>Exon<br/>SEQ ID<br/>NO:         Crop Hit<br/>Signal         Top Hit Accession<br/>Value         Top Hit<br/>No.         Top Hit<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14458         24246         2.32         0.0E+00         AB037820.1         NT           14470         24256         2.65         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14471         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24263         1.03         0.0E+00         AB037820.1         NT           14475         24263         1.03         0.0E+00         T56945.1         EST_HUMAN           14476         24263         1.11         0.0E+00         M69197.1         NT           14505         24294         3.14         0.0E+00         M69197.1         NT           14508         24298         1.32</td><td>Exon<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Pub.         (Top) Hit<br/>Pub.<br/>Signal<br/>Signal         Most Similar<br/>Pub.<br/>Signal         (Top) Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         <t< td=""><td>Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No:</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>PIO NO:         Expression<br/>Signal<br/>PIO NO:         (Top)
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        ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Palue         Top Hit Accession<br/>No.         Top Hit Accession<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24257         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB037820.1         NT           14476         24269         1.82         0.0E+00         AE53812         NT           14476         24269         1.03         0.0E+00         AE53812         NT           14476         24267         1.11         0.0E+00         BE30050.1         EST_HUMAN           14505         24294         3.14         0.0E+00         MB0917.1         NT           14508         24294<td>Exan<br/>NO:<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal         Most Similar<br/>FLAST         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00         AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1</td><td>Exon<br/>NO:-<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>14470         Most Similar<br/>Signal<br/>PLASTE<br/>Alubase<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE</td><td>Exan<br/>NO:<br/>1445B         ORF SEQ<br/>24246         Expression<br/>Signal<br/>Public         Most Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03         0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT     </td></td></t<><td>Expn<br/>SEQ ID<br/>ID NO:         ORF
SEQ<br/>Signal<br/>Signal         Expression<br/>Fallon         (Top) Hit<br/>Fallon         Top Hit Acession<br/>Fallon         Top Hit<br/>Database<br/>Source<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         24246         2.32         0.0E+00         AB037820.1         NT           14470         24259         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.65         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.03         0.0E+00         AB0451.1         NT           14470         24269         1.34         0.0E+00         AB0451.1         NT           14470         24260         3.14         0.0E+00         AB0451.1         NT           14505         24291         3.14         0.0E+00         AB0461.1         NT           14506</td><td>Exan<br/>NO:<br/>Inc.         ORF SEQ<br/>Secure<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Value         (Top) Hit<br/>No.<br/>Inc.         Top Hit Acession<br/>Source         Top Hit<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24256         2.0G         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14476         24262         1.82         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB030050.1         EST HUMAN           14502         24290         37.36         0.0E+00         M89197.1         NT           1</td><td>Excn SEQ ID DNO:         Cypression Signal NO:         Most Similar Value NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top 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24257         2.65         0.0E+00 AB037820.1         NT           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24258         2.65         0.0E+00 AB037820.1         NT           14471         24259         2.65         0.0E+00 AB037820.1         NT           14470         24259         2.55         0.0E+00 AB037820.1         NT           14471         24260         1.03         0.0E+00 AB037820.1         NT           14476         24263         1.03         0.0E+00 AB037820.1         NT           14477         24263         1.03         0.0E+00 AB0370.1         NT           14450         24263         1.11         0.0E+00 AB0370.1         NT           1450B         24297         1.12         0.0E+00 AB0370.1         NT           1450B         24298         1.34         0.0E+00 AB0370.1         NT      <tr< td=""></tr<></td></td></td> | Exon No:         CRF SEQ ID NO:         Expression Signal No:         Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit 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Exon SEQ ID NO: 10 NO: 10 NO: 10 NO: 14456         Cape FSEQ ID NO: 14456         Expression Signal Signal Public No: 24246         Top Hit Acession Public No: 24246         Top Hit Acession Signal Public No: 24256         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24266         Top Hit Acession No: 24268         Top Hit Acession No: 24268         Top Hit Acession No: 24268         Top Hit Acession No: 24268         Top Hit Acession No: 24268         Top Hit Acession No: 24268         Top Hit 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Signal Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession 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No:         Top Hit Acession No: | Exon No.:         CRF SEQ ID NO::         Expression Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:    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      Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top</td> <td>Exon No.:         CRF SEQ ID NO::         Expression Signal No:         Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top 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Hit Accession No: 24240         EST HUMAN           14470         24256         2.01         0.0E+00 Acos 641.1         NT           14470         24257         2.65         0.0E+00 Acos 6453812         NT           14471         24256         2.55         0.0E+00 Acos 6453812         NT           14474         24262         1.82         0.0E+00 Acos 6453812         NT           14474         24263         1.03         0.0E+00 Acos 6453812         NT           10108         19929         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.01         0.0E+00 Acos 6453812         NT           14505         24291         3.14         0.0E+00 Acos 646917.1</td> <td>Exon<br/>SEQ ID<br/>NO:         Crop Hit<br/>Signal         Top Hit Accession<br/>Value         Top Hit<br/>No.         Top Hit<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14458         24246         2.32         0.0E+00         AB037820.1         NT           14470         24256         2.65         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14471         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24263         1.03         0.0E+00         AB037820.1         NT           14475         24263         1.03         0.0E+00         T56945.1         EST_HUMAN           14476         24263         1.11         0.0E+00         M69197.1         NT         
 14505         24294         3.14         0.0E+00         M69197.1         NT           14508         24298         1.32</td> <td>Exon<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Pub.         (Top) Hit<br/>Pub.<br/>Signal<br/>Signal         Most Similar<br/>Pub.<br/>Signal         (Top) Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         Top Hit<br/>Pub.<br/>Signal         <t< td=""><td>Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No:</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>PIO NO:         Expression<br/>Signal<br/>PIO NO:         (Top) Hit<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Pa</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Palue         Top Hit Accession<br/>No.         Top Hit Accession<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24257         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB037820.1         NT           14476         24269         1.82         0.0E+00         AE53812         NT           14476         24269         1.03         0.0E+00         AE53812         NT           14476         24267         1.11         0.0E+00         BE30050.1         EST_HUMAN           14505         24294         3.14         0.0E+00         MB0917.1         NT           14508         24294<td>Exan<br/>NO:<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal         Most Similar<br/>FLAST         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00         AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1</td><td>Exon<br/>NO:-<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>14470         Most
Similar<br/>Signal<br/>PLASTE<br/>Alubase<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE</td><td>Exan<br/>NO:<br/>1445B         ORF SEQ<br/>24246         Expression<br/>Signal<br/>Public         Most Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03         0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT     </td></td></t<><td>Expn<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal         Expression<br/>Fallon         (Top) Hit<br/>Fallon         Top Hit Acession<br/>Fallon         Top Hit<br/>Database<br/>Source<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         24246         2.32         0.0E+00         AB037820.1         NT           14470         24259         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.65         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.03         0.0E+00         AB0451.1         NT           14470         24269         1.34         0.0E+00         AB0451.1         NT           14470         24260         3.14         0.0E+00         AB0451.1         NT           14505         24291         3.14         0.0E+00         AB0461.1         NT           14506</td><td>Exan<br/>NO:<br/>Inc.         ORF SEQ<br/>Secure<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Value         (Top) Hit<br/>No.<br/>Inc.         Top Hit Acession<br/>Source         Top Hit<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24256         2.0G         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14476         24262         1.82         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB030050.1         EST HUMAN           14502         24290         37.36         0.0E+00         M89197.1         NT           1</td><td>Excn SEQ ID DNO:         Cypression Signal NO:         Most Similar Value NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Ac</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>BLAST E         Expression<br/>No:         Most Similar<br/>Signal<br/>PLAST E         Top Hit Acession<br/>Value         Top Hit Acession<br/>No:         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           14456         24246         2.32         0.0E+00 BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24258         2.65         0.0E+00 AB037820.1         NT           14471         24259         2.65         0.0E+00 AB037820.1         NT           14470         24259         2.55         0.0E+00 AB037820.1         NT           14471         24260         1.03         0.0E+00 AB037820.1         NT           14476         24263         1.03         0.0E+00 AB037820.1         NT           14477         24263         1.03         0.0E+00 AB0370.1         NT           14450         24263         1.11         0.0E+00 AB0370.1         NT           1450B         24297         1.12         0.0E+00 AB0370.1         NT           1450B         24298         1.34         0.0E+00 AB0370.1         NT      <tr< td=""></tr<></td></td> | Exon No.:         CRF SEQ ID NO::         Expression Signal No:         (Top) Hit Top Hit Acession Signal No:         Most Similar No:         Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top
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No:         Top | Exon No.:         CRF SEQ ID NO::         Expression Signal No:         Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top Hit Acession No:         Top 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        14470         24257         2.65         0.0E+00 Acos 6453812         NT           14471         24256         2.55         0.0E+00 Acos 6453812         NT           14474         24262         1.82         0.0E+00 Acos 6453812         NT           14474         24263         1.03         0.0E+00 Acos 6453812         NT           10108         19929         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.03         0.0E+00 Acos 6453812         NT           10108         19930         1.01         0.0E+00 Acos 6453812         NT           14505         24291         3.14         0.0E+00 Acos 646917.1 | Exon<br>SEQ ID<br>NO:         Crop Hit<br>Signal         Top Hit Accession<br>Value         Top Hit<br>No.         Top Hit<br>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14458         24246         2.32         0.0E+00         AB037820.1         NT           14470         24256         2.65         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14471         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24259         2.55         0.0E+00         AB037820.1         NT           14474         24263         1.03         0.0E+00         AB037820.1         NT           14475         24263         1.03         0.0E+00         T56945.1         EST_HUMAN           14476         24263         1.11         0.0E+00         M69197.1         NT           14505         24294         3.14         0.0E+00         M69197.1         NT           14508         24298         1.32 | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>Signal         Expression<br>Figure<br>(Top) Hit<br>Pub.         (Top) Hit<br>Pub.<br>Signal<br>Signal         Most Similar<br>Pub.<br>Signal         (Top) Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal         Top Hit<br>Pub.<br>Signal <t< td=""><td>Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No:</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>PIO NO:         Expression<br/>Signal<br/>PIO NO:         (Top)
Hit<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Palue<br/>Pa</td><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Palue         Top Hit Accession<br/>No.         Top Hit Accession<br/>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24257         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB037820.1         NT           14476         24269         1.82         0.0E+00         AE53812         NT           14476         24269         1.03         0.0E+00         AE53812         NT           14476         24267         1.11         0.0E+00         BE30050.1         EST_HUMAN           14505         24294         3.14         0.0E+00         MB0917.1         NT           14508         24294<td>Exan<br/>NO:<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal         Most Similar<br/>FLAST         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00         AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1</td><td>Exon<br/>NO:-<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>14470         Most Similar<br/>Signal<br/>PLASTE<br/>Alubase<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE</td><td>Exan<br/>NO:<br/>1445B         ORF SEQ<br/>24246         Expression<br/>Signal<br/>Public         Most Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03         0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT     </td></td></t<> <td>Expn<br/>SEQ ID<br/>ID NO:         ORF
SEQ<br/>Signal<br/>Signal         Expression<br/>Fallon         (Top) Hit<br/>Fallon         Top Hit Acession<br/>Fallon         Top Hit<br/>Database<br/>Source<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         24246         2.32         0.0E+00         AB037820.1         NT           14470         24259         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.65         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.03         0.0E+00         AB0451.1         NT           14470         24269         1.34         0.0E+00         AB0451.1         NT           14470         24260         3.14         0.0E+00         AB0451.1         NT           14505         24291         3.14         0.0E+00         AB0461.1         NT           14506</td> <td>Exan<br/>NO:<br/>Inc.         ORF SEQ<br/>Secure<br/>Signal         Expression<br/>Figure<br/>(Top) Hit<br/>Value         (Top) Hit<br/>No.<br/>Inc.         Top Hit Acession<br/>Source         Top Hit<br/>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24256         2.0G         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14476         24262         1.82         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB030050.1         EST HUMAN           14502         24290         37.36         0.0E+00         M89197.1         NT           1</td> <td>Excn SEQ ID DNO:         Cypression Signal NO:         Most Similar Value NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Ac</td> <td>Exon<br/>NO:         ORF SEQ<br/>Signal<br/>BLAST E         Expression<br/>No:         Most Similar<br/>Signal<br/>PLAST E         Top Hit Acession<br/>Value         Top Hit Acession<br/>No:         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           14456         24246         2.32         0.0E+00 BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24258         2.65         0.0E+00 AB037820.1         NT           14471         24259         2.65         0.0E+00 AB037820.1         NT           14470         24259         2.55         0.0E+00 AB037820.1         NT           14471         24260         1.03         0.0E+00 AB037820.1         NT           14476         24263         1.03         0.0E+00 AB037820.1         NT           14477         24263         1.03         0.0E+00 AB0370.1         NT           14450         24263         1.11         0.0E+00 AB0370.1         NT           1450B         24297         1.12         0.0E+00 AB0370.1         NT           1450B         24298         1.34         0.0E+00 AB0370.1         NT      <tr< td=""></tr<></td> | Exon No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No: | Exon<br>NO:         ORF SEQ<br>Signal<br>PIO NO:         Expression<br>Signal<br>PIO NO:         (Top) Hit<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Palue<br>Pa | Exon<br>NO:         ORF SEQ<br>Signal         Expression<br>Signal         (Top) Hit<br>Palue         Top Hit Accession<br>No.         Top Hit Accession<br>Source           14458         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00         AB037820.1         NT           14471         24257         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB037820.1         NT           14476         24269         1.82         0.0E+00         AE53812         NT           14476         24269         1.03         0.0E+00         AE53812         NT           14476         24267         1.11         0.0E+00         BE30050.1         EST_HUMAN           14505         24294         3.14         0.0E+00         MB0917.1         NT           14508         24294 <td>Exan<br/>NO:<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal         Most Similar<br/>FLAST         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source         Top Hit Acession<br/>Acluse         Top Hit Acession<br/>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00        
AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1</td> <td>Exon<br/>NO:-<br/>14476         ORF SEQ<br/>24246         Expression<br/>Signal<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>14470         Most Similar<br/>Signal<br/>PLASTE<br/>Alubase<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE<br/>PLASTE</td> <td>Exan<br/>NO:<br/>1445B         ORF SEQ<br/>24246         Expression<br/>Signal<br/>Public         Most Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03         0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT     </td> | Exan<br>NO:<br>14476         ORF SEQ<br>24246         Expression<br>Signal         Most Similar<br>FLAST         Top Hit Acession<br>Acluse         Top Hit Acession<br>Source         Top Hit Acession<br>Acluse         Top Hit Acession<br>Source           14458         24246         2.32         0.0E+00         AFD86641.1         NT           14470         24257         2.65         0.0E+00         AFD86641.1         NT           14470         24258         2.55         0.0E+00         AFD86641.1         NT           14470         24268         2.55         0.0E+00         AFD86641.1         NT           14470         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         2.55         0.0E+00         AFD86641.1         NT           14477         24269         1.82         0.0E+00         AFS8122.1         NT           14477         24269         1.03         0.0E+00         AFS812.1         NT           14476         24280         3.14         0.0E+00         AFS812.1         NT           14502         24280         3.14         0.0E+00         AFS812.1         NT           14508         24280         1.34         0.0E+00         AFS8467.1 | Exon<br>NO:-<br>14476         ORF SEQ<br>24246         Expression<br>Signal<br>PLASTE<br>PLASTE<br>PLASTE<br>14470         Most Similar<br>Signal<br>PLASTE<br>Alubase<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE<br>PLASTE | Exan<br>NO:<br>1445B         ORF SEQ<br>24246         Expression<br>Signal<br>Public         Most Similar<br>Public         Top Hit Acession<br>Public         Top Hit Acession<br>Public         Top Hit Acession<br>Source           1445B         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14476         24256         2.65         0.0E+00         AR037820.1         NT           14470         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR037820.1         NT           14474         24269         2.65         0.0E+00         AR03812 NT         NT           14474         24269         1.03        
0.0E+00         AG83812 NT         NT           14476         24269         1.03         0.0E+00         AG83812 NT         NT           14478         24269         1.13         0.0E+00         AG83812 NT         NT           14478         24280         3.14         0.0E+00         AG8197.1         NT           14505         24280         3.14         0.0E+00         AG8197.1         NT | Expn<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal         Expression<br>Fallon         (Top) Hit<br>Fallon         Top Hit Acession<br>Fallon         Top Hit<br>Database<br>Source<br>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14465         24246         2.32         0.0E+00         AB037820.1         NT           14470         24259         2.65         0.0E+00         AB037820.1         NT           14474         24269         2.55         0.0E+00         AB037820.1         NT           14474         24269         2.65         0.0E+00         AB037820.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.82         0.0E+00         AB0451.1         NT           14474         24269         1.03         0.0E+00         AB0451.1         NT           14470         24269         1.34         0.0E+00         AB0451.1         NT           14470         24260         3.14         0.0E+00         AB0451.1         NT           14505         24291         3.14         0.0E+00         AB0461.1         NT           14506 | Exan<br>NO:<br>Inc.         ORF SEQ<br>Secure<br>Signal         Expression<br>Figure<br>(Top) Hit<br>Value         (Top) Hit<br>No.<br>Inc.         Top Hit Acession<br>Source         Top Hit<br>Source           14456         24246         2.32         0.0E+00         BE081527.1         EST_HUMAN           14470         24256         2.0G         0.0E+00         AB037820.1         NT           14470         24258         2.65         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         2.55         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14474         24262         1.82         0.0E+00         AB037820.1         NT           14476         24262         1.82         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB037820.1         NT           14476         24263         1.11         0.0E+00         AB030050.1         EST HUMAN           14502         24290         37.36         0.0E+00         M89197.1         NT           1 | Excn SEQ ID DNO:         Cypression Signal NO:         Most Similar Value NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Acession NO:         Top Hit Ac | Exon<br>NO:         ORF SEQ<br>Signal<br>BLAST E         Expression<br>No:         Most Similar<br>Signal<br>PLAST E         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>Source         Top Hit Acession<br>Source           14456         24246         2.32         0.0E+00 BE081527.1         EST_HUMAN           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24257         2.65         0.0E+00 AB037820.1         NT           14470         24258         2.65         0.0E+00 AB037820.1         NT           14471         24259         2.65         0.0E+00 AB037820.1         NT           14470         24259         2.55         0.0E+00 AB037820.1         NT           14471         24260         1.03         0.0E+00 AB037820.1         NT           14476         24263         1.03         0.0E+00 AB037820.1         NT           14477         24263         1.03         0.0E+00 AB0370.1         NT           14450         24263         1.11         0.0E+00 AB0370.1         NT           1450B         24297         1.12         0.0E+00 AB0370.1         NT           1450B         24298         1.34         0.0E+00 AB0370.1         NT <tr< td=""></tr<> |

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Table 4
Single Exon Probes Fxnressed

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	ZING FINGER PROTEIN 132	Homo sapiens hypothetical protein DK F7n762F1312 (DK F7n762F1312)	Homo sapiens chromosome 21 segment HS21C003	Homo saplens hypothetical protein FL 120073 (FL 120073) mRNA	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1- J61 segments: and Tor-C-elpha nene exons 1-4	Human Tor-C-delta gene, exons 14; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1- J6; semments: and Tor-C-alcha dese	H.sapiens MeCP-2 cene	H.sapiens MeCP-2 dene	Human collagenase type IV (CLG4) gene exon 2	Homo sapiens chromosome 21 segment HS210080	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I) mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2) mPMA	H.sapiens MICA gene	Homo sapiens zinc finger protein (KIAA0412) mRNA	Homo sapiens mRNA for KIAA0633 protein, partial cds	Mus musculus zinc finger protein Interacting with K protein 1 (Zik1), mRNA	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGFA6) mRNA	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	Homo sapiens gene encoding filensin, exon 8	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7	Homo sapiens MHC class 1 region	Homo saplens opioid receptor, delta 1 (OPRD1) mRNA	Homo saplens splice variant AKAP350 mRNA partial cas	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens partial TTN dene for fifth	Homo sapiens titin (TTN) mRNA	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 44 and partial cds
le Exon Prot	Top Hit Datábase Source	SWISSPROT	77	L L		12	Į.	L	Į.	NT	TN	TN	- LA	L,	NT.	 	NT	۲٦.	F	L7	TN	T.	LNT	TN				E			NT
Sing	Top Hit Acession No.	P52740	8922180 NT	AL163203.2	8923080 NT	7661979 NT	_					2.2	5032150 NT	6806918 NT		4585642 NT	3.1	6677648 NT	5174560 NT	4758199 NT	-	7705546 NT		0.0E+00 AF055066.1 N	4505508 NT	F091711.1	4507720 NT	4507720 NT	0.0E+00 AJ277892.1 N	4507720 NT	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 AL16320	0.0E+00	0.0E+00	0.0E+00 M94081.	0.0E+00 M94081	0.0E+00 X94628.1	0.0E+00 X94628.1	0.0E+00 M55582.	0.0E+00 AL163280	0.0E+00	0.0E+00	0.0E+00 X92841.1	0.0E+00	0.0E+00 AB01453	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y16723.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF091711	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D63562.1
	Expression Signal	4.1	76.0	8.0	7.78	0.95	1.66	1.66	1.69	1.69	1.08	3.22	0.99	0.82	1.44	1.97	1.18	2.26	1.05	8.64	1.2	1.61	1.33	24.91	2.43	2.46	5.48	5.48	0.86	12.01	0.95
	ORF SEQ ID NO:	24415	24417	24419	24424	24428	24429	24430	24432	24433	24436	24437	24447	24458	24460	24463	24464	24466	24467	24469	24471	24472		24477		24480	23791	23792	24484	24490	24493
	Exen SEQ ID NO:	14629	14631	14633	14637	14641	14642	14642	14644	14644	14647	14648	14660	14671	14673	14676	14677	14679	14680	14682	14684	14685	14686	4690 690	14692	14693	14013	14013	14697	14706	14709
	Probe SEQ ID NO:	4744	4746	4748	4752	4756	4757	4757	4759	4759	4762	4763	4776	4786	4788	4791	4792	4794	4/95	4797	4799	988	4801	4806	4808	4809	4812	4812	4814	4824	4827

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							1	1		-	1		1					1		2 .5	일 등	١	1	$\int$		ſ	T	Т
	Top Hit Descriptor	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylalytranstransferase) (FDPS) mRNA	Homo sapiens sialytransferase 8 (alpha-N-acetylneuraminate: alpha-2,8-sialytransferase, GD3 synthase) (SIAT8) mRNA	Human mRNA for transcription factor AREBS complete cde	Human mRNA for transcription factor AREBS, complete cds	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete eds)	Homo sabiens chromosome 21 segment HS21Cha4	UI-H-BI3-alv-f-02-0-UI st NCI CGAP Stins Home cantans of NA close 1446 CE 2000 CC	Homo sapiens hypothetical protein FL/11190 (FL/11190) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) gene, alternative splice products. partial cds	Homo sapiens titin (TTN) gene, alternative solice products, partial cds	Homo saplens titin (TTN) mRNA	Human ribosomal protein L21 mRNA, complete cds	601303729F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE 3638118 5'	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	Homo sapiens mRNA for KIAA1043 protein, partial cds	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens chromosome Xq28 melanoma antigen family A2a (WAGEA2A), melanoma antigen family A12 (WAGEA12), melanoma antigen family A2b (WAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDH), and 15	Homo sapiens chromosome Xq28 metanoma antigen family A2a (WAGEA2A), metanoma antigen family A12 (WAGEA12), metanoma antigen family A2b (WAGEA2B), metanoma antigen family A3 (MAGEA3), caltractin (CAI T) NADION dehirdrogenees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicensees ilicens	Homo sapiens tifn (TTN) mRNA	Homo sapiens tign (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens E2F transcription factor 2 (F2F2) mRNA	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene exon 3	Homo saplens chromosome 21 segment HS21C009
	Top Hit Database Scurce	TN TN		N-	LN	Į Į	N	EST HUMAN	N	N.	TN	Į.	Z	NT	EST_HUMAN	FN	ŢN	FZ	ΔŢ	ΙΝ	TN	-	5	17	5			NT
	Top Hit Acession No.	4503684 NT	4506952 NT			3.1	2	8.1	8922926 NT	4507720 NT	2.1	2.1			3.1	4758199 NT	.1	8923441 NT	8923441 NT			1507720	4507720 NT	4507720 NT	4507720 NT	4758225 NT	0.0E+00 AF016705.1	0.0E+00 AL163209.2
Most Similar	(Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 D15050.1	0.0E+00 D15050.1	0.0E+00 AB026898	0.0E+00 AL163284	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF058332	0.0E+00 AF05833;	0.0E+00	0.0E+00 U14967.1	0.0E+00 BE408863	0.0E+00	0.0E+00 AB028968	0.0E+00	0.0E+00	0.0E+00 U82671.2	0.0E+00 U82671.2	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.52	1.06	1.31	1.31	0.86	1.34	1.45	12	7.99	2.81	2.81	2.95	4.34	2.58	5.37	0.99	1.66	1.66	1.06	1.06	5.81	5.81	3.51	7.76	1.17	1.35	1.33
	ORF SEQ ID NO:	24496	24105		24509	24515	24530	24536		24490	24544	24546	24552			24569	24574	24584	24585	24596	24597	23791	23792	24602	24603		24619	1
	SEQ ID NO:	14713	14319	14726	14726				ļ	-1			14774	14777	14789	14794	14804	14817	14817	14830	14830	14013	14013	14834	14835	14843	14853	14862
1	Probe SEQ ID NO:	4831	4837	4845	4845	4854	4871	4879	4885	4886	4888	4888	4894	4897	4910	4915	4925	4930	4939	4953	4953	4957	4957	4929	4960	4968	4978	4987

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Table 4
Single Exon Probes Expressed in Heart

Single Exoli Plobes Expressed in Realt	Top Hit Database Source	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene	Homo sapiens partial TTN gene for titin	Homo saplens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo saplens titin (TTN) mRNA	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)	Homo sapiens vascular endothellal cadherin 2 mRNA, complete ods	Homo sapiens vascular endothellal cadherin 2 mRNA, complete cds	Homo sapiens cyclophilin (USA-CYP) mRNA	Homo sapiens G-protein coupled receptor (RE2), mRNA	Homo saplens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTIN) mRNA	Homo saplens titin (TTN) mRNA	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA	Human cellular fibronectin mRNA	Human cellular fibronectin mRNA	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) cene, complete cats	Homo saplens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Hono sapiens titin (TTN) mRNA	Human olfactory receptor-like gene, complete cds	Human offactory receptor-like gene, complete ods	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	Homo sapiens glypican 3 (GPC3) mRNA	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA	Homo saplens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
alfille -		호	노	4507720 NT	4507720 NT	4507720 NT	4507720 NT	¥	호	Z	5454153 NT	6677700 NT	4507720 NT	4507720 NT	4507720 NT	4507720 NT	4557362 NT	Ϋ́	TN	Ä	1507720 NT	4507720 NT	4507720 NT	LN	TN	4507720 NT	4507720 NT	TN	5360213 NT	IN	4885474 NT	4885474 NT	4758697 NT
ן מ	Top Hit Acession No.	0.0E+00 D50657.1	0.0E+00 AJ277892.1	45077	45077	45077	45077	0.0E+00 X52988.1	0.0E+00 AF240635.1	0.0E+00 AF240635.1			45077	45077	45077	45077		0.0E+00 M10905.1	0.0E+00 M10905.1	0.0E+00 U91328.1		45077	45077	L35475.1	L35475.1	45077	45077	0.0E+00 AF195658.1	53602	0.0E+00 AE000327.1	48854	. 48854	47586
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	37.78	2.29	3.02	4.23	2.89	2.89	2.43	1.84	1.84	1.01	1.22	11.22	11.22	14.9	14.9	1.33	1.03	1.03	1.06	3.04	6.27	6.27	1.34	1.34	9:38	9:38	0.94	1.35	0.8	1.06	0.96	1.59
	ORF SEQ ID NO:		24639	24640	24642	23791	23792	24660	24681	24682	24686	24698	23791	23792	23791	23792	24708	24713	24714	24715	24726	23791	23792	24743	24744	23791	23792	24765	24766	24768	24778	24793	24794
	Exan SEQ ID NO:	14865	14875	14876	14878	14013	14013	14892	14909	. 14909	14912	14926	14013	14013	14013	14013	14935	14940	14940	14941	14950	14013	14013	14967	14967	14013	14013	14992	14993	14997	15007	15026	15028
	Probe SEQ ID NO:	4990	5000	5001	5003	5005	5005	5018	5037	5037	5040	5054	5055	5055	5056	5056	5065	2070	5070	5071	2080	9609	5096	5098	5098	5099	5099	5124	5126	5130	5140	5159	5162

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Table 4
Single Exon Probes Expressed in Heart

כווולנים דילאו בפספת ווו ופפור	Exon ORF SEQ Expression (Top) Hit Accession Signel No: Signel Value Source Source Source Source Top Hit Descriptor	15031 24797 1.12 0.0E+00 AF245703.1 INT Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds	15031 24798 1.12 0.0E+00 AF245703.1 NT Homo saplens toll-like receptor 8 (TLR8) mRNA, complete cds	15050 24814 1.72 0.0E+00 AF006061.1 NT Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds	10.43 0.0E+00 4507720 NT	23792 10.43 0.0E+00 4507720 NT	15052 24816 6.75 0.0E+00 4507720 NT Homo sapiens titin (TTN) mRNA	15056 1.38 0.0E+00 AL163285.2 NT Homo sapiens chromosome 21 segment HS21C085		24823 3.97 0.0E+00	15059 24824 0.96 0.0E+00 4502398 NT Homo saplens beaded filament structural protein 1, filensin (BFSP1) mRNA	15086 15.86 0.0E+00 AF093093.1 NT Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15	0.0E+00 AF137286.1 NT	24831 2.25 0.0E+00 AF137286.1 NT	15150 24917 2.99 0.0E+00 9256579 NT Homo sapiens protocadhem alpha 13 (PCDHA13), mRNA	24926 3.82 0.0E+00 BE931080.1 EST_HUMAN	24930 3.12 0.0E+00 AF182034.1	15162 24931 3.12 0.0E+00 AF182034.1 NT Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds	24940 1.92 0.0E+00 X56163.1 NT	24941 1.92 0.0E+00 X56163.1 NT	- HUMAN		25034 1.67 0.0E+00 BE794412.1 EST HUMAN	25035 1.67 0.0E+00 BE794412.1 EST_HUMAN	15232 25037 5.46 0.0E+00[M29908.1 NT Homo sapiens eosinophil peroxidase (EPP) gene, exon 7	15234 25038 1.81 0.0E+00 A1791363.1 EST HUMAN HEAVY CHAIN PRECURSOR V-I REGION (HIMAN).	25044 5.42 0.0E+00 11421038 NT	T HUMAN	15247 25052 1.92 0.0E+00 BE538857.1 EST HUMAN 601061489F1 NIH MGC 10 Homo sapiens CDNA clone IMAGE:3447839 5	25075 1.31 0.0E+00 BE292784.1 EST_HUMAN	25080 1.8 0.0E+00 BF526328.1   EST_HUMAN	25081 1.8 0.0E+00 BF526328.1 EST_HUMAN	
								056				980																244					_
	Probe ES SEQ ID SEG NO: N	L .	5165 1	5186 1	5187 1		5189 1	5193 1	5195		5196 1				5226 1						5307 1	5308 1	5309 1	5309 1		5313 11		<u> </u>	5327 1				5348 1

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Table 4
Single Exon Probes Expressed in Heart

Exan ORF SEQ ID NO:	g	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
15272 25	25101	5.24	0.0E+00	0.0E+00 AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
15272 25	25102	5.24	0.0E+00	0.0E+00 AF257737.1	TN	Homo sepiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
	25114	1.45	0.0E+00	0.0E+00 D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
15282 25	25115	1.45	0.0E+00	0.0E+00 D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
15294 25	25141	1.67	0.0E+00	11420819 NT	IN	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
15305 25	25158	3.26	0.0E+00	0.0E+00 BF529931.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
15305 2E	25159	3.26	0.0E+00	0.0E+00 BF529931.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5
15308 25	25161		0.0E+00	0.0E+00 BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5
15315 25	25362	4.21	0.00+00	11434392 NT	LN	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
15341		2.43	0.0E+00	0.0E+00 AW867316.1	EST_HUMAN	MR0-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
15351 25	25405	3.05	0.0E+00	0.0E+00 BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
L	25406			0.0E+00 BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
15365 25	25420	1.31	0.0E+00	11420819 NT	IN	Homo sapiens offactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
15365 25	25421	1.31	0.0E+00	11420B19 NT	IN.	Homo sapiens offactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
15372 25	25429		0.0E+00	0.0E+00 AF064254.1	TN	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
15372 25	25430	5.35	0.0E+00	0.0E+00 AF064254.1	LN.	Homo sapiens very long-chain acyl-CoA synthetase homotog 1 mRNA, complete cds
15376 25	25435	2.9	0.0E+00	0.0E+00 AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
	436			0.0E+00 AJ224639.1	IN	Homo sapiens Surf-5 and Surf-6 genes
15390 25	25453			M85719.1	EST_HUMAN	EST02238 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCM48
15394 25	25459	3.67	0.0E+00	0.0E+00 AW405472.1	EST_HUMAN	UI-HF-BL0-adh-d-02-0-UI,r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 57
15408 25	25471	5.74	0.0E+00	0.0E+00 AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
15408 25	25472	5.74	0.0E+00	0.0E+00 AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
15408 25	25473	5.74	0.0E+00	0.0E+00 AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
15410 2	25475	1.88	0.0E+00	0.0E+00 U36261.1	LN	Human befa-prime-adaptin (BAM22) gene, exon 13
	27.2		L	7 3003074	144141111111111111111111111111111111111	2995b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
	20010	2	0.0=+00	U.UE+UU AA1959U5.1	ES HOMAN	MICSIN HEAVI CHAIN, SKELETAL MUSCLE (HUMAN);
	5516		0.0E+00	0.0E+00 AJ006345.1	LN-	Homo sapiens KVLQT1 gene
15449 2	25517	1.5	0.0E+00	0.0E+00 AJ006345.1	TN	Homo sapiens KVLQT1 gene
15454 2	25524	2	0.0E+00	0.0E+00 AI207616.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
15464 2	25534	3.98	0.0E+00	11416801 NT	TN	Hamo sepiens protocadherin beta 2 (PCDHB2), mRNA
15471 2	25542	6.76	0.0E+00	0.0E+00 BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_B Homo sapiens cDNA clone IMAGE:3677843 5
15472 29	25543	1.58	0.0E+00	10048478 NT	1.	Mus musculus aczonin (Acz), mRNA
15473 28	25544	3.03	0.0E+00	0.0E+00 U86961.1	EZ	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
	1					

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Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete zq81d03.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5 similar to Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA Homo saplens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA zc08h06.r1 Soares_paraffyroid_tumor_NbHPA Homo sepiens cDNA clone IMAGE:321755 5' 2208h06.r1 Soares_paraffyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5 zr40h01.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to zr40h01.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.; SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.; 602036272F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184321 Homo sepiens familial mental retardation protein 2 (FMR2) gene, exon 14 601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 6 601645287F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:3930453 5' 801558060F1 NIH_MGC_58 Homo sepiens cDNA clone IMAGE:3827775 5' 601558060F1 NIH_MGC_58 Homo sepiens cDNA clone IMAGE:3827775 5' 601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5 602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5 601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5 601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5 AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 Human G protein-coupled receptor GPR-9-6 gene, complete cds Fop Hit Descriptor RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA Human T cell surface glycoprotein CD-6 mRNA, complete cds Human T cell surface glycoprotein CD-6 mRNA, complete cds TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN.; Homo sapiens cadherin 20 (CDH20) mRNA, complete cds Homo sapiens peptide transporter 3 (LOC51296), mRNA Homo sapiens xylosyltransferase II (XT2), mRNA Homo sapiens xylosyltransferase II (XT2), mRNA Human anion exchanger (AE1) gene, exons 1-20 Single Exon Probes Expressed in Heart EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST_HUMAN** EST_HUMAN Top Hit Database EST_HUMAN HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN HUMAN Source EST 9789986|NT 눋 눋 11433071 NT 11435630 NT 11545913 NT 11545913 NT **Fop Hit Acession** 0.0E+00 AA193506.1 BE257173.1 0.0E+00 AA193506.1 0.0E+00 AA204740.1 BF569905.1 0.0E+00 AF217289.1 BE828144.1 0.0E+00|BE958636.1 0.0E+00 BE280197.1 0.0E+00 BE889610.1 0.0E+00 BF031742. 0.0E+00 AF012618.1 0.0E+00 BF338835. 0.0E+00 AU137772. 0.0E+00 W33069.1 0.0E+00 W33069.1 0.0E+00 U86961.1 0.0E+00 U34625.1 0.0E+00 U45982.1 0.0E+00 U34625.1 L35930.1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00.0 0.0E+00 0.0E+00 **0.0**元+0.0 0.0E+00 0.0E+00 0.0E+00 (Top) Hit BLAST E Most Simils Value 2.93 1.74 1.66 1.66 1.54 1.54 10.66 7 2.47 1.89 <del>1</del>.4 3.57 8 13.03 13.03 4.14 3.57 3.57 2.8 1.38 1.63 1.41 3.4 1.47 Expression Signal 25742 25566 25588 25589 25593 25613 25614 25634 25636 25642 25654 25655 25668 25672 25690 25691 25770 25771 25772 25790 25800 25811 25671 ORF SEQ ÖNQ 15510 15545 15664 15489 15515 15545 15548 19450 15574 15589 15589 5663 SEQ ID 15480 15482 15530 15530 15546 15561 15574 15638 15649 15664 15682 15690 15701 1551 15551 15561 ÿ Probe SEQ ID 5564 5574 5596 5597 5615 5615 5631 5631 5632 5634 5638 5649 5649 5660 5663 5680 5680 5755 5756 5756 5775 5784 5795 5566 5730 5741 ÿ

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'	UI-HF-BLO-acc-g-12-0-UI.st NIH MGC 37 Homo sapiens cDNA clone IMA CE: 3058754 31	以27503.r1 Soares placenta Nb2HP Homo saniens cDNA clone IMAGE・140033 5	Human gene for the light and heavy chains of myeloneroxidase	601305368F1 NIH MGC 39 Homo sapiens cDNA clone IMAGE 3636516 51	601305368F1 NIH MGC 39 Homo sapiens cDNA clone IMAGE:3639616 5'	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005380 5	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 51	ws25c07.xt NCI_CGAP_GC6 Homo saplens cDNA clone IMAGF-2498220 31	601105344F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE 3087983 51	601105344F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE-2987983 6	UI-HF-BLO-aco-h-02-0-UI.r1 NIH MGC 37 Homo sapiens cDNA clone IMAGE 3050031 F	UI-HF-BLD-aco-h-02-0-UI.r1 NIH MGC 37 Homo sepiens cDNA clone IMAGE:3050031 5	AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT 1a (CACNA1G) mRNA, complete cds	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 6' similar to TR:O15390 015390 GT24, [3] TR:O43840 TR:O43206 :	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:015390 015390 GT24, [3] TR:043840 TR:043208	601587561F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3841847 5'	601512058F1 NIH MGC 71 Homo saplens cDNA clone IMAGE:3913311 S'	601512058F1 NIH MGC 71 Home sapiens cDNA clone IMAGE:3313 15	Human antigen CD27 gene, exons 1-2	Homo sapiens chromosome 21 segment HS21C004	Hamo sapiens chromosome 21 segment HS21C004	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA	#31f11.x1 NCI_CGAP_GC8 Homo saplens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE_P17553 WNT-3 PROTO-ONCOGENE PROTEIN PERCI IDSOB	Homo sapiens zinc finder homeodomain protein (ATRE1.4) mRNA complete cuts	ZW52c03.r1 Soares total fetus Nb2HF8 9w Home caniens cDNA Alme IMAGE:772ccc F1	QV3-BN0047-300800-278-c06 RMnn47 Home caniens chiva	AU125928 NT2RM4 Homo saplens cDNA clone NT2RM40n2430 F	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	LN.	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	ŢN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	NT	LN	TN	EST HUMAN	N.	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	0.0E+00 AV650020.1	0.0E+00 AW575598.1	H01255.1	0.0E+00 X15377.1	0.0E+00 BE735989.1	0.0E+00 BE735989.1	0.0E+00 AU119245.1	0.0E+00 AU119245.1	0.0E+00 Al989483.1	0.0E+00 BE293153.1	0.0E+00 BE293153.1	0.0E+00 AW406348.1	0.0E+00 AW 406348.1	0.0E+00 AV719444.1	0.0E+00 AF190860.1	0.0E+00 AW163640.1	0.0E+00 AW163640.1	3.1	3.1	3.1		4.2	AL163204.2	6005983 NT	0.0E+00 Al638412.1	.32832.1	0.0E+00 AA434584.1	0.0E+00 BE925875.1	0.0E+00 AU125928.1	3E169131.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 H01255.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE79987	0.0E+00 BE88981	0.0E+00 BE88981	0.0E+00 L24493.1	0.0E+00	0.0E+00 AL16320	0.0E+00	0.0E+00	0.0E+00 L32832.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE16913
	Expression Signal	8.1	2.81	4.21	1.99	4.25	4.25	11.57	11.57	1.56	4.81	4.81	1.36	1.36	1.69	2.24	3.45	3.45	4.79	7.23	7.23	3.71	2.15	2,15	3.54	4.13	1.79	3.58	1.48	1.44	7.44
	ORF SEQ ID NO:		25848		25857	25862	25863		25870			25883	25931	25932	25951	25958	25964	25965	25978	25981	26982	25988	25991	25992	25999	26001	26002	26007	26019	26044	26076
	Exon SEQ ID NO:	15732	15736			15749	15749	15753	15753	15760	15765	15765	15807	15807	15826	15835	15841	15841	15856	15860	15860	15866	15869	15869	15875	15877	15878	15885	15896	15916	15944
	Probe SEQ ID NO:	5826	5830	5832	5838	5843	5843	5847	5847	5854	5859	5859	5901	5901	592·I	5930	5936	5836	5951	5955	5955	2961	5964	88 88	2970	5973	5974	5980	5991	6011	6041

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	II.5-GN0032-180900-145-d07 GN0032 Homo seniens cDNA	2088e03.rf Shatanene Hel a rell ca 0277318 Line control Control	11.3-ST0024-230799-001-801 ST0024 Homo sanians chila	IL3-ST0024-230799-001-B01 ST0024 Home seniers - ONA	Homo sapiens CD6 antinen (CD6) mRNA	801339977F1 NIH MGC 53 Homo septems ATMA street 11/4 AT A September 51	601443667E1 NIH MGC 65 Homo sapiens CDNA clans INA CE-2017207 FI	601443667F1 NIH MGC 65 Homo sapiens cDNA clane IMAGE-3847867 F	7b49f03.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN	CM1.HT08777J060900_307_41 HT0877 U.S	23403 rt Spares NhHMD: St Home conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the 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of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the conjunction of the c	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA	602/85859E1 NIH MCC 45 Home confers about 1	Human MYCI 2 gane complete Ads	Homo saniens cadharin 20 (CDH20) mDNA completed	Homo sabiens cadherin 20 (CDH20) mRNA commissional	Homo sapiens melanoma antican family b 2 (AAA CECS)	601448954F1 NIH MGC 19 Homo capiens child class like actions at	H. saplens mRNA for latent transforming growth factor-hele hinding and it is not as	H.sapiens mRNA for latent transforming growth factor-theta hinding protein (1 TDD 2)	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA complete cds	Homo sapiens ciliary dynein heavy chein o (DNAHo) may, complete cus	Homo sapiens NALP1 mRNA, commilete cals	602/85852F1 NIH MGC 45 Homo sapiens chiNA close 1846 CE 42346775 F1	Human type IV sodium channel alpha notwontide (CNIAA)	601889823F1 NIH MGC 17 Homo sabiens clova Alama MARCE 44 2504 21	University and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second 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	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	IN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	IN	EST HUMAN	NT	L	NT	LZ	EST HUMAN	NT	M	NT	N	L	T HUMAN		EST HUMAN	LN	T HI MAAN	П
	Top Hit Acession No.	0.0E+00 BF085667.1	AA190755.1	0.0E+00 Al940621.1	0.0E+00 Al940621.1	11435626 NT	BE566381.1	0.0E+00 BE867889.1	0.0E+00 BE867889.1	BE550162.1	BE550162.1	0.0E+00 BF088376.1	AA195106.1	11034810 NT	BF569905.1	103069.1	0.0E+00 AF217289.1	0.0E+00 AF217289.1	11420775 NT	0.0E+00 BE262941.1						0.0E+00 BF569905.1		3.1		T	0.0E+00 BE254103.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 AA1907	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE5563	0.0E+00	0.0E+00	0.0E+00 BE55016	0.0E+00 BE55010	0.0E+00	0.0E+00 AA1951	0.0E+00	0.0E+00 BF56990	0.0E+00 J03069.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z37976.	0.0E+00 Z37976.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L01978.1	0.0E+00	0.0E+00 [131302	0.05+00/	0.0E+00
	Expression Signal	1.81	3.15	6.08	6.08	3.07	1.98	13.15	13.15	2.07	2.07	1.46	3.84	10.28	2.57	2.32	2.8	2.8	2.75	5.63	2.32	2:32	2.83	2.83	1.35	2.18	3.58	5.61	1.78	1.34	1.41
	ORF SEQ ID NO:		26191				24867	24872	24873	26130	26131	26150			26118		26157	26158	24876	24842	24843	24844	24845	24846	24851	26213	26217	26224	26227	26241	26242
	<u> 0</u>		16046	16054		_ [	15104	15109	15109	16995	15995	16012	16015	15973	15982	15990	16019	16019	15112	15125	15126	15128	15127	15127	15132	16064	16067	16075	16078	16091	16092
	Probe SEQ ID NO:	6042	6063	6071	6071	9209	6094	6609	609	6101	6101	6118	6121	6126	6135	6142	6146	6146	6154	6168	6169	9169	6170	9179	6175	6178	6181	93	6183	6225	6226

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Exon NO:         ORF SEQ SIGNal SIGNAL         From the Similar Value SIGNAL         Most Similar Value No:         Top Hit Aces SIGNAL           16103 16116 16126 16126 16126 16137 16126 16137 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 161		Top Hit Descriptor	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'	AU143706 Y79AA1 Homo sapiens cDNA clons Y79AA1002365 5'	601431819F1 NIH MGC 72 Homo sapiens cDNA clone IMAGE:3917164 5'	601431819F1 NIH_MGC_72 Homo capiens cDNA done IMAGE:3917164 6	Homo sapiens keratin 12 (KRT12) gene, complete cds	Homo sapiens keratin 12 (KRT12) gene, complete cds	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDK), mKNA	qc67a07.x1 Scares_placenta_8tc9weeks_ZNbHP8tc9W Homo sapiens cUNA clone invAce::1 146444 s similar to SW:ARSD_HUMAN P61689 ARYLSULFATASE D PRECURSOR ;contains element HGR	repetitive element;	qc67a07.x1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR	repetitive element;	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mKNA	602035089F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4182839 5	zn60f09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5 similar to 1 K:C800502 G806562 NEBULIN.;	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	H.sapiens DNA for ZNGP2 pseudogene, exon 4	Human P2xt receptor mRNA, complete cds	Human P2x1 receptor mkNA, complete cds	EST368573 MAGE resequences, MAGD Homo saplens cDINA	EST362586 MAGE resequences, MAGA Homo sapiens cUNA	x539a05.y1 NCI_CGAP_LU31 Hamo septens CJNA clone IMAGE:2078640 3 SIMILIE TO IN. CLOROSO CLOSOSO HINF3/FH TRANSCRIPTION FACTOR GENESIS;	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001651 5	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA	zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	cn17405.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17405 random	
Exon NO:         ORF SEQ SIGNal SIGNAL         From the Similar Value SIGNAL         Most Similar Value No:         Top Hit Aces SIGNAL           16103 16116 16126 16126 16126 16137 16126 16137 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 16150 161	ום דייטיון ווחיי	Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	Z.	N	NT	N		EST_HUMAN		EST_HUMAN	TN	NT	EST HUMAN	EST_HUMAN	NT	NT	N	NT	Į.	EST_HUMAN	EST HUMAN	  EST_HUMAN	EST_HUMAN	N	EST HUMAN	H HIMAN	10-10-10-10-10-10-10-10-10-10-10-10-10-1
Exan SEQ ID ORF SEQ Expression (Top) Hit SEQ ID NO: Signal 16109 Hit SEQ ID NO: Signal 16109 Hit SEQ ID NO: Signal 16109 Hit SIGNAL 16109 161109 16126 26253 5.9 0.0E+00 161109 26259 1.31 0.0E+00 161109 26306 3.63 0.0E+00 161109 26306 3.63 0.0E+00 161109 26324 25.51 0.0E+00 161109 26325 25.51 0.0E+00 161109 26325 25.51 0.0E+00 161109 26325 25.51 0.0E+00 161109 26352 6.72 0.0E+00 161109 26352 6.72 0.0E+00 16201 26353 6.72 0.0E+00 16201 26353 11.09 0.0E+00 16201 26372 26329 11.09 0.0E+00 16201 26372 26329 11.09 0.0E+00 16201 26372 26329 11.09 0.0E+00 16201 26372 26339 11.09 0.0E+00 16201 16202 26363 11.09 0.0E+00 16201 16202 26363 11.09 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16202 26343 54.65 0.0E+00 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 16201 1620	פווט	rop Hit Acession No.	U133213.1	U143706.1	E891286.1	E891286.1	F137286.1	F137286.1	11436699			1128344.1		N128344.1	11426392	11426392	3F337375.1	AA128453.1	AF005213.1	AF005213.1	X70172.1	<b>U45448.1</b>	U45448.1	AW956503.1	AW950516.1	AW239326.1	AU117553.1	11427135	AA211663.1	A1750584 4	
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Exan SEQ ID ID NO: NO: NO: 16103 26253 16119 26280 15137 24830 15137 24831 16150 26306 16166 26324 16170 26326 16170 26329 16170 26329 16191 26353 16191 26353 16202 26362 16202 26363 16212 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 16221 26314 162			5.9	244	131	1.31	1.97	1.97	3.63	3.63		25.51		25.51	18.73	18.73	14.06	5.1	6.72	6.72	7.55	11:09	11.09	1.43	2.54	1.67	1.8	6,			
			26253	+	26279	26280	24830	24831	26305	26306								<u> </u>				اً ا									70400
		Exan SEQ ID NO:	16103	16110	18128	16126	15137	15137	16150	16150		16166		16166	16168	16168	16170	16172	16191	16191	16200	16202	16202	16210	l	1			16272		16321
			6927	1020	0220	0200	8773	6273	6286	6286		6302		8302	6304	6304	6306	6308	6328	6328	6337	6339	6339	6347	6349	6380	8400	8404	6717	3	8462

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	on17405.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTRC cn17405 rendom	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds	Homo saplens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete ods	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain (semanhorin) 54 (SEMA5A) mRNA	Homo sapiens transient receptor potential channel 5 (TRPCs) mRNA	601885465F1 NIH MGC 57 Homo sapiens cDNA clone IMAGE-4103729 F.	AU129622 NT2RP2 Homo saplens cDNA clone NT2RP2005913 5'	Homo saplens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5	601593156F1 NIH MGC 9 Homo saplens cDNA clone IMAGE 3947365 5	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 6'	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5	601481713F1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3884258 5'	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5	201106.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE 568410 51	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 51	Human amylolid-beta protein (APP) gene, exon 11	Human amyloid-beta protein (APP) gene, exon 11	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone INAGE:728719 5 similar to TR:G300482 G300482 POI = PEVFERSE TRANSCEDIA SE LOADO OF PERSONS SERVICES SIMILAR TO TREGATOR SERVICES SIMILAR TO TREGATOR SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICE	AL142402 Y794A1 Home saniene chNA clare V70A A4000277 E	602/53008F1 NIH MGC 81 Homo seniers CDNA clone MA CE 4304428 E	DK-Z0761P092 r1 761 (synonym: hamy?) Homo sepiens cDNA clara DK-Z2-Z64Daga E	DKF20761P092 r1 761 (synonym: hamv2) Home seniens cDNA clone DKF27761P092 s	601485254F1 NIH MGC 69 Home saciens cDNA clane IMAGE 3887772 st	UI-HF-BNO-akj-f-01-0-UI.r1 NIH MGC 50 Homo saplens cDNA clone IMAGE:3077406 FI	nilar to		
	Top Hit Database Source	EST_HUMAN	TN	Ā	LX	Z.	EST HUMAN		1	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	TN	MAMILIA TRA	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	AI752561.1	0.0E+00 AF064205.1	0.0E+00 AF064205.1	11417342 NT	6912735 NT		AU129622.1	4501848 NT	BE739870.1	BE739870.1	AU120424.1	AU120424.1	1.1	5.1	0.0E+00 AA149791.1	0.0E+00 BE736046.1	M34872.1	M34872.1	4A397551 1		2		0.0E+00 AL120124.1	0.0E+00 BE877693.1	AW500549.1	4W157233.1	3E745597.1	3E745597.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AI752561	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF21790	0.0E+00 AU12962	0.0E+00	0.0E+00 BE73987	0.0E+00 BE73987	0.0E+00 AU12042	0.0E+00 AU12042	0.0E+00 BE787610	0.0E+00 BE78761	0.0E+00	0.0E+00	0.0E+00 M34872.1	0.0E+00 M34872.1	0.0E+00 AA39755	0.0E+00 AU14240	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW50054	0.0E+00 AW15723	0.0E+00 BE745597	0.0E+00 BE745597
	Expression Signal	4.25	1.59	1.59	1.3	1.98	5.37	2.98	6.49	4.97	4.97	60.88	60.88	1.52	1.52	1.29	3.72	3.97	3.97	1.65	7.54	8.73	1.96	1.96	1.31	1.35	14.35	1.16	1.16
	ORF SEQ ID NO:	26487	26530	26531	26551	26569	26571	26576					26593	26614	26615	26690	26719	26729	26730	26749	26750	-	26783	26784		26810	26813	26842	26843
	Exan SEQ ID NO:	16321	16358	16358	16374	16389	16392	16397	16408	16413	16413	16414	16414	16432	16432	16502	16525	16534	16534	16554	16557	16568	16594	16594	16610	16621	16626	16854	16654
	Probe SEQ ID NO:	6462	6439	6439	6515	9230	6534	6539	6550	6555	6555	6556	6556	6574	6574	6622	6645	6654	6654	6674	2299	8899	6714	6714	6730	6742	6747	6775	6775

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens Xq pseudoautosomal region; segment 1/2	7d76a04 xt NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3278862 3' similar to TR:095793 095793 STAUFEN PROTEIN.;	wI80b10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone INAGE:2429275 3' similar to SW-COGT HI IMAN PEOSAL MATRIX METALL OPPORTEMINES 14 PORT INCOME.	601334790F1 NIH MGC 39 Home septems CDNA clone IMAGE SARRERS FI	601334790F1 NIH MGC 39 Homo sapiens cDNA clone IMAGE-3688655 5	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	273s08.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);	QV3-DT0045-221289-046-c07 DT0045 Homo seniens cDNA	QV3-DT0045-221299-046-c07 DT0045 Homo saplens cDNA	601452412F1 NIH MGC 66 Homo sapiens cDNA clane IMAGE:3858179 5	601452412F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3856179 5'	Homo sapiens chromosome 21 segment HS21C009	Homo saplens chromosome 21 segment HS21C009	601431238F1 NIH MGC 72 Home sapiens cDNA clone IMAGE:3016569 51	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 13 (MAP3K13) mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13) mRNA	H. saplens mRNA for gamma-glutamytransferase	H.sapiens mRNA for gamma-glutamyltransferase	H.sapiens mRNA for gamma-glutamyltransferase	xo46e01.x1 NCI_CGAP_UtI Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN):	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02	601236488F1 NIH MGC 44 Homo saniens cDNA clane MACE 3809700 F1	282e04.r1 Soares owarv filmor NhHOT Homo cantens a PMA along 1MA CE 722262 E1	601900571F1 NIH MGC 19 Homo seniens CDNA clone IMAGE: 44002 3	UI-H-BI1-adr-e-12-0-UI st NCI CGAP Subs Home seriens CNN alone 11/10-0-12-20-20	UI-H-BI1-adr-e-12-0-UI-S1 NCI CGAP Sub3 Homo saniens CDNA clone INA CE:2717567 3	601150051F1 NIH_MGC 19 Homo saplens cDNA clone IMAGE-3502838 5'	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'	
Sic Liver of	Top Hit Database Source	IN	EST_HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	NT	LN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	NT	EST HUMAN	F	NT	Z-L	N	NT	EST_HUMAN	EST HIMAN	Т	Т	EST HUMAN	Т	Т	EST_HUMAN	П	
5	Top Hit Acession No.	0.0E+00 AJ271735.1	0.0E+00 BE674157.1	A1885671.1	0.0E+00 BE563650.1	0.0E+00 BE563650.1	11427235 NT	11427235 NT	0.0E+00 AA398511.1	0.0E+00 AW364874.1	0.0E+00 AW364874.1	0.0E+00 BE612586.1	0.0E+00 BE612586.1	0.0E+00 AL163209.2		0.0E+00 BE890797.1	4768695 NT	4758695 NT				0.0E+00 AW513513.1	052650 1	0.0E+00 BE378495.1			0.0E+00 AW139673.1	-	0.0E+00 BE260272.1		
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 AI885671	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X98922.1	0.0E+00 X98922.1	0.0E+00 X98922.1	0.0E+00	0.0E+00 D52650 1	0.0E+00	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 BF700165	
	Expression Signal	2.72	22	1.36	1.31	1.31	1.44	1.44	3.89	1.45	1.45	1.21	1.21	1.25	1.25	2.01	2.4	2.4	2.85	2.85	2.85	1.36	3.64	4.46	1.31	4.32	1.41	1.41	2.39	1.83	
	S. D	26852	26878	26879	L	26888	26897	26898		82692		26942	26943	26956	26957		26984	26985	27026	27027	27028		27083	27081	27083		27088	27089	27104	27106	
	_ \cdot	16662	16689	16690	16696	16696	16703	16703	16730	16735		16748	16748	16758	16758	16778	16791	- 1	1	16833	16833	16870	16872	16888	16892	16893	16898	16898	16915	16917	
	Probe SEQ ID NO:	6783	6810	6811	6817	6817	6824	6824	6851	6856	6856	6989	6989	6879	6879	6899	6913	6913	6955	6955	6955	6993	6995	7011	7015	7016	7021	7021	7038	7040	

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		7	Т	7	Т	7	7	7	т-	Т	Т	7	7	_	-	<del>-</del>	-7	7	<del>- /</del>	۳-	٠,	4	11-11	<del></del>	4	1100			1),	<u> 31 .11</u> .	<u>)) 1</u>	ą.
Single Exon Probes Expressed in Heart	Top Hit Descriptor	602127664F1 NIH MGC 56 Homo sepiens cDNA clone iMAGE-428452 51	802127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5	or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S RIBOSOMAL_PROTEIN L7A (HUMAN):	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1 mRNA	Homo sapiens ankrin 1, erythrocytic (ANK1), transcript variant 1, mRNA	Homo sapiens ITGB4 gene for integrin beta 4 subunit exons 3.41	AV718377 FHTB Hamo sapiens cDNA clone FHTBAAF11 5'	xw73c07.xf NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECLIRSOR (HI MAN)	AU124051 NT2RM2 Homo saplens cDNA clone NT2RM2001575 5'	Homo saciens mRNA for KIAA0454 mortein nearles cole	hf48a09.x1 Scares NFL T GBC S1 Home capiens CDNA close 114A CE 2022 202	Inf48a09.x1 Soares NFL T GBC S1 Homo sapiens CDNA clone IMAGE: 2025005	DKFZp434C1814 s1 434 (synonym: htess) Homo seniens cDNA clans DKFZp434C1814 s1	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 31	Homo saplens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds	Homo seniens mRNA for KIAA1512 motein mortin adv	Homo sapiens fumor protein 573 (TP73) mRNA	Human ig rearranged H-chain epsilon-3 pseudonene constant region	Homo sapiens mRNA for KIAA0823 protein, partial cds	Homo sapiens mRNA for KIAA0823 protein, partial cds	AV660739 GLC Homo sapiens cDNA clone GLCGKG123'	Homo sapiens polycystin-L (PKDL), mRNA	601141119F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3140740 K	601141119F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3140740 5'	Human mRNA for GABA-A receptor, alpha 1 subunit	wq34a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:IMGB3_HUMAN	O15480 MELANOMA-ASSOCIATED ANTIGEN B3;	Homo sapiens protocadherin alpha 8 (PCDHA8), mRNA	EST370381 MAGE resequences, MAGE Homo saplens cDNA	Human endogenous retrovirus, complete genome	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
Jie Exon Pro	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	Z	LN LN	N.	EST_HUMAN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	TN	NT	N L	IN	N.	NT	EST_HUMAN	7706638 NT	EST HUMAN	EST_HUMAN	TN		EST_HUMAN	Ļ	EST HUMAN	Ę	ト
	Top Hit Acession No.	0.0E+00 BF700165.1	0.0E+00 BF700165.1		0947037	10947037 NT	0.0E+00 Y11107.3	-		1.		3.1			0.0E+00 AL040428.1	*	7	22857	K01241.1	0.0E+00 AB020630.1	AB020630.1	4V660739.1	7706638		2.1			_	3256595	1.1	9635487 NT	11436995 NT
	Most Similar (Top) Hit BLAST E Value				0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF133901	0.05+00	0.0E+00	0.0E+00 K01241.1	0.0E+00	0.0E+00 AB020630	0.0E+00 AV660739	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X14766.1	70.0	0.0E+00 AI954607.	0.0E+00	0.0E+00 AW95831	0.0E+00	0.0E+00
	Expression Signal	1.83	1.83	6.35	3.54	3.54	1.28	1.45	3.64	1.57	2.64	4.41	4.41	2.84	2.84	1.17	18.6	3.97	1.25	2.65	2.65	1.96	3.43	3.86	3.86	1.91		2.12	4.49	45.	1.49	6.88
	ORF SEQ ID NO:	27107	27108	27137		27143	27159		27169		27218	27219	27220		27242	27243	27244		27268	27272	27273	27277	27280	27298	27299	27313	00020	21320	2/324	27333	2/340	709/7
	Exan SEQ ID NO:	16917	16917	16946	16950	16950	16985	16972	16976	16979	17024	17025	17025	17053	17053	17054	17055	17075	17081	17084	17084	17087	17090	17108	17108	17118	17107	17131	16171	1/140	2 2	10171
	Probe SEQ ID NO:	7040	7040	7069	7073	7073	7088	7095	7099	7102	7147	7148	7148	7176	7176	7177	7178	7198	7204	7207	7207	7210	7213	7331	7231	7241	7250	7257	4C7 /	7260	2002	1,4001

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Single Exon Probes Expressed in Heart

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Top Hit Descriptor	Homo sapiens mRNA for KIAA0578 protein, partial cds	601589294F1 NIH_MGC_7 Homo sapiens cDNA clane IMAGE:3943463 5	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 51	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5	EST50505 Gall bladder I Homo sapiens cDNA 5' end	EST50505 Gall bladder I Homo saplens cDNA 5' end	be09f05.y1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus BcI-xL mRNA, complete cds (MOUSE);	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus muscutus	Bcl-xL mRNA, complete cds (MOUSE);	602023150F1 NCI_CGAP_Brn67 Hamo sapiens cDNA clone IMAGE:4158300 5'	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5	ow60h01x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN.:	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	qm09s06x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A.;	qm09s06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A :	EST366028 MAGE resequences, MAGC Homo saplens cDNA	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'	C06158 Human pancreatic Islet Homo sapiens cDNA clone hbc5605	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605	601578683F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3927548 5	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
Top Hit Detabase Source	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	IN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	INT	INT
Top Hit Acession No.	0.0E+00 AB011150.1	0.0E+00 BE794823.1	BE883843.1	0.0E+00 BE883843.1	0.0E+00 AA344601.1	AA344601.1	0.0E+00 BE207063.1			BF348013.1	BE712515.1	AL042278.1	0.0E+00 Al088043.1	11560151 NT	11560161 NT	0.0E+00 AI290909.1	A1290909-1		0.0E+00 AF153466.1	0.0E+00 BE255829.1	0.0E+00 BE781382.1	0.0E+00 BE781382.1	AW163779.1	0.0E+00 BE263191.1	C06158.1	C06158.1	BE746215.1	11437282 NT	11437282 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 BE88384	0.0E+00	0.0E+00	0.0E+00 AA34460	0.0E+00		0.0E+00	0.0E+00 BF34801	0.0E+00 BE71251	0.0E+00 AL 04227	0.0E+00	0,0E+00	0.0E+00	0.0E+00	0 0E+00 Al290909	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW1637	0.0E+00	0.0E+00 C06158.	0.0E+00 C06158.	0.0E+00 BE74621	0.0E+00	0.0E+00
Expression Signal	1.44	2.56	1.24	1.24	1.6	1.6	1.38		1.38	2.71	3	11.81	1.27	2.06	2.06	8.86	8.86	1.69	3.92	4.9	1.37	1.37	7.21	2.85	3.98	3.98	3.22	1.93	1.93
ORF SEQ ID NO:		27366	27374	27375	27383	27384	27426		27427		27457	27479	27503			26632	26633				27529	27530	27531	27541		27563	27566	27574	27575
Exon SEQ ID NO:	17166	17167	17174	17174	17184	17184	17227	l	17227		17252	17273	17292	L	16442	16444	16444	16445	17259	17321	17323	17323	17324	17335	17358	17358			17369
Probe SEQ ID NO:	7290	7291	7298	7298	7308	7308	7360		7360	7368	7383	7406	7425	7429	7429	7431	7431	7432	7450	7461	7463	7463	7464	7475	7488	7488	7490	7499	7499

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Single Exon Probes Expressed in Heart

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onigie Ekoni riobes Ekpresseu III near	Top Hit Descriptor	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'	Homo sapiens keratin 2e (KRT2E) gene, complete cds	Homo sapiens keratin 2e (KRT2E) gene, complete cds	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	Homo sepiens chromosome 9 duplication of the T cell receptor beta locus and trypsinoden gene families	ULHF-BN0-akj-c-07-0-UI.r1 NIH MGC 50 Homo sapiens cDNA done IMAGE:3077384 57	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds	AIGF≃androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA	AU132349 NT2RP3 Homo saplens cDNA clone NT2RP3004260 5'	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 6	60159558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5	60159558F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3949383 5'	Homo sapiens ĶIAA0345 gene product (KIAA0345), mRNA	AU132349 NT2RP3 Hamo sapjens cDNA clane NT2RP3004260 5'	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds	Homo sapiens leucocyte immunoglobulir-like receptor-1 mRNA, complete cds	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'	va72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE.2899977 3' similar to gb:Xo2152_cds1 L- LACTATE DEHYDROGENASE M CHAIN (HUMAN):	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5
וום באטוו רוטי	Top Hit Database Source	L	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	IN	EST HUMAN	NT .	TN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	N	EST_HUMAN	NT	NT	NT	EST HUMAN	EST_HUMAN	EST HUMAN	LN	EST_HUMAN
3115	Top Hit Acession No.	11437282 NT						0.0E+00 AW 500293.1		0.0E+00 AF029308.1	0.0E+00 AW 500526.1	0.0E+00 AF009668.1	0.0E+00 S78466.1	0.0E+00 S78466.1	0.0E+00 BE563320.1				1.1	0.0E+00 BE740490.1	2067					11	0.0E+00 BE280793.1	0.0E+00 AW236269.1	7235	0.0E+00 AU143673.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.00-100	0.0E+00	0.0E+00
	Expression Signal	1.93	1.47	2.59	2.59	1.47	1.76	1.76	1.25	1.25	2.45	1.34	2.56	2.56	2.57	1.62	2.17	2.17	7.73	. 7.73	1.76	2.22	1.86	. 2.72	2.72	1.65	2.44	1.74	1.91	5.98
	ORF SEQ ID NO:	27576	27509	27591	27592	27612	27626	27627	27629	27630	L		27691	27692	27693	27701	27722			1				27776			27795	27800		27826
	Exon SEQ ID NO:	17369	17302	17381	17381	17399	17410	17410	17414	17414	17431	17458	17472	17472	17473	17481	17500	17500	17509	17509	17516	17532	17533	17551	17551	17558	17570	17578	17586	17603
	Probe SEQ ID NO:	7499	7514	7530	7530	7548	7559	7559	7563	7563	7580	7607	7621	7621	7622	7630	7650	7650	7659	7659	7666	7682	7683	7701	7701	7708	7720	7728	7736	7753

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Single Exon Probes Expressed in Heart

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Top Hit Descriptor	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'	Homo saplens killer cell inhibitory receptor KIRCI gene, exons 2.3 and 4.	Homo sapiens HEF like Protein (HEFL), mRNA	Homo sapiens HEF like Protein (HEFL), mRNA	AU136637 PLACE1 Homo saplens cDNA clone PLACE1004737 5	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial 7NF143 gene	Homo sapiens partial RANBP7 gene for RanBP7//moorin7 and partial 2NE/43 gene	ZP97h11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE-628197 5	231f01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE おなるなち Fr	최31f01.r1 Soares, pregnant, uterus, NbHPU Homo sapiens cDNA clone IMAGE : Fin RA45 등	Homo sapiens KIF4 (KIF4) mRNA, complete cds	601570712F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE 3845403 5	601570712F1 NIH MGC 21 Homo sabiens cDNA clone IMAGE-RAZARA R'	Homo saplens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504) mRNA	Homo sapiens mRNA for actin binding protein ABP620 commister onle	Homo saplens mRNA for estroden receptor hela complete cols	Homo sapiens mRNA for estrogen receptor beta, complete cds	zq08h11.r1 Stratagene muscle 837209 Homo saplens cDNA clone IMAGE:628965 5' similar to TR:G407097	502037045F1 NCI CGAP Brink Paniers CDNA class (MACE 1464000 F)	602037045F1 NCI CGAP Brief4 Homo sapiens CDNA Aprie 1848 CE-448200 E	FB23A4 Fetal brain, Strategene Homo sapiens CDNA clone FR23A4 3 and	nab45e12.x1 Soares NSF F8 9W OT PA P S1 Homo saniens cDNA clone IMAGE: 3285274 31	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'	xu74b01x1 NCI_CGAP_Kld8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN HIMAN).	601078764F1 NIH MGC 12 Homo saniens cDNA close IMA CE 3464773 F	601467419F1 NIH MGC 67 Homo saniens cDNA clone IMAGE:387700 E	RC2-BT0642-150200-012-d03 RT0642 Homo semiens cPNA	RC2-BT0642-150200-012-d03 BT0642 Home saniens cDNA	601573895F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE: 3835409 R	601573895F1 NIH_MGC_9 Hamo sapiens cDNA clone IMAGE:3835198 5	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
. Top Hit Database Source	EST HUMAN	LN LN	N N	L L	EST HUMAN	EST HUMAN	F	NT	EST HUMAN	EST HUMAN	EST_HUMAN	TN	EST HUMAN	EST HUMAN	7	TN	TN	NT	בכד עוואאוו	Т	HUMAN	Г	Г	EST_HUMAN		Т	Т	Т	Т		EST_HUMAN	EST_HUMAN
Top Hit Acession No.	AU143673.1	AF072408.1	11421001 NT	11421001 NT	AU136637.1	AU136637.1	0.0E+00 AJ295844.1	0.0E+00 AJ295844.1	AA196387.1	AA131248.1	AA131248.1	0.0E+00 AF179308.1	BE730772.1	BE730772.1	11560151 NT	0.0E+00 AB029290.1	AB006590.1	4B006590.1	441947701	3F340331.1	3F340331.1		0.0E+00 BF436218.1	0.0E+00 AV654765.1	0.0E+00 AW517960 1	0.0E+00 BE549213.1	0.0E+00 BE781742.1	0.0E+00 BE082720.1	3E082720.1	0.0E+00 BE743215.1	0.0E+00 BE743215.1	1.5711075.1
Most Similar (Top) Hit BLAST E Value	0.0E+00 AU14367	0.0E+00 AF07240	0.0E+00	0.0E+00	0.0E+00 AU13663	0.0E+00 AU13663	0.0E+00	0.0E+00	0.0E+00 AA196387	0.0E+00 AA13124	0.0E+00 AA13124	0.0E+00	0.0E+00 BE73077	0.0E+00 BE73077;	0.0E+00	0.0E+00	0.0E+00 AB006590	0.0E+00 AB006590	0.05+00	0.0E+00 BF340331	0.0E+00 BF340331	0.0E+00 T03078.1	0.0E+00	0.0E+00	0.01100	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE082720	0.0E+00	0.0E+00	0.0E+00 AV711075
Expression Signal	5.98	7.52	2.48	2.48	2.96	2.96	2.13	2.13	4.01	1.17	1.17	1.46	3.45	3.45	1.24	1.64	5.19	5.19	3.27	5.43	5.43	1.37	2.35	2.05	3.55	90'9	1.65	2.23	2.23	1.69	1.69	2.33
ORF SEQ ID NO:	27827	27830	27832	27833		27869	27879	27880			27916	27937		27960		27987	27991	27992	27993	27994	27995	28036	28065		28072	28074	28092	28101	28102	28111	28112	28170
Exon SEQ ID NO:	17603						L	17645	17654	17673	17673	17692			17742	17747	17753	17753	17754	17755	17755	17796	17822	17823	17832	17834	17851	17858	17858	17865	17865	17924
Probe SEQ ID NO:	7753	7756	7758	7758	7785	7785	7795	7795	7804	7823	7823	7842	7865	7865	7892	7897	7903	7903	7904	7905	7905	7946	7972	7973	7982	7984	8001	8008	8008	8015	8015	8032

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA	EST375636 MAGE resequences, MAGH Homo sapiens cDNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' sImilar to TR:060566 0e0568 VDX;	TCAAP3D0817 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sepiens cDNA clone TCAAP0817	wb28a12.x1 NCI_CGAP_GC8 Homo saplens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element:	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element	Homo sapiens NOD2 protein (NOD2) mRNA	Homo sapiens NOD2 protein (NOD2) mRNA	UI-HF-BL0-acm-d-04-0-UI-r1 NIH MGC 37 Homo sapiens cDNA clone IMAGE:3059383 5'	Homo saplens hypothetical protein FLJ20079 (FLJ20079), mRNA	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA	Homo sapiens 6-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA	wu32b06.x1 Soares_Dieckgraefe_cdon_NHCD Homo saplens cDNA clone IMAGE 2521715 31	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'	Homo saplens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	601674332F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3957343 51	2p95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN SKEI FTAI MISCI F (HI MAN)	601588829F1 NIH MGC 7 Homo sabiens cDNA clone IMAGE:3043015 51	AV727362 HTC Homo saplens cDNA clone HTCAOH08 5'	AV727362 HTC Homo sapiens cDNA done HTCAQH06 5'	xy04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852225 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN):	AU135741 PLACE1 Homo sepiens cDNA done PLACE1002794 5'	
	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	1	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST LIMAN	LO LO	LN L	EST_HUMAN	TN	R	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	LΝ	. 1	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	
, <del> </del> -	Top Hit Acession No.		0.0E+00 AW813783.1	Ļ	11431124 NT	11431124 NT	0.0E+00 AW057621.1	0.0E+00 BE243270.1	0.0E+00 Al652239.1	0.0E+00 AIR52238 1	11545911 NT	11545911 NT	0.0E+00 AW404795.1	11424829 NT	4504536 NT	4504536 NT		0.0E+00 BE882109.1		8923939	3333	0.0E+00 BE903304.1	0.0E+00 AA195905.1		0.0E+00 AV727362.1	0.0E+00 AV727362.1	0.0E+00 AW516055.1	0.0E+00 AU135741.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.05+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	00+100	0.00.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	
	Expression Signal	2.33	6.11	6.43	2.5	2.5	1.99	1.92	4.86	4 86	291	2.91	2.01	4.8	9.16	9.16	2.73	3.04	10.56	22.36	22.36	1.91	4.05	4.69	6.8	6.8	17.96	217	
	ORF SEQ ID NO:	28171		28178		28192	28195	28200	28201	28202	28209	28210	28221	28224	28225	28226	28227	28231	28233	28234	28235	28247	25516	28269	28277	28278	28296	28301	
	Exan SEQ ID NO:		17926	17931	17942	17942	17945	17950	17951	17951	L	<u> </u>	17972		ļ	Į	17971	17980	17984	- 1	- 1	18000	15448	18022	18031	18031		18049	
	Probe SEQ ID NO:	8032	8034	8040	8051	8051	8054	8059	0908	8060	8908	8068	8081	8084	8085	8085	8086	8083	8093	8095	8095	8110	8113	8134	8143	8143	8156	8161	

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oliigie Exuli riones Expresseu III nealt	Top Hit Descriptor	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;	H.sapiens mRNA for H1 histamine receptor	HSC3IC031 normalized Infant brain cDNA Homo sapiens cDNA clone c-3ic03	Homo sapiens RGH1 gene, retrovirus-like element	xw66f01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);	UI-H-Bi3-ah-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3	UI-H-BI3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'	Homo sapiens ribosomal protein L31 (RPL31) mRNA	Homo saplens mRNA for KIAA0667 protein, partial cds	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'	Homo sapiens mRNA for KIAA0545 protein, partial cds	Homo saplens of cardiac alpha-myosin heavy chain gene	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-	LACTATE DEHYDROGENASE M CHAIN (HUMAN);	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:17527723'	qf43c03.x1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772.3'	QV4-ST0234-121199-032-b06 ST0234 Homo sapiens cDNA	AU116908 HEMBA1 Homo saplens cDNA clone HEMBA1000255 5'	Homo sapiens insulin receptor (INSR), mRNA	QV0-UM0083-170400-191-d06 UM0093 Homo sapiens cDNA	QV0-UM0083-170400-191-d06 UM0093 Homo sapiens cDNA	602037014F1 NC _CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184979 57	601148357F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3163310 5'	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17	Homo sapiens of cardiac alpha-myosin heavy chain gene
שונים באחון	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	IN	EST_HUMAN	NT	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	INT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	L L	NT
) IIO	Top Hit Acession No.	0.0E+00 AW59333.1	0.0E+00 AW593333.1	0.0E+00 AW 593333.1	234897.1	F13069.1	J10083.1	0.0E+00 AW338094.1	0.0E+00 AW451230.1	0.0E+00 AW451230.1	4506632 NT	0.0E+00 AB014567.1	0.0E+00 BE298449.1	0.0E+00 AB011117.1	Z20656.1	0.0E+00 BE792155.1	0.0E+00 BF684061.1	0.0E+00 AU118386.1		0.0E+00 AW236269.1	0.0E+00 AI149809.1	AI149809.1	0.0E+00 AW391937.1	0.0E+00 AU116908.1	11424726 NT	0.0E+00 AW804516.1	0.0E+00 AW804516.1	0.0E+00 BF340308.1	0.0E+00 BE261209.1	U50326.1	Z20656.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z34897.1	0.0E+00 F13069.1	0.0E+00 D10083.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z20656.1	0.0E+00	0.0E+00	0.0E+00.		0.0E+00	0.0E+00	· 0.0E+00 A1149809.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00 U50326.1	0.0E+00 Z20656.1
	Expression Signal	3.45	3.45	3.45	1.82	2.8	2.12	2.92	5.64	5.64	14.21	2.03	2.35	1.88	59.52	3.47	25.37	6.16		2.72		6.77	3.05	4.62	18.63	1.78	1.78	2.14	49.5	2.53	68.7
	ORF SEQ ID NO:	28304	28305	28306				28328	ŀ	28330			28346		28363	28371		28374				28379	28380					28394			28404
	Exan SEQ ID NO:	18054	18054	18054	18056	18057	18064	18077	18078	18078	10179	18081	18092	18106	18109	18120	18121	18124	ı	- 1			18131	18142		18151			-		18162
	Probe SEQ ID NO:	8166	8166	8166	8168	8169	8176	8191	8192	8192	8194	8196	8208	8224	8227	8240	8241	8244		8245	8250	8250	8251	8262	8265	8271	8271	8272	8273	8282	8283

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8287		28409	3.52	0.0E+00	0.0E+00 BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
8287	7 18166		3.52	0.0E+00	0.0E+00 BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
8307	18184	28431	24.55	0.0E+00	0.0E+00 AA740782.1	EST HUMAN	ob32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element
8313	18190	28439	3.12	0.0E+00	0.0E+00 AF252303.1	NT.	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
8326	3 18203		149.55	0.0E+00	0.0E+00 C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4817
8333		28460	2.17	0.0E+00	0.0E+00 AA746375.1	EST HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Hamo sapiens cDNA clone IMAGE:1309009 5'
8333			2.17	0.0E+00	0.0E+00 AA746375.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
8341		28470	2.41	0.0E+00	0.0E+00 M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
8341		28471	2.41	0.0E+00	0.0E+00 M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
8344		28472	1.82	0.0E+00		EST_HUMAN	QV2-HT0698-020800-295-407 HT0698 Homo sapiens cDNA
8345			8.08	0.0E+00	0.0E+00 AL157608.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo saplens cDNA clone DKFZp761J2116 5'
8357	18234	28482	10.53	0.0E+00	0.0E+00 AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
8375		28503	1.86	0.0E+00	0.0E+00 BF366553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
8395			3.78	0.0E+00	1.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
8395	18271	28524	3.78	0.0E+00	0.0E+00 BE182360.1	EST_HUMAN	PMo-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
8405			3.46			EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
8410		28539	1.74	0.0E+00	0.0E+00 AW500307.1	EST_HUMAN	UI-HF-BNO-akg-d-02-0-UI.r1 NIH_MGC_50 Homo saplens cDNA clone IMAGE:3077019 5'
8410		28540	1.74	0.0E+00	0.0E+00 AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
8442		28574	4	0.0E+00	0.0E+00 BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
8443			1.96	0.0E+00	1	EST_HUMAN	ao86g11.x1 Schiller meningloma Homo sapiens cDNA clone IMAGE:1952804 3'
8443	3 18317	28576	1.96	0.0E+00	0.0E+00 AI459545.1	EST_HUMAN	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:19528043'
8455	18328	28587	88.73	0.0E+00	0.0E+00 F00884.1	EST HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
							HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone
8455	5 18328	28588	88.73	0.0E+00	0.0E+00 F00884.1	EST_HUMAN	77E12
8480			3.88	0.0E+00	4758827 NT	NT	Homo sapiens neurexin III (NRXN3) mRNA
8481		28619	4.54	0.0E+00		EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
8483		28620	16	0.0E+00	4.1	EST_HUMAN	UI-H-BI2-age-h-01-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
8484			3.77	0.0E+00	5.1	EST HUMAN	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
8484			3.77	0.0E+00		EST_HUMAN	RC0-CT0380-210100-032-c10 CT0380 Hamo saplens cDNA
8488			6.91	0.0E+00		NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
8488	3 18361	28626	6.91	0.0E+00	0.0E+00 AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds

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Single Exon Probes Expressed in Heart	Top Hit Descriptor Source	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E18 EST_HUMAN 55KDA-ASSOCIATED PROTEIN.;	ba04d07.yf NIH_MGC_7 Home sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B_ EST_HUMAN 55KDA-ASSOCIATED PROTEIN: ;		T_HUMAN	EST_HUMAN RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA	EST_HUMAN RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA	pp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627833 5' similar to gb:X03740 EST_HUMAN MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	EST_HUMAN   UI-H-BI4-aok-b-10-0-UI.s1 NOI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'			EST_HUMAN   601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5		T_HUMAN	NT Homo sapiens mRNA for KIAA1316 protein, partial cds	NT Homo sapiens mRNA for KIAA1316 protein, partial cds					EST_HUMAIN   dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'	NT Human gamma actin-like pseudogene, complete cds	wf20e11.x1 Soares_Dieckgraafe_colon_NHUC Homo saplens cDNA clone IMAGE:2351180 3: similar to EST HUMAN   gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);	EST_HUMAN 601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5	EST_HUMAN 601889823F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4123948 5	Г	EST_HUMAN 601439605F1 NIH_MGC_72 Homo sapiens cDNA done IMAGE:3924577 5'		EST_HUMAN   601861947F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:4081715 5	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B EST HUMAN 55KDA-ASSOCIATED PROTEIN.:
ın Heart	Тор	MGC_7 Homo sapiens cDNA cl ATED PROTEIN.;	_MGC_7 Homo sapiens cDNA cl ATED PROTEIN.;	lyosin, heavy polypeptide 4, skele	20900-385-b12 UM0091 Homo s	10500-110-h04 HT0230 Homo sa	10500-110-h04 HT0230 Homo sa	tagene muscle 937209 Homo sap Y CHAIN, SKELETAL MUSCLE	10-0-UI.s1 NOI_CGAP_Sub8 Ho	10-0-UI.s1 NCI_CGAP_Sub8 Ho	<b>JE1 Homo sapiens cDNA clona F</b>	IH_MGC_69 Homo sapiens cDN	IH_MGC_69 Homo sapiens cDN	IH_MGC_55 Homo sapiens cDN	nRNA for KIAA1316 protein, parti	ıRNA for KIAA1316 protein, parti	stinoblastoma-like 2 (p130) (RBL	etinoblastoma-like 2 (p130) (RBL:	ukaryotic translation initiation fact	IH_MGC_81 Homo sapiens cDN	MGC_3 Homo sapiens cDNA cl	actin-like pseudogene, complete o	res_Dieckgraefe_colon_NHUC H 3AMMA-1 CHAIN C REGION (H	IH_MGC_17 Homo sapiens cDN	IH_MGC_17 Homo saplens cDN	30800-333-e04 NN0054 Homo s	IIH_MGC_72 Homo sapiens cDN	odgin-like protein (GLP), mRNA	IIH_MGC_53 Homo saplens cDN	MGC_7 Homo sapiens cDNA o
robes Expressec	9			Homo sapiens n	П										Homo sapiens n	Homo saplens n	Homo sapiens re	Homo sapiens re				Human gamma		Т		Г	П	Homo saplens g		
gle Exon F	Top Hit Databas Source	EST_HUMA	EST_HUMA	F	EST_HUMA	EST_HUMA	EST_HUM	EST_HUM	EST_HUM	EST_HUM	EST_HUM	EST_HUM/	EST_HUM	EST_HUM	LN LN	NT	NT	NT	M	EST_HUM	EST_HUM/	NT	  EST HUM	EST_HUM	EST_HUM/	EST_HUM/	EST HUM	NT	EST_HUM	EST HIM
Sin	Top Hit Acession No.	0.0E+00 BE206848.1	0.0E+00 BE206846.1	11024711 NT	0.0E+00 BF093687.1	0.0E+00 BE148076.1	0.0E+00 BE148076.1	0.0E+00 AA195905.1	0.0E+00 BF507876.1	0.0E+00 BF507876.1	0.0E+00 AU135170.1			0.0E+00 BF240536.1	0.0E+00 AB037737.1	0.0E+00 AB037737.1	11430868 NT	11430868 NT	4503544 NT	0.0E+00 BF576267.1	0.0E+00 AW328173.1	0.0E+00 M55083.1	0.0E+00 Al660968.1	0.0E+00 BF306996.1	0.0E+00 BF306996.1	0.0E+00 BF362462.1	0.0E+00 BE897051.1	8923698 NT	0.0E+00 BF207662.1	0.0E+00.BE206846.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	.0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	2.59	2.59	2.85	2.01	2.9	2.9	6.47	4.47	4.47	2.16	5.62	5.62	10.32	3.05	3.05	3.49	3.49	6.1	2.49	5.44	120.65	3.18	3.64	3.64	26.88	4.07	2.89	2.24	4.61
	ORF SEO ID NO:	28628	28629	28648	28651	28653	28654	28665	28687	28688	28692	28696	78697		28713	28714	28717	28718	28734	28741	28744		28750		28753	l 		28793		28833
	Exon SEQ ID NO:	18363	18363	18383	1	18390	18390	18398	18418	18418	18423	18427		18435	18445	18445	18449	18449	18463	18470	18472	18475	18479	<u>L</u> _	18481	18486	18504	18512	18514	18550
	Probe SEQ ID NO:	8490	8490	8511	8514	8518	8518	8526	8546	8546	8553	8557	8557	8566	8577	8577	8581	8581	8596	8603	8605	8098	8612	8614	8614	8620	8639	8648	8650	8661

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Table 4
Single Exon Probes Expressed in Heart

ba04d07.y1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:2823373 5' similar to TR:O76022 076022 E18. h22b10.x1 NCl_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316699 3' sImilar to TR:Q13458 Q13458 wn83g03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ 7f27f12.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:3285919 3' similar to TR:O00409 O00409 wz91h01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 ni42c08.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHAnz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 nz11c07.s1 NCI_CGAP_GCB1 Hamo sapiens cDNA clone IMAGE:1287469 3' similar to TR:Q13686 DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 51 DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5 Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds Homo saplens polycystic kidney disease-associated protein (PKD1) gene, complete cds wp06g08x1 NCL_CGAP_Kid12 Homo capiens cDNA clone IMAGE:2464094 3 601501090F1 NIH_MGC_70 Homo saplens cDNA clone IMAGE:3902926 5' 601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5 601572186T1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:3839012 3 601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3 dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5 AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5 AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5 AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5 Top Hit Descriptor MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA QV0-CT0225-101299-071-f06 CT0225 Homo sapiens cDNA Homo sapiens KIAA0247 gene product (KIAA0247), mRNA IL5-HT0731-020500-077-f05 HT0731 Homo sapiens cDNA ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN); Q13686 ALKB HOMOLOG PROTEIN.; CE11040 ZINC FINGER, C2H2 TYPE; Q13686 ALKB HOMOLOG PROTEIN. CHECKPOINT SUPPRESSOR 1.: 55KDA-ASSOCIATED PROTEIN. RECEPTOR (HUMAN) TRIO.: EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST_HUMAN Top Hit Database EST_HUMAN EST HUMAN Source 눋 Top Hit Acession 11435244 0.0E+00 AW753028.1 0.0E+00 AW006022.1 0.0E+00 AW387776.1 0.0E+00 AW387776.1 0.0E+00 BE185656.1 0.0E+00|AA760913.1 0.0E+00|BE206846.1 0.0E+00|AA558707.1 0.0E+00 AW327895. BE910546.1 0.0E+00|BE676347.1 0.0E+00|AA760913.1 0.0E+00 BF002333.1 0.0E+00 AL046540.1 0.0E+00 AL046540.1 0.0E+00 AI923116.1 0.0E+00 BE748899.1 0.0E+00 BE748899.1 0.0E+00 AU141882. AU141882. ģ 0.0E+00 A1934954.1 0.0E+00 BE622317. 0.0E+00 L39891.1 0.0E+00 L39891.1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 (Top) Hit BLAST E **Jost Simila** 4.73 2.36 4.74 12.53 4.18 4.18 2.78 2.78 4.02 1.91 10.47 3.19 4.61 7.41 2.33 10.47 2.97 2.35 2.97 257 Expression 28834 28836 28800 24915 28842 28812 28813 28823 28863 28864 28130 28876 28888 28925 28943 28962 28963 ORF SEQ 28869 28924 28982 28941 ÖNO 18550 18518 SEQ ID 18552 18557 15148 18529 18539 18580 18580 17886 18589 18589 18599 18640 18640 18653 19474 18673 18673 18690 18558 18611 18584 18650 ġ SEQ ID 8670 8843 8663 8668 8669 8700 8712 8712 8724 8737 8772 8722 8724 8728 8772 8784 8797 8840 8861 8878 8661 8861 8827 8827 8837 8837 ÿ

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Table 4
Single Exon Probes Expressed in Heart

a alega della alega Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, atternatively Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 UI-HF-BNO-ama-c-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5 Homo sepiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA Homo saplens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA Human von Willebrand factor pseudogene corresponding to exons 23 through 34 601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5' 601237691F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3609623 5 601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5' 602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5 601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5' RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA 602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5 601676357F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3958935 5 601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5 601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5 601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 6 601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5 601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5' Human lambda-immunoglobulin constant region complex (germline) Human lambda-immunoglobulin constant region complex (germline) Top Hit Descriptor RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); Homo sapiens KIAA0247 gene product (KIAA0247), mRNA Human beta-prime-adaptin (BAM22) gene, exon 5 77E12 spliced spliced EST HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** Top Hit Database EST_HUMAN **EST HUMAN EST HUMAN** Source 눋 눋 눋 Ę 11435244 NT 11427345 NT 11427345 NT 7669505 NT 11024711 NT 11427345 7669505 Top Hit Acession 0.0E+00 AW505430.1 0.0E+00 AF223391.1 BE297175.1 BE379254.1 BE379254.1 BE794758.1 BE698861.1 0.0E+00 AA211663.1 0.0E+00 AF223391.1 BE698861.1 0.0E+00 BE879633.1 0.0E+00 M60676.1 BE409993. BF681641.1 BF681641.1 0.0E+00 BE903372. BF309120.1 BE879633. BF312552. 0.0E+00 X51755.1 0.0E+00 X51755.1 0.0E+00 F00884.1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 (Top) Hit BLAST E 0.0E+00 0.0E+00 0.0E+00 0.06.+50 Most Simila Value 2.57 5.52 2.04 2.04 4.08 3.25 31.52 63.21 37.53 2.93 6.35 2.32 5.66 3.22 6.15 6.15 3.02 3.02 20.36 1.98 1.98 31.56 36.47 34.29 1.93 1.93 36.47 Expression Signal 28989 26434 29005 29006 29014 29018 29036 28983 28987 28990 29015 29019 29026 ORF SEQ 29007 29017 29021 29034 29035 29037 29062 29063 29066 29076 29077 29078 29081 ÖΝQ 18725 SEQ ID 18696 18710 18712 18742 18742 18775 18690 18694 18696 16272 18724 18724 18724 19475 15883 18711 18723 18725 18732 18786 18786 18792 18727 18727 18741 18741 18771 18771 18787 ġ 8916 8885 8885 988 8088 8088 SEQ ID 8902 8903 8904 8915 8916 8878 8883 8916 8917 8917 8919 8919 8924 8933 8933 8934 8934 8964 8965 8962 8969 8981 8981 8982 8987 ÿ

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Top Hit Descriptor	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds	Homo sapiens of cardiac alpha-myosin heavy chaln gene	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 6	Homo sapiens chromosome 21 segment HS21C046	qe17b12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:17392313'	Hamo sapiens gene for AF-6, complete cds	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mKNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	DKFZp434K0819_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434K0819 5	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5	IL-BT030-271098-001 BT030 Homo sapiens cDNA	yv40e08.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;	Homo sapiens adenylosuccinate lyase gene, complete cds	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sepiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA	Homo sapiens X-linked anhidrotitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	TOUROUTES	Homo sapiens low density lipoprocein-related protein Z (LNT Z), Illinum	hg31e06x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element,contains element MER22 repetitive element;	RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5 flanking region and partial cds	Human endogenous retrovirus, complete genome	an05h04.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'	QV-BT065-020399-103 BT065 Homo saplens cDNA	
Top Hit Database Source	EST_HUMAN	NT		EST_HUMAN	NT	EST_HUMAN	NT	NT	NT	NT		NT	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	FST HUMAN	NT	LN LN	TN	NT	<u> </u>	Z !	Ł	EST HUMAN	EST HUMAN	N	N.	EST HUMAN	EST HUMAN	
Top Hit Acessian No.					0.0E+00 AL163246.2		9.1	AL163246.2	11417862 NT	5802973 NT		0.0E+00 AF240786.1		11418318 NT	AL046544.1	0.0E+00 Al903497.1	0 0E+00 N54484 1	0 0F+00 AF108656 1			10092587 NT	7 0000	0.0E+00 AF003528.1	11430460 NT	0.0E+00 AW590082.1	0 0E+00 BE090210.1	0.0E+00 AF068757.1	9635487 NT	0.0E+00 A 204914.1	-	
Most Similar (Top) Hit BLAST E Value	0.0E+00 F00884.1	0.0E+00 U84744.1	0.0E+00 Z20656.1	0.0E+00	0.0E+00	0.0E+00 AI190993	0.0E+00	0.0E+00 AL 163246	0.0E+00	0.0E+00		0.0E+00	0.0E+00 AL04193	0.0E+00	0.0E+00 AL04654	0.0三十00	00+00	0 0F+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00							
Expression Signal	31.52	7.35	92.9	2.54	2.67	3.43	2.24	2.2	2.73	5.48		1.63	2.82	3.07	4.39	2.36	7.0	338	3.21	3.21	2.75		2.7	2.48	3.23	161	233	1.56	1.59	1.58	
ORF SEQ ID NO:	29082	29096	23098	24893								25066							20601					25183	25064						
Exan SEQ ID NO:	18792	18803	18805	19747	19594	19605	18829	18843	18849	18864		19563	19571	19711	18910	19610	1		1.		19612	1	١	19412	10544	L	L			L	┚
Probe SEQ ID NO:	8987	0006	9002	9017	9031	9033	9043	3062	9071	0606		9123	9133	9158	9167	9180	9	9210	9236	9236	9246		9276	9309	0220	0382	9426	OAR	9498	9529	-

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					gb:M64099	gb:M64099				3A Homo sapiens						γ								
Top Hit Descriptor	HTM1-654F HTM1 Homo sapiens cDNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA cione IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	Human gamma-cytoplasmic actin (ACTGP9) pseudogene	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens	CUNA CIONE I CBAP4466	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Homo saplens G protein-coupled receptor 24 (GPR24), mRNA	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5	Homo saptens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA	Human endogenous retrovirus pHE.1 (ERV9)	Homo sapiens oxytocin receptor (OXTR), mRNA	RC1-HT0595-200400-012-f12 HT0595 Homo sapiens cDNA	DKFZp434J0618_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0618
Top Hit Database Source	EST_HUMAN	NT	ΝΤ	NT	EST_HUMAN	EST_HUMAN	LN TA	₽N	NT		EST_HUMAN	FX	N	NT	NT	TN	NT	NT	NT	NT.	NT	LN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	0.0E+00 BE439792.1		6912457	0.0E+00 AF036365.1 ·	0.0E+00 H30132.1	0.0E+00 H30132.1	0.0E+00 D50659.1	11418189 NT	11418189 NT		0.0E+00 BE246780.1		11526291 NT	4885312 NT	0.0E+00 AB029900.1	9558724 NT	0.0E+00 AL163246.2	FN 8169089	7657020 NT	TN 28567387	0.0E+00 X57147.1	11434874 NT	.1	0.0E+00 AL048911.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0Ё+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.05+00		0.0E+00	00+30:0		
Expression Signal	1.68	1.98	1.98	2.33	2.87	2.87	32.21	3.99	3.99		5.21	1.64	2.39	3.19	2.21	1.5	2.79	1.41	2.13	2.42	1.51	1.29	1.56	1.28
ORF SEQ ID NO:		21724	21725	25267	21426	21427		25244	25245		25214	24829		24886		25233		20354		25177				
Exan SEQ ID NO:	19596	11841	11841	19161	11561	11561	19179	19181	19181	l	19239	15089	19249	15092	19269	19291	19757	10546	l	.19388	19407	19621	19591	19431
Probe SEQ ID NO:	9540	9551	9551	9571	9584	9584	9597	8289	9599		9685	Z696	8696	9721	9734	9773	9794	9800	9878	9913	9938	9946	9966	9971

CLAIMS

A spatially-addressable set of single exon nucleic-acid probes for measuring gene expression in a sample derived
 from human heart comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 4. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,981 - 19,771.
- 5. A spatially-addressable set of single exon nucleic acid 25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 20,000 single exon nucleic acid probes.
- 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

- 8. A spatially-addressable set of single exon nucleic acid 5 probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokarvotic and bacteriophage vector sequence.
- 9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 10. A spatially-addressable set of single exon nucleic acid
  15 probes as claimed in any of claims 1 9 characterised in
  that said set of probes is addressably disposed upon a
  substrate.
- 11. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 11.
- 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart

  30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.

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- 15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 29,119, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.
- 16. A single exon nucleic acid probe as claimed in any one
  15 of claims 13 to 15 wherein said single exon nucleic acid
  probe comprises between 15 and 25 contiguous nucleotides of
  said SEQ ID NO.
- 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 25 kb in length.
  - 18. A single exon nucleic acid probe as claimed in any one of claims 13 17, wherein said probe is DNA, RNA or PNA.

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- 19. A single exon nucleic acid probe as claimed in any one of claims 13 18, wherein said probe is detectably labeled.
- 30 20. A single exon nucleic acid probe as claimed in any one of claims 13 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 21. A single exon nucleic acid probe as claimed in any one of claims 13 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human heart, comprising:

contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

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24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 25. A nucleic acid sequence as set out in any of SEQ ID 5 NOs: 1 19,771 which encodes a peptide.
  - 26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 19,771.
- 10 27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 19,772 29,119.

#### 1/10

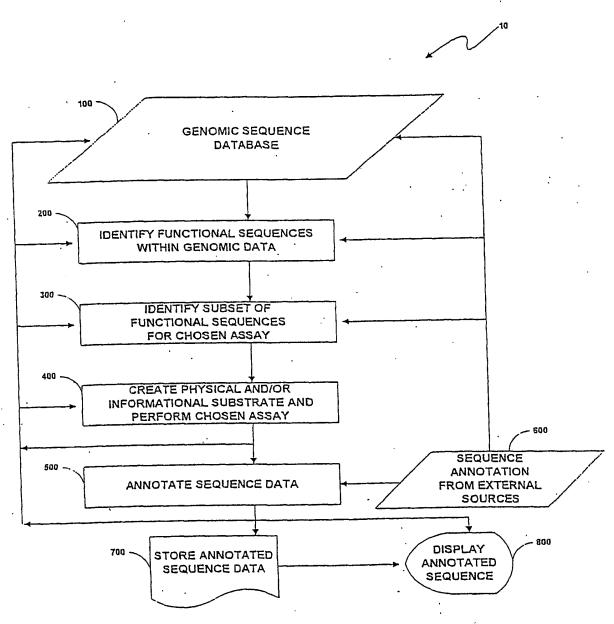


Fig. 1

WO 01/57274

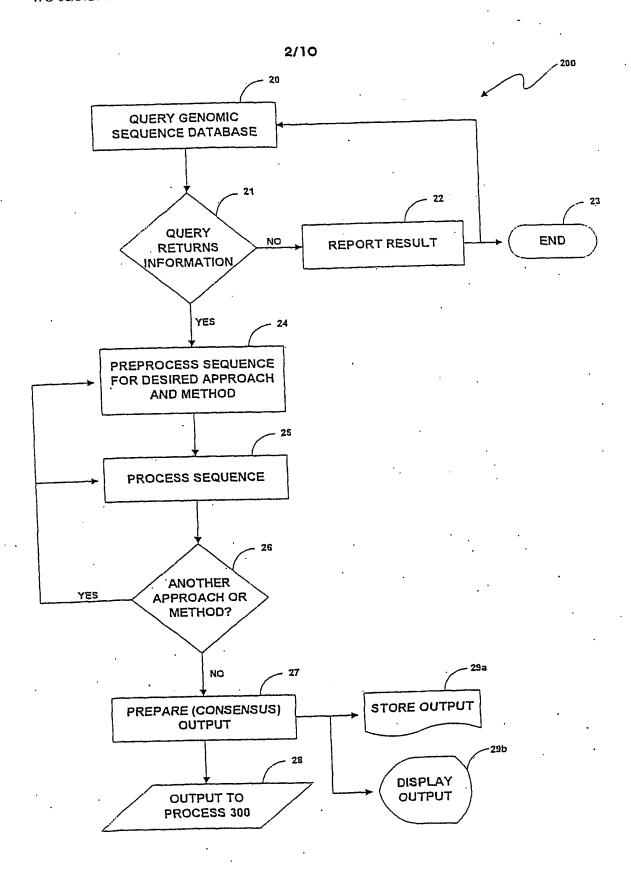


Fig. 2

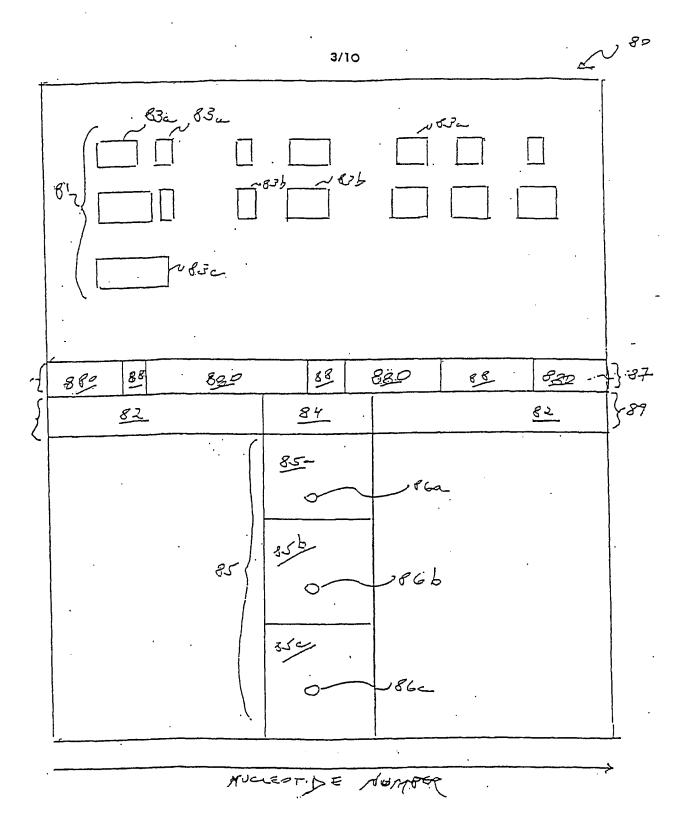


Fig. 3

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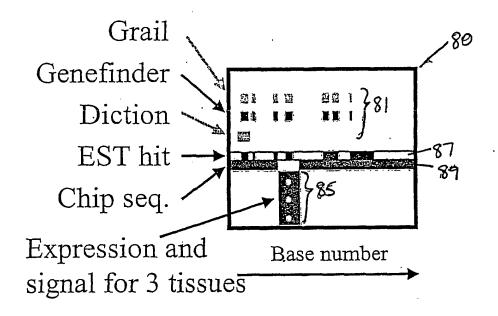


Fig. 4

## 5/10

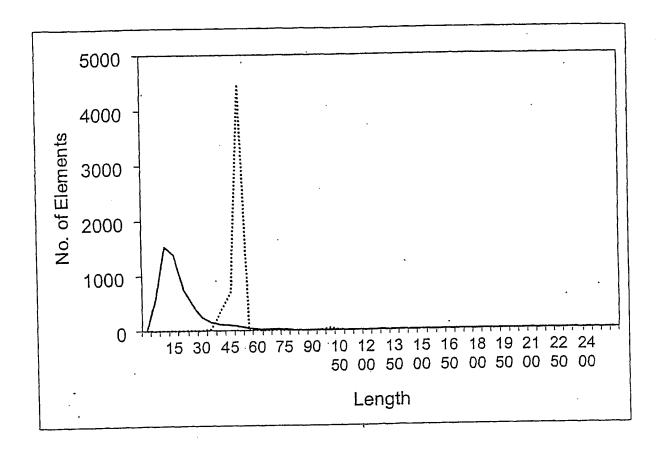


Fig. 5

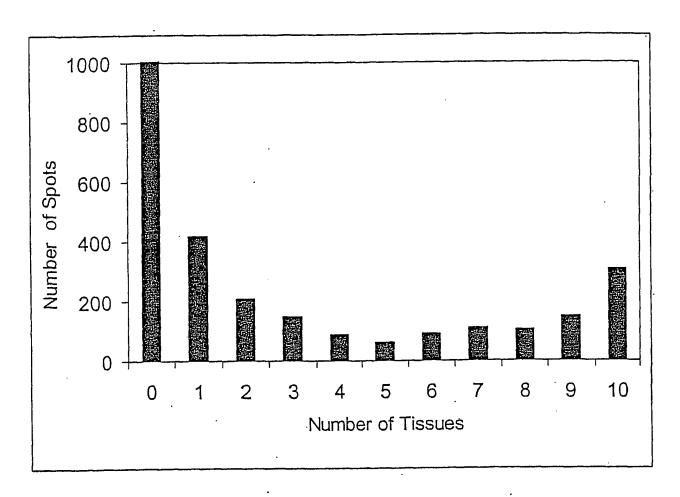


Fig. 6

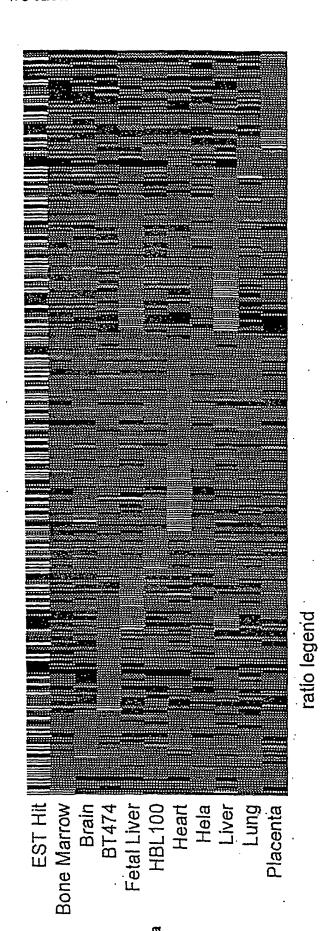


Fig. 7b

₩ 4 € 0.4 ±

Fig. 7

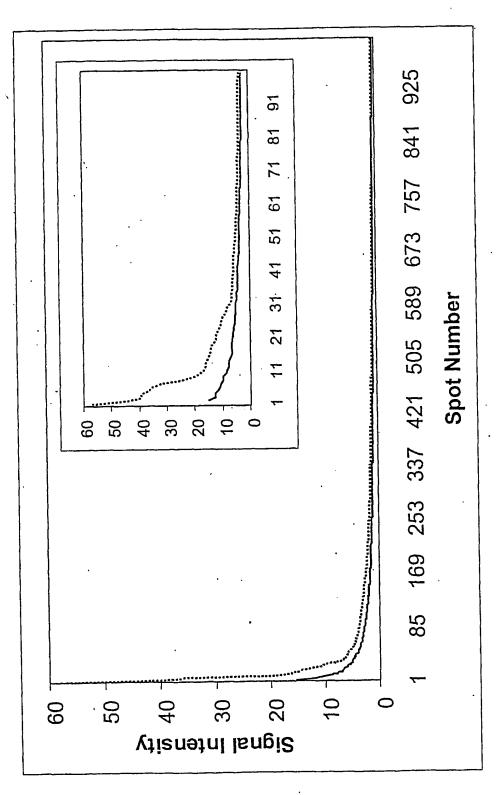


Fig. 8

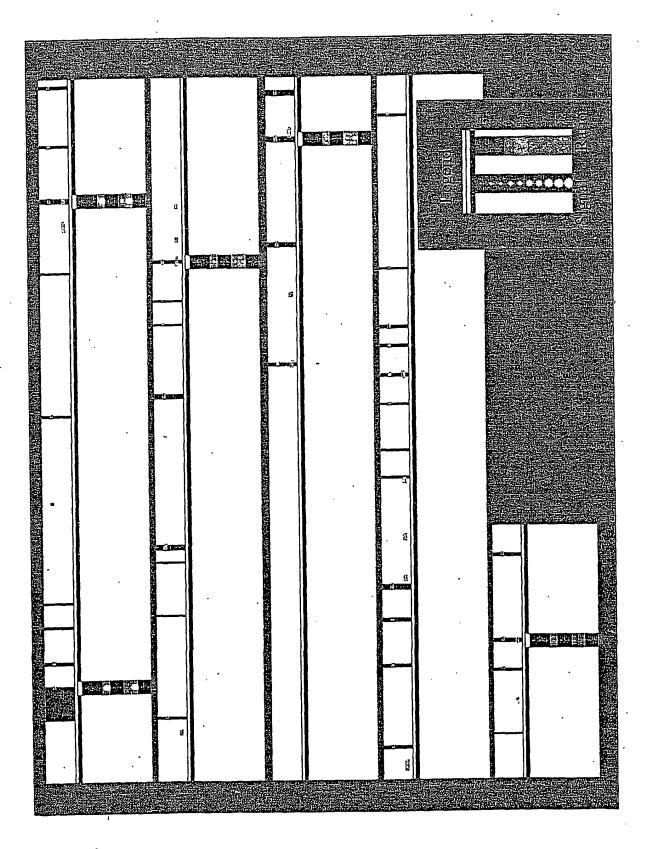
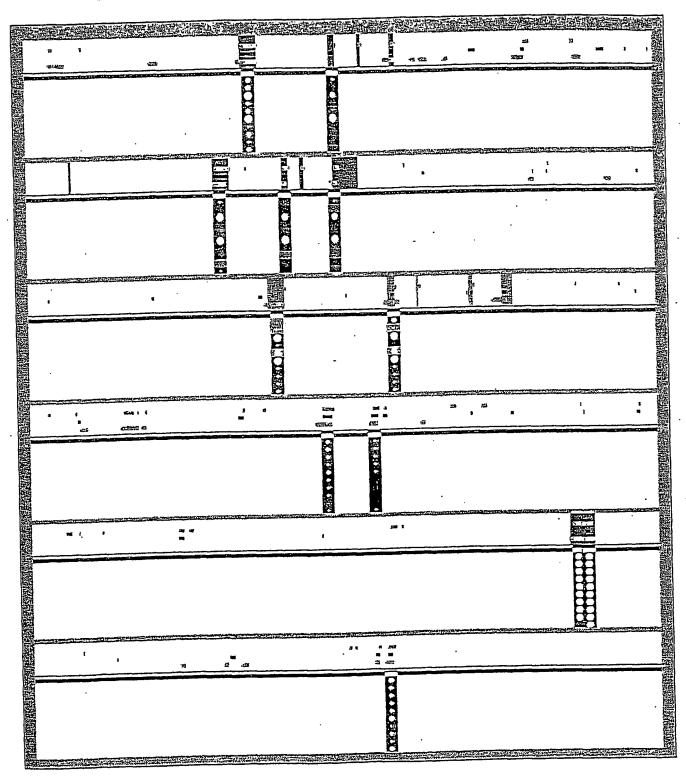


Fig. 9

10/10

Fig. 10



## (19) World Intellectual Property Organization International Bureau



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#### PCT

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(22) International Fili	ng Date: 30 January	2001 (30.01.2001	) LS
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(30) Priority Data:	4 February 2000 (	(04.02.2000) 11:	(84) Do Ki

- US 60/207,456 26 May 2000 (26.05.2000) 09/608,408 30 June 2000 (30.06.2000) US US 3 August 2000 (03.08.2000) 09/632,366 60/234,687 21 September 2000 (21.09.2000) US 27 September 2000 (27.09.2000) US 60/236,359 4 October 2000 (04.10.2000) GB 0024263.6
- (71) Applicant (for all designated States except US): AEOM-ICA, INC. [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94086 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 968 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, P.O. Box 1327, Piscataway, NJ 08855 (US).

- B1) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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see PCT Gazette No. 51/2001 of 20 December 2001, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.

#### INTERNATIONAL SEARCH REPORT

ernational Application No

Relevant to claim No.

PCT/US 01/00666

# A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12Q1/68

C. DOCUMENTS CONSIDERED TO BE RELEVANT

According to International Patent Classification (IPC) or to both national classification and IPC

#### B. FIELDS SEARCHED

Category *

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EPO-Internal, PAJ, WPI Data, BIOSIS

Citation of document, with indication, where appropriate, of the relevant passages

X	DATABASE EBI 'Online! EMBL; Accession Number: AL049837, 11 May 1999 (1999-05-11) HEILIG ET AL.: "Human chromosom sequence BAC R-959A22 of librar; from chromosome 14 of Homo sapic (Human)"	y RPCI-11	13-21, 25,27
Y	XP002182997 the whole document	-/	1-12, 22-24,26
X Furth	ner documents are listed in the continuation of box C.	X Patent family members are listed i	n annex.
"A" docume conside "E" earlier d filling de "L" docume which I citation "O" docume other m "P" docume later th	nt which may throw doubts on priority claim(s) or is cited to establish the publication date of another in or other special reason (as specified) and the special reason (as specified) and the special reason and disclosure, use, exhibition or neans and prior to the international filling date but an the priority date claimed	"T" later document published after the inter or priority date and not in conflict with to cited to understand the principle or the invention  "X" document of particular relevance; the cannot be considered novel or cannot involve an inventive step when the document of particular relevance; the cannot be considered to involve an inventive step when the document is combined with one or more ments, such combination being obvious in the art.  "&" document member of the same patent for	he application but ory underlying the almed invention be considered to: urment is taken alone almed invention entive step when the e other such docu- s to a person stilled
	actual completion of the international search 2 July 2002	Date of mailing of the International sear 0 7. 08. 2002	ch report

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31–70) 340–2040, Tx. 31 651 epo nl, Fax: (+31–70) 340–3016 Authorized officer

Botz, J

## INTERNATIONAL SEARCH REPORT

ternational Application No
PCT/US 01/00666

C.(Continu	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category *	with the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of t	Relevant to claim No.
X	DATABASE EBI 'Online! EMBL; AA414703, 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project"	13-21, 25,27
Y	XP002205620 the whole document	1-12, 22-24,26
X	DATABASE EBI 'Online! EMBL; Accession Number: 002711, 1 July 1997 (1997-07-01) BENIT ET AL.: "Cloning of a new murine endogenous retrovirus MuERV-L with strong similarity to the human HERV-L element and with a gag coding sequence closely related to the FVI restriction gene"	15-21,27
Υ	XP002037954 the whole document	1-12, 22-24,26
Y	LIEW ET AL .: "A catalogue of genes in the cardiovascular system as identified by expressed sequence tags" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, USA, vol. 91, October 1994 (1994–10), pages 10645–10649, XP002185728 table 2	1-27
Y	LIPSHUTZ ET AL.: "High density synthetic oligonucleotide arrays" NATURE GENETICS, vol. 21, January 1999 (1999-01), pages 20-24, XP002115232 NEW YORK, NY, US the whole document	1–27
A	DATSON ET AL.: "Scanning for genes in large genomic regions: cosmid based exon trapping of multipleexpons in a single product" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, vol. 24, no. 6, 1996, pages 1105-1111, XP002081565 Surrey, GB the whole document	
A	WO 98 30722 A (MACK DAVID H.) 16 July 1998 (1998-07-16) page 63, paragraph 2	

International application No. PCT/US 01/00666

## INTERNATIONAL SEARCH REPORT

Box I	Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)				
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:					
1.	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:				
	Claims Nos.:  1-12, 15-21 (partially not searched) because they relate to parts of the international Application that do not comply with the prescribed requirements to such an extent that no meaningful international Search can be carried out, specifically:  see FURTHER INFORMATION sheet PCT/ISA/210				
з. 🔲	Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).				
Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)				
This inter	mational Searching Authority found multiple inventions in this international application, as follows:				
	see additional sheet				
1. 🔲	As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.				
2	As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.				
	As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  1-27 (partially)				
4. 🔲	No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:				
Remark c	The additional search fees were accompanied by the applicant's protest.     X   No protest accompanied the payment of additional search fees.				

### FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-12, 15-21 (partially not searched)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id. as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (se claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 19780. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 9989).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 9989, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search

#### FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 19780.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1 - 27 (partially)

Invention number 1:

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising Seq. Id. 9989). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 19780).

2. Claims: 1 - 27 (partially)

Invention 2

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising Seq. Id. 9989). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by Seq. Id. 2 (in particular the one defined by Seq. Id. 19780).

3. Claims: 1 - 27 (partially)

Inventions 3 - 9980

A nucleic acid probe comprising SEQ ID n (where n ranges from 2 - 9980 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon Seq. Id. no." in the same row that contains Seq. Id. n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by Seq. Id. n, in particular the one defined by the Seq. Id. no. in the column "ORF Seq. Id. no." of the same row where Seq. Id. n is listed.

## INTERNATIONAL SEARCH REPORT

Information on patent family members

remational Application No

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
WO 9830722 A	16-07-1998	AU EP JP US WO US	6035698 A 0973939 A1 2001508303 T 6303301 B1 9830722 A1 2002028454 A1 2002039739 A1	03-08-1998 26-01-2000 26-06-2001 16-10-2001 16-07-1998 07-03-2002 04-04-2002

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## 

(43) International Publication Date 9 August 2001 (09.08.2001)

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- (25) Filing Language:

English

(26) Publication Language:

English

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09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

- (71) Applicant (for all designated States except US): AEOM-ICA, INC. [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94086 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 968 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, P.O. Box 1327, Piscataway, NJ 08855 (US).

- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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- without international search report and to be republished upon receipt of that report
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- (48) Date of publication of this corrected version:

20 December 2001

(15) Information about Correction:

see PCT Gazette No. 51/2001 of 20 December 2001, Sec-

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.